



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 161552

TO: Louis V Wollenberger
Location: rem/3B61/2C18
Art Unit: 1635
Friday, August 19, 2005
Case Serial Number: 10/774721

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *POB*

barbara.obryen@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:25:21 ; Search time 72.5 Seconds
(without alignments)
473.956 Million cell updates/sec

Title: US-10-774-721-37
Perfect score: 21
Sequence: 1 gugccugcggaacuggctt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 2 | 13.8 | 65.7 | 20 | 1 | US-08-835-770-24 | Sequence 24, Appl |
| C 3 | 13.8 | 65.7 | 20 | 1 | US-08-628-731-24 | Sequence 24, Appl |
| C 4 | 13.2 | 62.9 | 19 | 3 | US-08-637-732A-26 | Sequence 26, Appl |
| C 5 | 13.2 | 62.9 | 21 | 1 | US-08-271-942A-57 | Sequence 57, Appl |
| C 6 | 13.2 | 62.9 | 21 | 3 | US-08-779-916A-57 | Sequence 57, Appl |
| C 7 | 13.2 | 62.9 | 21 | 5 | PCT-US95-08604-57 | Sequence 57, Appl |
| C 8 | 12.8 | 61.0 | 19 | 1 | US-08-271-946A-13 | Sequence 13, Appl |
| C 9 | 12.8 | 61.0 | 19 | 1 | US-08-271-942A-13 | Sequence 13, Appl |
| C 10 | 12.8 | 61.0 | 19 | 3 | US-08-779-916A-13 | Sequence 13, Appl |
| C 11 | 12.8 | 61.0 | 19 | 3 | US-08-750-232-13 | Sequence 13, Appl |
| C 12 | 12.8 | 61.0 | 19 | 5 | PCT-US95-08604-13 | Sequence 13, Appl |
| C 13 | 12.8 | 61.0 | 19 | 5 | PCT-US95-08606-13 | Sequence 13, Appl |
| C 14 | 12.4 | 59.0 | 20 | 4 | US-09-657-346A-126 | Sequence 126, App |
| C 15 | 12.2 | 58.1 | 17 | 3 | US-09-275-680-7 | Sequence 7, Appli |
| C 16 | 12.2 | 58.1 | 20 | 3 | US-09-366-257-38 | Sequence 38, Appl |
| C 17 | 12.2 | 58.1 | 20 | 3 | US-09-844-634-62 | Sequence 62, Appl |
| C 18 | 12.2 | 58.1 | 21 | 4 | US-09-762-195-8 | Sequence 8, Appli |
| C 19 | 12.2 | 58.1 | 21 | 4 | US-09-762-195-17 | Sequence 17, Appl |
| C 20 | 11.8 | 56.2 | 17 | 3 | US-09-375-318-50 | Sequence 50, Appl |
| C 21 | 11.8 | 56.2 | 20 | 4 | US-10-177-573-15 | Sequence 15, Appl |
| C 22 | 11.6 | 55.2 | 18 | 2 | US-08-897-340-26 | Sequence 26, Appl |
| C 23 | 11.6 | 55.2 | 18 | 3 | US-08-757-024-823 | Sequence 823, App |
| C 24 | 11.6 | 55.2 | 18 | 3 | US-09-252-329-26 | Sequence 26, Appl |
| C 25 | 11.6 | 55.2 | 18 | 4 | US-09-093-972C-823 | Sequence 823, App |
| C 26 | 11.6 | 55.2 | 19 | 3 | US-08-757-024-809 | Sequence 809, App |
| C 27 | 11.6 | 55.2 | 19 | 3 | US-08-757-024-822 | Sequence 822, App |

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| 28 | 11.6 | 55.2 | 19 | 4 | US-09-093-972C-809 | Sequence 809, App |
| 29 | 11.6 | 55.2 | 19 | 4 | US-09-093-972C-822 | Sequence 822, App |
| C 30 | 11.6 | 55.2 | 20 | 1 | US-08-286-889-50 | Sequence 50, Appl |
| C 31 | 11.6 | 55.2 | 20 | 1 | US-08-485-618-50 | Sequence 50, Appl |
| C 32 | 11.6 | 55.2 | 20 | 1 | US-08-362-652-50 | Sequence 50, Appl |
| C 33 | 11.6 | 55.2 | 20 | 1 | US-08-640-672-19 | Sequence 19, Appl |
| C 34 | 11.6 | 55.2 | 20 | 1 | US-08-605-672-50 | Sequence 50, Appl |
| C 35 | 11.6 | 55.2 | 20 | 2 | US-08-482-293A-50 | Sequence 50, Appl |
| C 36 | 11.6 | 55.2 | 20 | 2 | US-08-577-858A-19 | Sequence 19, Appl |
| C 37 | 11.6 | 55.2 | 20 | 2 | US-08-943-363-50 | Sequence 50, Appl |
| C 38 | 11.6 | 55.2 | 20 | 3 | US-08-757-024-794 | Sequence 794, App |
| C 39 | 11.6 | 55.2 | 20 | 3 | US-08-757-024-808 | Sequence 808, App |
| C 40 | 11.6 | 55.2 | 20 | 3 | US-08-757-024-821 | Sequence 821, App |
| C 41 | 11.6 | 55.2 | 20 | 3 | US-09-366-257-12 | Sequence 12, Appl |
| C 42 | 11.6 | 55.2 | 20 | 3 | US-09-193-043-50 | Sequence 50, Appl |
| C 43 | 11.6 | 55.2 | 20 | 3 | US-09-688-307A-50 | Sequence 50, Appl |
| C 44 | 11.6 | 55.2 | 20 | 4 | US-09-350-259-50 | Sequence 50, Appl |
| C 45 | 11.6 | 55.2 | 20 | 4 | US-09-093-972C-794 | Sequence 794, App |

ALIGNMENTS

RESULT 1
US-08-136-811-24/c
; Sequence 24, Application US/08136811
; Patent No. 5510239
; GENERAL INFORMATION:
; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
; APPLICANT: Clarence Frank
; TITLE OF INVENTION: Oligonucleotide Interference with
; TITLE OF INVENTION: Multidrug Resistance
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,811
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-136-811-24

Query Match 65.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCUGUCGGGAACUGGCT 20


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; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer T60"
US-08-637-732A-26

Query Match 62.9%; Score 13.2; DB 3; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 UGCCUGUCGGGAACUGGC 19
Db 2 TGCCAGTCGGGAACGCG 19

RESULT 5
US-08-271-942A-57/c
; Sequence 57, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,942A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human

QY 1 GUGCCUGUCGGGAACUGG 18
Db 21 GCGTCTGTGGGAACTGG 4
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; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
US-08-271-942A-57

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Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACUGG 18
Db 21 GCGTCTGTGGGAACTGG 4

RESULT 6
US-08-779-916A-57/c
; Sequence 57, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; APPLICANT: Hui, May
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
US-08-779-916A-57

Query Match 62.9%; Score 13.2; DB 3; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACUGG 18
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; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
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US-08-750-232-13

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Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACTGG 18
Db 19 GTCTGTGGGAACTGG 4

RESULT 12
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; Sequence 13, Application PC/TUS9508604
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
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; APPLICATION NUMBER: PCT/US95/08604
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,942
; APPLICATION NUMBER: 08-JUL-1994
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
;
PCT-US95-08604-13

Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACTGG 18
Db 19 GTCTGTGGGAACTGG 4

RESULT 13
PCT-US95-08606-13/c
; Sequence 13, Application PC/TUS9508606
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
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; APPLICATION NUMBER: PCT/US95/08606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,946
; APPLICATION NUMBER: 08-JUL-1994
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
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; NAME/KEY: primer for exon 1 of human RB1 gene
PCT-US95-08606-13

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Best Local Similarity 68.8%; Pred. No. 3.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db      19 GTCTGTGGGGAAC TGG 4

RESULT 14
US-09-657-346A-126/c
; Sequence 126, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-346A-126

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Best Local Similarity 78.6%; Pred. No. 5.7e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GUCGGGAACUGGCT 20
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Db      16 GTCGGGAAC TGCCT 3

RESULT 15
US-09-275-680-7
; Sequence 7, Application US/09275680
; Patent No. 6221630
; GENERAL INFORMATION:
; APPLICANT: Hopper, James E
; TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
; TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
; TITLE OF INVENTION: Yeast
; FILE REFERENCE: 98428
; CURRENT APPLICATION NUMBER: US/09/275,680
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7

Query Match          58.1%; Score 12.2; DB 3; Length 17;
Best Local Similarity 64.7%; Pred. No. 7e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GCCUGUCGGGAACUGGC 19
      |||:|:|
Db      1 GCCTGTTGACAACTGGC 17

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Job time : 76.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 05:29:57 ; Search time 842 Seconds
(without alignments)
1208.503 Million cell updates/sec

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Perfect score: 21
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Scoring table: IDENTITY_NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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3: gb_in:
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9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 2 | 19 | 90.5 | 21 | 6 | CQ860126 | CQ860126 Sequence |
| C 3 | 18.4 | 87.6 | 20 | 6 | CQ860119 | CQ860119 Sequence |
| C 4 | 13.8 | 65.7 | 20 | 6 | AR037349 | AR037349 Sequence |
| C 5 | 13.8 | 65.7 | 20 | 6 | AR040632 | AR040632 Sequence |
| C 6 | 13.8 | 65.7 | 20 | 6 | I19643 | I19643 Sequence 24 |
| C 7 | 13.4 | 63.8 | 16 | 6 | AX471987 | AX471987 Sequence |
| C 8 | 13.2 | 62.9 | 21 | 6 | I25270 | I25270 Sequence 57 |
| C 9 | 12.8 | 61.0 | 16 | 6 | CQ858638 | CQ858638 Sequence |
| C 10 | 12.8 | 61.0 | 19 | 6 | AR163030 | AR163030 Sequence |
| C 11 | 12.8 | 61.0 | 19 | 6 | I24629 | I24629 Sequence 13 |
| C 12 | 12.8 | 61.0 | 19 | 6 | I25226 | I25226 Sequence 13 |
| C 13 | 12.8 | 61.0 | 21 | 6 | CQ848735 | CQ848735 Sequence |
| C 14 | 12.4 | 59.0 | 20 | 6 | AR271882 | AR271882 Sequence |
| C 15 | 12.2 | 58.1 | 20 | 6 | AR215747 | AR215747 Sequence |
| C 16 | 12.2 | 58.1 | 21 | 6 | BD190401 | BD190401 Phosphati |
| C 17 | 12.2 | 58.1 | 21 | 6 | BD190410 | BD190410 Phosphati |
| C 18 | 12.2 | 58.1 | 21 | 6 | AR452563 | AR452563 Sequence |
| C 19 | 12.2 | 58.1 | 21 | 6 | AR452572 | AR452572 Sequence |

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| C 20 | 12.2 | 58.1 | 21 | 6 | AX024461 | AX024461 Sequence |
| C 21 | 12.2 | 58.1 | 21 | 6 | AX024470 | AX024470 Sequence |
| C 22 | 12.2 | 58.1 | 21 | 6 | AX614231 | AX614231 Sequence |
| C 23 | 11.8 | 56.2 | 17 | 6 | AR240883 | AR240883 Sequence |
| C 24 | 11.8 | 56.2 | 20 | 6 | AX708916 | AX708916 Sequence |
| C 25 | 11.8 | 56.2 | 20 | 6 | AX708918 | AX708918 Sequence |
| C 26 | 11.6 | 55.2 | 18 | 6 | AR075066 | AR075066 Sequence |
| C 27 | 11.6 | 55.2 | 18 | 6 | AR141884 | AR141884 Sequence |
| C 28 | 11.6 | 55.2 | 18 | 6 | E15984 | E15984 Oligonucleo |
| C 29 | 11.6 | 55.2 | 20 | 6 | AR020500 | AR020500 Sequence |
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| C 31 | 11.6 | 55.2 | 20 | 6 | AR052377 | AR052377 Sequence |
| C 32 | 11.6 | 55.2 | 20 | 6 | AR053223 | AR053223 Sequence |
| C 33 | 11.6 | 55.2 | 20 | 6 | AR055175 | AR055175 Sequence |
| C 34 | 11.6 | 55.2 | 20 | 6 | AR158046 | AR158046 Sequence |
| C 35 | 11.6 | 55.2 | 20 | 6 | I15822 | I15822 Sequence 50 |
| C 36 | 11.6 | 55.2 | 20 | 6 | I92526 | I92526 Sequence 50 |
| C 37 | 11.6 | 55.2 | 20 | 6 | AR222696 | AR222696 Sequence |
| C 38 | 11.6 | 55.2 | 20 | 6 | AR399783 | AR399783 Sequence |
| C 39 | 11.6 | 55.2 | 20 | 6 | AX449014 | AX449014 Sequence |
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| C 42 | 11.6 | 55.2 | 21 | 6 | AR529567 | AR529567 Sequence |
| C 43 | 11.6 | 55.2 | 21 | 6 | AX095592 | AX095592 Sequence |
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ALIGNMENTS

RESULT 1
LOCUS CQ860125 21 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 37 from Patent WO2004072293.
ACCESSION CQ860125
VERSION CQ860125.1 GI:51982013

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL
Patent: WO 2004072293-A 37 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source Location/Qualifiers
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/note="Artificiel"

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Qy 1 GUGCCUGUCGGGAACUGGCTT 21

Db 1 GTGCCTGTCTCGGGAACUGGCTT 21

RESULT 2

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LOCUS CQ860126 21 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 38 from Patent WO2004072293.
ACCESSION CQ860126

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| Db | 20 CCTGCCTGGAACCTGGCT 4 | | |
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| LOCUS | AX471987 | 16 bp | DNA linear PAT 09-AUG-2002 |
| DEFINITION | Sequence 6 from Patent WO2053171. | | |
| ACCESSION | AX471987 | | |
| VERSION | AX471987.1 GI:22207038 | | |
| KEYWORDS | | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | 1 | | |
| AUTHORS | Alzheimer,C., Goppelt,A. and Koegel,H. | | |
| TITLE | Use of intermediate-conductance potassium channels and modulators for the diagnosis and treatment of illnesses having disturbed keratinocyte activity | | |
| JOURNAL | Patent: WO 02053171-A 6 11-JUL-2002; | | |
| FEATURES | LUDWIG MAXIMILIANS UNI (DE) | | |
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| Query Match | | 63.8%; Score 13.4; DB 6; Length 16; | |
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| Matches | | 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0; | |
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| Db | 1 CTGGCGGGAACCTGGC 15 | | |
| RESULT 8 | | | |
| LOCUS | I25270/c | 21 bp | DNA linear PAT 07-OCT-1996 |
| DEFINITION | Sequence 57 from patent US 5550020. | | |
| ACCESSION | I25270 | | |
| VERSION | I25270.1 GI:1605140 | | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 21) | | |
| AUTHORS | Gallie,B.L., Dunn,J.M. and Stevens,J.K. | | |
| TITLE | Method, reagents and kit for diagnosis and targeted screening for retinoblastoma | | |
| JOURNAL | Patent: US 5550020-A 57 27-AUG-1996; | | |
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| Matches | | 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0; | |
| QY | | | |
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| RESULT 9 | | | |
| LOCUS | CQ858638/c | 16 bp | DNA linear PAT 31-AUG-2004 |
| DEFINITION | Sequence 100 from Patent WO2004069991. | | |
| ACCESSION | CQ858638 | | |
| VERSION | CQ858638.1 GI:51852605 | | |
| KEYWORDS | | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | 1 | | |
| AUTHORS | Hansen,B., Thue,C.A., Petersen,K.D., Westergaard,M. and Wissenbach,M. | | |
| TITLE | Oligomeric compounds for the modulation of survivin expression | | |
| JOURNAL | Patent: WO 2004069991-A 100 19-AUG-2004; | | |
| FEATURES | Santaris Pharma A/S (DK) | | |
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| LOCUS | AR163030/c | 19 bp | DNA linear PAT 17-OCT-2001 |
| DEFINITION | Sequence 13 from patent US 6270963. | | |
| ACCESSION | AR163030 | | |
| VERSION | AR163030.1 GI:16233504 | | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 19) | | |
| AUTHORS | Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E. | | |
| TITLE | Method for testing for mutations in DNA from a patient sample | | |
| JOURNAL | Patent: US 6270963-A 13 07-AUG-2001; | | |
| FEATURES | Location/Qualifiers | | |
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| Best Local Similarity | | 68.8%; Pred. No. 3.1e+05; | |
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| Db | 19 GTCTGTGGGGAACCTGG 4 | | |
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| LOCUS | I24629/c | 19 bp | DNA linear PAT 07-OCT-1996 |
| DEFINITION | Sequence 13 from patent US 5545527. | | |
| ACCESSION | I24629 | | |
| VERSION | I24629.1 GI:1604499 | | |

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Stevens,J.K. and Dunn,J.M.
TITLE       Method for testing for mutations in DNA from a patient sample
JOURNAL     Patent: US 5545527-A 13 13-AUG-1996;
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ORIGIN
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Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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LOCUS      125226
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ACCESSION  I25226
VERSION     I25226.1 GI:1605096
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE      Method, reagents and kit for diagnosis and targeted screening for
           retinoblastoma
JOURNAL    Patent: US 5550020-A 13 27-AUG-1996;
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DEFINITION Sequence 195 from Patent WO2004065628.
ACCESSION  CQ848735
VERSION     CQ848735.1 GI:51470163
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Fu,G.
TITLE      Quantitative multiplex detection of nucleic acids
JOURNAL    Patent: WO 2004065628-A 195 05-AUG-2004;
           Fu, Guoliang (GB)
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Db      19 GTCTGTGGGGAAGTGG 4

RESULT 14
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DEFINITION Sequence 126 from patent US 6503754.
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VERSION     AR271882.1 GI:29703450
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Zhang,H. and Wyatt,J.
TITLE      Antisense modulation of BH3 interacting domain death agonist
           expression
JOURNAL    Patent: US 6503754-A 126 07-JAN-2003;
FEATURES   Location/Qualifiers
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Best Local Similarity 78.6%; Pred. No. 4.9e+05;
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DEFINITION Sequence 62 from patent US 6410324.
ACCESSION  AR215747
VERSION     AR215747.1 GI:23314003
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Bennett,C.F. and Watt,A.T.
TITLE      Antisense modulation of tumor necrosis factor receptor 2 expression
JOURNAL    Patent: US 6410324-A 62 25-JUN-2002;
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Best Local Similarity 70.6%; Pred. No. 6.2e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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ORGANISM    Unclassified.
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AUTHORS     Stevens,J.K. and Dunn,J.M.
TITLE       Method for testing for mutations in DNA from a patient sample
JOURNAL     Patent: US 5545527-A 13 13-AUG-1996;
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Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCCUGUCGGGAACUGG 18
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Db      19 GTCTGTGGGGAAGTGG 4

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ACCESSION  I25226
VERSION     I25226.1 GI:1605096
KEYWORDS   .
SOURCE     Unknown.
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REFERENCE  1 (bases 1 to 19)
AUTHORS    Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE      Method, reagents and kit for diagnosis and targeted screening for
           retinoblastoma
JOURNAL    Patent: US 5550020-A 13 27-AUG-1996;
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Best Local Similarity 68.8%; Pred. No. 3.1e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db      19 GTCTGTGGGGAAGTGG 4

RESULT 13
CQ848735
LOCUS      CQ848735
DEFINITION Sequence 195 from Patent WO2004065628.
ACCESSION  CQ848735
VERSION     CQ848735.1 GI:51470163
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Fu,G.
TITLE      Quantitative multiplex detection of nucleic acids
JOURNAL    Patent: WO 2004065628-A 195 05-AUG-2004;
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FEATURES   Location/Qualifiers
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RESULT 14
AR271882/c
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DEFINITION Sequence 126 from patent US 6503754.
ACCESSION  AR271882
VERSION     AR271882.1 GI:29703450
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Zhang,H. and Wyatt,J.
TITLE      Antisense modulation of BH3 interacting domain death agonist
           expression
JOURNAL    Patent: US 6503754-A 126 07-JAN-2003;
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DEFINITION Sequence 62 from patent US 6410324.
ACCESSION  AR215747
VERSION     AR215747.1 GI:23314003
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Bennett,C.F. and Watt,A.T.
TITLE      Antisense modulation of tumor necrosis factor receptor 2 expression
JOURNAL    Patent: US 6410324-A 62 25-JUN-2002;
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Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Copyright (c) 1993 - 2005 Compugen Ltd.

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| C 9 | 12.8 | 61.0 | 19 | 2 AAT11532 | Aat11532 Retinobla |
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| C 35 | 11.8 | 56.2 | 20 | 12 ADJ22087 | Adj22087 Human end |
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ALIGNMENTS

RESULT 1
ADR27688/c
ID ADR27688 standard; DNA; 20 BP.

XX ADR27688;
XX 04-NOV-2004 (first entry)

DE OB-RGRP antisense oligonucleotide, AS 10.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.

OS Synthetic.

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| 13-AUG-2004. | |
| 10-FEB-2003; 2003FR-00001543. | |

us-10-774-721-37.rng

Fri Aug 19 08:52:56 2005

```
XX 10-FEB-2003; 2003FR-00001543.
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and their
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (yfp) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 87.6%; Score 18.4; DB 13; Length 20;
XX Best Local Similarity 75.0%; Pred. No. 24;
XX Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
XX
XX 2 UGCCUGUCGGGAACUGGCTT 21
XX :|||:|:|||||:|||||
XX 20 TGCCTGTTCGGGAACCTGGCAT 1
XX
XX RESULT 2
XX AAQ86849/c
XX ID AAQ86849 standard; DNA; 20 BP.
XX
XX AAQ86849;
XX
XX 13-DEC-1995 (first entry)
XX
XX Antisense oligonucleotide ISIS 8363 hybridises to MRP gene.
XX
XX Untranslated region; coding sequence; chemotherapeutic drug treatment;
XX antisense; modulation; multidrug resistance protein; drug; cancer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..20
XX /tag= a
XX /note= "contains phosphorothioate internucleotide
XX linkages"
XX
XX WO9510938-A1.
XX
XX 27-APR-1995.
```

```
XX 23-SEP-1994; 94WO-US010827.
XX 18-OCT-1993; 93US-00136811.
XX (ISIS-) ISIS PHARM INC.
XX Baracchini E, Bennett CF;
XX WPI; 1995-169974/22.
XX
XX New oligo:nucleotide cpds., esp. for cancer therapy - which are
XX specifically hybridisable with nucleic acid encoding multi:drug
XX resistance-associated protein.
XX
XX Claim 7; Page 11; 36pp; English.
XX
XX Oligonucleotides AAQ86826-50 are antisense oligonucleotides used to
XX modulate the expression of the multidrug resistance protein (MRP) by
XX hybridising with the multidrug resistance (MDR) gene or its RNA message.
XX This sequence is targeted to the 3' untranslated region (3'UTR) of the
XX MDR gene. The oligonucleotides can be used to improve the efficacy of
XX chemotherapeutic drug treatment of a disease such as cancer or to prevent
XX multidrug resistance developing during drug treatment of a disease
XX
XX Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 65.7%; Score 13.8; DB 2; Length 20;
XX Best Local Similarity 76.5%; Pred. No. 4.9e+03;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4 CCUGUCGGGAACUGGCT 20
XX ||:| | |||||:||||
XX 20 CCTGCCTGGAACTGGCT 4
XX
XX RESULT 3
XX AAV53600/c
XX ID AAV53600 standard; DNA; 20 BP.
XX
XX AAV53600;
XX
XX 25-MAR-2003 (revised)
XX 20-NOV-1998 (first entry)
XX
XX Nucleotide sequence of a phosphorothioate oligonucleotide 24.
XX
XX Phosphorothioate oligonucleotide; antisense; inhibition; cancer; human;
XX multidrug resistance; multiresistant protein; MRP; chemotherapy;
XX leukotriene; inflammatory condition; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /note= "phosphorothioate backbone"
XX
XX US5801154-A.
XX
XX 01-SEP-1998.
XX
XX 08-APR-1997; 97US-00835770.
XX
XX 18-OCT-1993; 93US-00136811.
XX 16-APR-1996; 96US-00628731.
XX
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dean NM, Baracchini E;
XX WPI; 1998-494825/42.
XX
XX
```


XX Anti:sense oligo:nucleotide(s) inhibiting multi:drug resistance protein
PT expression - useful for increasing the efficacy of drugs that certain
PT conditions have become resistant to e.g. small cell lung cancer.
XX
PS Claim 11; Col 12; 29pp; English.
XX
CC This is the nucleotide sequence of the phosphorothioate oligonucleotide
CC used in the method of the invention, involving the use of antisense
CC oligonucleotides to inhibit multidrug resistance. The oligonucleotides
CC are used for the antisense inhibition of multiresistant proteins (MRPs).
CC These proteins are commonly found in some cancers which initially respond
CC to chemotherapy, but overexpression of the protein leads to chemotherapy
CC drug resistance. They are administered with the drugs to attempt to
CC enhance efficacy of the drugs. MRPs are also expressed in other ailments,
CC and as such, the oligonucleotides can be used to treat these conditions,
CC as well. The sequences are based on the human MRP and are used to treat
CC conditions such as cancers, especially small-cell lung cancer, prevention
CC of development of multidrug resistance during chemotherapy, and treatment
CC of conditions characterised by leukotriene production, especially
CC inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 2; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.9e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCUGUCGGGAACUGGCT 20
Db ||:|||||:||||
20 CCTGCCTGGAACCTGGCT 4

RESULT 4
ABQ78935
ID ABQ78935 standard; DNA; 16 BP.
XX
AC ABQ78935;
XX
XX
DT 04-NOV-2002 (first entry)
XX
DE Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
XX
KW Mouse; intermediate-conductance potassium channel; dermatological;
KW antiinflammatory; keratolytic; vulnery; antipsoriatic; atopic eczema;
KW contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose;
KW hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIK1;
KW PCR; primer; ss.
XX
OS Mus musculus.
XX
XX
PN WO200253171-A2.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-EP015317.
XX
PR 28-DEC-2000; 2000DE-01065475.
PR 20-MAR-2001; 2001US-0277453P.
XX
PA (SWIT-) SWITCH BIOTECH AG.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
XX
PI Goppelt A, Alzheimer C, Koegel H;
XX
XX WPI; 2002-643295/69.
XX
XX Use of intermediate-conductance potassium channel proteins for the
PT diagnosis, prevention and treatment of disorders associated with
PT disturbed keratinocyte activity, especially psoriasis.
XX
PS Example 3; Page 119; 121pp; German.
XX

CC The invention relates to a novel use of intermediate-conductance
CC potassium channel proteins. The proteins of the invention have
CC dermatological, antiinflammatory, keratolytic, vulnery, and
CC antipsoriatic activity. The method is used especially in the field of
CC damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo,
CC hyperkeratosis, actinic keratosis, hypertrophic scars, keloids, lentigo,
CC aged skin, ulcers and especially psoriasis. The sequence represents a PCR
CC primer for the mouse potassium channel protein mIK1 of the invention
XX
SQ Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 63.8%; Score 13.4; DB 6; Length 16;
Best Local Similarity 80.0%; Pred. No. 7.6e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGC 19
Db ||:|||||:||||
1 CTGGCGGGAACCTGGC 15

RESULT 5
AAQ88255
ID AAQ88255 standard; DNA; 19 BP.
XX
AC AAQ88255;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1995 (first entry)
XX
DE Neisseria pilC gene constant region probe TR60.
XX
KW PilC protein; pilin; pathogenic type 4 pilus bacteria; vaccine;
KW detection; bacterial adhesin; phase variation; constant region; probe;
KW Neisseria gonorrhoeae; Neisseria meningitidis; Pseudomonas aeruginosa;
KW ss.
XX
OS Synthetic.
XX
XX DE4336530-Cl.
XX
PD 13-APR-1995.
XX
PF 26-OCT-1993; 93DE-04336530.
XX
PR 26-OCT-1993; 93DE-04336530.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Meyer TFF, Rudel T, Rylf RR, Scheuerpflug IB;
XX
XX WPI; 1995-140328/19.
XX
XX Recombinant PilC-proteins derived from Neisseria gonorrhoeae - and their
PT prodn. methods; useful for immunisation against pathogen type 4 pilus
PT carrying bacteria or their detection.
XX
XX Claim 5; Page 12; 29pp; German.
XX
CC Sequences coding for pilin PilC proteins from Neisseria spp. have been
CC isolated (see AAQ88239-Q88241). The pilC1 and pilC2 genes from
CC N.gonorrhoeae have 84% identity. Probes were designed based on regions of
CC shared homology (see AAQ88242-88261) and these constant region probes
CC were used in Southern hybridisations to identify other pilC genes in
CC N.gonorrhoeae strain MS11 and N.meningitidis strain A1493. Also, the same
CC probes were used to screen a Pseudomonas aeruginosa strain and identified
CC a pilC-like sequence. Gene sequences which hybridise with any of the
CC constant region probes are claimed. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. No. 9.7e+03;

| | |
|------------|---|
| CC | those of RB wild-type DNA, patients can be diagnosed early which may |
| CC | avoid the need for radiotherapy. Any difference in length of exons |
| CC | between a suspected RB patient and those from wild-type RB1 indicates |
| CC | either a deletion or insertion mutation. Further sequencing of suspect |
| CC | exons can pinpoint the mutation. The method is directed to the diagnosis |
| CC | of and targeted genetic screening for retinoblastoma in family members of |
| CC | a retinoblastoma patient |
| XX | |
| SQ | Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other; |
| | |
| | Query Match 61.0%; Score 12.8; DB 2; Length 19; |
| | Best Local Similarity 68.8%; Pred. No. 1.5e+04; |
| | Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0; |
| | |
| QY | 3 GCCUGUCGGGAACUGG 18 |
| Db | 19 GTCTGTGGGGAAC TGG 4 |
| | |
| | RESULT 10 |
| AAT12851/c | |
| ID | AAT12851 standard; DNA; 19 BP. |
| XX | |
| AC | AAT12851; |
| XX | |
| DT | 22-OCT-1996 (first entry) |
| XX | |
| DE | PCR 5' primer for exon 1 of human RB1 (retinoblastoma-1) gene. |
| XX | |
| KW | PCR; polymerase chain reaction; retinoblastoma; tumour suppressor; |
| KW | cancer; mutation; identification; diagnosis; cystic fibrosis; |
| KW | hierarchy assay; method; specificity; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO9607761-A2. |
| XX | |
| PD | 14-MAR-1996. |
| XX | |
| PF | 07-JUL-1995; 95WO-US008606. |
| XX | |
| PR | 08-JUL-1994; 94US-00271946. |
| XX | |
| PA | (VISI-) VISIBLE GENETICS INC. |
| XX | |
| PI | Dunn JM, Stevens JK, Capatos D, Matthews DE; |
| XX | |
| DR | WPI; 1996-171632/17. |
| XX | |
| PT | Testing for a disease-associated mutation in a gene - using a hierarchy |
| PT | of tests selected to optimise performance while minimising cost. |
| XX | |
| PS | Example 1; Page 32; 63pp; English. |
| XX | |
| CC | AAT12839-T12899 (excluding AAT12878) are PCR primers used to amplify |
| CC | various regions of the RB-1 genome, including exons 1-27, the promoter |
| CC | region and a control sequence unrelated to RB-1 from chromosome 15. The |
| CC | primers are used in an example of a method for testing a disease- |
| CC | associated mutation in a gene, the gene may not necessarily be a tumour |
| CC | suppressor gene like the retinoblastoma gene another example is the |
| CC | cystic fibrosis transmembrane conductance regulator (CFTR) gene which may |
| CC | be analysed using the same method. The primers are used in various |
| CC | groupings to produce a hierarchical assay useful to test a group of |
| CC | patients suspected to have a genetic mutation. The method allows the |
| CC | optimum (or near optimum) diagnostic algorithm by considering the cost |
| CC | and the sensitivity and specificity of each test |
| XX | |
| SQ | Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other; |
| | |
| | Query Match 61.0%; Score 12.8; DB 2; Length 19; |
| | Best Local Similarity 68.8%; Pred. No. 1.5e+04; |
| | Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0; |

| | |
|----------|---|
| QY | 3 GCCUGUCGGGAACUGG 18 |
| Db | 19 GTCTGTGGGGAAC TGG 4 |
| | |
| | RESULT 11 |
| ADQ31737 | |
| ID | ADQ31737 standard; DNA; 21 BP. |
| XX | |
| AC | ADQ31737; |
| XX | |
| DT | 21-OCT-2004 (first entry) |
| XX | |
| DE | Multiplex amplification of human SNP fragments, primer #153. |
| XX | |
| KW | Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP; |
| KW | single nucleotide polymorphism. |
| XX | |
| OS | Homo sapiens. |
| OS | Synthetic. |
| XX | |
| PN | US2004146866-A1. |
| XX | |
| PD | 29-JUL-2004. |
| XX | |
| PF | 24-JAN-2003; 2003US-00349780. |
| XX | |
| PR | 24-JAN-2003; 2003US-00349780. |
| XX | |
| PA | (FUGG/) FU G. |
| XX | |
| PI | Fu G; |
| XX | |
| DR | WPI; 2004-552653/53. |
| XX | |
| PT | Analyzing multiple targets in polynucleotide, by providing multiple |
| PT | primers with target nucleic acids, digesting nucleic acid products with |
| PT | cognate restriction enzymes, amplifying digested products, and detecting |
| PT | amplified products. |
| XX | |
| PS | Example 2; SEQ ID NO 195; 65pp; English. |
| XX | |
| CC | The invention relates analysing multiple targets in polynucleotide, |
| CC | involves providing a set or sets of multiple primers with target nucleic |
| CC | acids in separate reactions of primer extension or amplification, where |
| CC | the reactions produce nucleic acid products in that each nucleic acid |
| CC | fragments comprise at least one restriction site, digesting nucleic acid |
| CC | products of the separate reactions on the restriction sites with cognate |
| CC | restriction enzymes, joining digested products derived from the separate |
| CC | reactions together, where randomly joining nucleic acid fragments from |
| CC | the separated reactions are created, amplifying the joined products, and |
| CC | detecting the amplified products. Also included are an oligonucleotide |
| CC | primer for detecting target nucleic acid sequence (comprising a 3' |
| CC | complementary portion and 5' non-complementary portion, where the 5' non- |
| CC | complementary portion comprises a restriction enzyme site, where the |
| CC | restriction site acts as detection marker in the process of detecting |
| CC | target nucleic acid sequence, where the detection signal generated from |
| CC | enzymatic manipulation on restriction site of reaction product is |
| CC | indicative of the presence of target nucleic acid sequence) and a kit for |
| CC | use in analysis and detection of multiple targets in a polynucleotide |
| CC | (comprising a set or sets of multiple primers, universal primers, |
| CC | restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all |
| CC | enzymes, and dNTPs). The method is useful for analysing multiple targets |
| CC | in a polynucleotide and for genotyping mutations, preferably single |
| CC | nucleotide polymorphisms (SNPs), and for analysing differential gene |
| CC | expression profiles, genomic methylation patterns and any specific |
| CC | nucleic acids from any source. The method enables analysis of multiple |
| CC | targets quantitatively. An experiment was performed, using the method of |
| CC | the invention, where SNPs were detected in 70 human genomic DNA |
| CC | fragments, simultaneously. The present sequence is a primer used in the |
| CC | above experiment. |
| XX | |
| SQ | Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 U; 0 Other; |

Query Match 61.0%; Score 12.8; DB 13; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.6e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCUGUCGGGAACUGG 18
|||:|:| |||:|:|
Db 1 GCCTGTGGGTAAC TGG 16

RESULT 12
AAL38283/c
ID AAL38283 standard; DNA; 20 BP.
XX
AC AAL38283;
XX
DT 29-AUG-2003 (revised)
DT 15-AUG-2002 (first entry)
XX
DE Mouse BH3 interacting domain death mRNA agonist inhibitor SEQ ID 126.
XX
KW Hepatotrophic; immunomodulatory; cytostatic; antiinflammatory; hepatitis;
KW haemostatic; BH3 interacting domain death agonist; liver disease;
KW haematopoietic disorder; developmental disorder; immunological disorder;
KW hyperproliferative disorder; apoptosis; mouse; chimeric; 2'-methoxyethyl;
KW 2'-MOE; phosphorothioate backbone; murine; ds.
XX
OS Mus musculus.
OS Chimeric.
XX
PN WO200220547-A1.
XX
PD 14-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-US027316.
XX
PR 07-SEP-2000; 2000US-00657346.
PR 07-MAR-2001; 2001US-00800631.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Zhang H, Wyatt JR;
XX
DR WPI; 2002-393838/42.
XX

Novel antisense compound targeted to nucleic acid molecule encoding the
BH3 interacting domain death agonist, useful for treating animals with
diseases associated with BH3 interacting domain death agonist, e.g.
hepatitis.

Claim 3; Page 89; 171pp; English.
The invention relates to a compound 8 to 50 nucleotides in length
targeted to a nucleic acid molecule encoding a BH3 interacting domain
death agonist, where the compound specifically hybridises with and
inhibits the expression of the BH3 interacting domain death agonist. The
compound of the invention is useful for inhibiting the expression of the
BH3 interacting domain death agonist in cells or tissues. The compound is
also useful for treating an animal having a disease or condition
associated with the BH3 interacting domain death agonist, e.g.
haematopoietic disorder, hyperproliferative disorder, a developmental
disorder, immunological disorder, or a disease or condition of the liver
e.g., hepatitis, or a condition associated with apoptosis. The compound
is useful for diagnostics, therapeutics, prophylaxis and as research
reagents and kits. This polynucleotide sequence represents an antisense
oligonucleotide inhibitor of the DNA from mouse BH3 interacting domain
death agonist RNA of the invention. NOTE: This sequence is a chimeric
oligonucleotide 20 nucleotides in length, which is flanked on both sides
by five-nucleotide 'wings'. The wings are composed of 2'-methoxyethyl (2'
-MOE) nucleotides. The internucleoside (backbone) linkages are
phosphorothioate (P=S) throughout the oligonucleotide. (Updated on 29-AUG
-2003 to standardise OS field)

SQ Sequence 20 BP; 5 A; 8 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 2.5e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GUCGGGAACUGGCT 20
|:|||||:|
Db 16 GTCGGGAAC TGCCT 3

RESULT 13
ADP46888
ID ADP46888 standard; DNA; 21 BP.
XX
AC ADP46888;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human c-Cbl siRNA antisense strand, SEQ ID 224.
XX
KW Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour;
KW fat deposition; metabolic rate; lean muscle mass; body fat; Cbl;
KW multi-adaptor protein; feeding disorder; glucose uptake disorder;
KW metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl;
KW siRNA; short interfering RNA; ds; RNA interference; gene silencing.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004055181-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-AU001676.
XX
PR 16-DEC-2002; 2002AU-00953393.
PR 14-NOV-2003; 2003AU-00906285.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Molero JC, James D;
XX
DR WPI; 2004-488065/46.
XX

Identifying compounds capable of modulating feeding behavior, fat
deposition, metabolic rate, or the ratio of lean muscle mass to body fat
by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity
and hypolipidemia.

Claim 86; SEQ ID NO 224; 213pp; English.
The present invention relates to a method for identifying a compound that
is capable of modulating feeding behaviour, fat deposition, metabolic
rate, or the ratio of lean muscle mass to body fat in a subject. The
method comprises performing an assay to measure a metabolism-associated
phenotype that has been determined for a genetically modified non-human
animal that comprises a genetic modification within an allele of its Cbl
locus, and determining the effect of the compound on the phenotype. The
genetic modification reduces or prevents expression of a functional
endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
protein that is involved in ligand-induced down regulation of receptor
tyrosine kinases. The method of the invention is useful in the treatment
of feeding disorders or disorders of glucose uptake and metabolism, such
as diabetes, obesity and hyperlipidaemia. The present sequence is the
antisense strand for a human c-Cbl siRNA. The siRNA is useful in
modulating a metabolism-associated phenotype in a cell, tissue or animal
subject.

Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 59.0%; Score 12.4; DB 12; Length 21;
Best Local Similarity 71.4%; Pred. No. 2.5e+04;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACU 16
|||:|||||:
Db 7 GCCTCTCGGGAAC 20

RESULT 14
AAH24024
ID AAH24024 standard; DNA; 17 BP.
XX
AC AAH24024;
XX
DT 29-AUG-2001 (first entry)
XX
DE Yeast GAL7 gene upstream UASgal site, SEQ ID NO:7.
XX
KW UASgal site; cis-acting transcription control element; Gal4; Gal3; Gal80;
KW stoichiometrically balanced expression; yeast;
KW galactose-inducible expression; expression construct; promoter; GAL7; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN US6221630-B1.
XX
PD 24-APR-2001.
XX
PF 24-MAR-1999; 99US-00275680.
XX
PR 24-MAR-1999; 99US-00275680.
XX
PA (PENN-) PENN STATE RES FOUND.
XX
PI Hopper JE;
XX
DR WPI; 2001-307557/32.
XX
PT Expression construct for inducing and sustaining high level recombinant
PT polypeptide production in yeast, comprises nucleic acids encoding a trans
PT -acting transcription factor, selectable marker and yeast origin of
PT replication.
XX
PS Disclosure; Col 15; 22pp; English.
XX
CC The invention relates to high copy number expression constructs for high
CC level polypeptide expression in yeast. The yeast expression constructs
CC comprise a nucleic acid sequence encoding a set of trans- acting
CC transcription factors, a nucleic acid encoding a yeast selectable marker
CC providing an inefficiently or efficiently selected phenotype, a nucleic
CC acid encoding a yeast or bacterial origin of replication (ori), and a
CC unique restriction site downstream of a promoter containing a cis- acting
CC transcription control element that is regulated by the transcription
CC factors which are encoded by the expression construct. In a specific
CC embodiment of the invention, the expression construct provides for
CC galactose-inducible protein expression. Such constructs contain DNA
CC encoding the transcription factors Gal3, Gal4 and Gal80, and a UASgal cis
CC -acting control element within the promoter which drives expression of
CC the inserted gene of interest. The vector-encoded transcription factors
CC are expressed in stoichiometrically-balanced amounts, which is
CC particularly important for a galactose-inducible system, as Gal4, when
CC not balanced by stoichiometric levels of Gal3 and Gal80, becomes a
CC constitutive transcription factor, and can become toxic to the cell. The
CC constructs of the invention express the transcription factors at levels
CC higher than those found in native yeast cells, thereby ensuring
CC expression of the gene of interest. The expression constructs provide
CC robust, high level expression of a gene of interest (which can encode an
CC endogenous or heterologous polypeptide) in yeast. Sequences AAH24019-
CC AAH24035 represent actual UASgal sites found within the promoters of
CC various yeast galactose-inducible genes which may be used as the cis-
CC acting control element in a galactose-inducible expression construct of
CC the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 58.1%; Score 12.2; DB 4; Length 17;
Best Local Similarity 64.7%; Pred. No. 3e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGAACUGGC 19
|||:|:|:|:
Db 1 GCCTGTGACAACTGGC 17

RESULT 15
AAZ95350
ID AAZ95350 standard; DNA; 20 BP.
XX
AC AAZ95350;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human mtPEPCK phosphorothioate antisense oligonucleotide SEQ ID NO:38.
XX
KW Human; mitochondrial phosphoenolpyruvate carboxykinase; PEPCK-M; PCK2;
KW PEPCK-mitochondrial; mtPEPCK; antisense oligonucleotide; modulation;
KW phosphorothioate; inhibition; diagnosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
PN US6030837-A.
XX
PD 29-FEB-2000.
XX
PF 03-AUG-1999; 99US-00366257.
XX
PR 03-AUG-1999; 99US-00366257.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI McKay R, Cowsert LM, Butler MM;
XX
DR WPI; 2000-205209/18.
XX
CC New antisense compound targeted to a nucleic acid molecule encoding human
CC mitochondrial phosphoenolpyruvate carboxykinase useful for treating a
CC human with a mitochondrial phosphoenolpyruvate carboxykinase-associated
CC disease.
XX
PS Claim 3; Col 39; 32pp; English.
XX
CC AAZ95320 to AAZ95359 represent antisense oligonucleotides targeted to a
CC nucleic acid molecule encoding human mitochondrial phosphoenolpyruvate
CC carboxykinase (also known as PEPCK-mitochondrial; PEPCK-M; PCK2 and
CC mtPEPCK), where the oligonucleotide specifically hybridise with and
CC inhibit the expression of human mtPEPCK. The antisense oligonucleotides
CC can be used for inhibiting the expression of mtPEPCK in human cells or
CC tissues in vitro and can also be used for treating an animal,
CC particularly a human suspected of having or being prone to a condition or
CC disease associated with expression of mtPEPCK. They can also be used in
CC diagnostics and as research reagents in sandwich and other assays
XX
SQ Sequence 20 BP; 1 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 58.1%; Score 12.2; DB 3; Length 20;
Best Local Similarity 58.8%; Pred. No. 3.1e+04;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACUG 17
|:|:|:|:|:
Db 4 GTGTCTCTCGGCAC 20

Search completed: August 18, 2005, 06:25:06
Job time : 238 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:17:36 ; Search time 1765 Seconds
(without alignments)
452.889 Million cell updates/sec

Title: US-10-774-721-37
Perfect score: 21
Sequence: 1 gugccugcggaacuggctt 21
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
.Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 11.2 | 53.3 | 19 | 8 | AZ763411 1M0558B24 |
| 2 | 9.8 | 46.7 | 17 | 9 | AJ589126 Arabidops |
| 3 | 9.8 | 46.7 | 19 | 8 | AZ486389 1M0314E21 |
| 4 | 9.8 | 46.7 | 20 | 8 | AZ593689 1M0405C21 |
| 5 | 9.6 | 45.7 | 16 | 1 | AL039794 DKFZp434B |
| 6 | 9.6 | 45.7 | 18 | 1 | AL039892 DKFZp434G |
| 7 | 9.6 | 45.7 | 18 | 1 | AL043072 DKFZp434B |
| 8 | 9.6 | 45.7 | 19 | 1 | AL042746 DKFZp434C |
| 9 | 9.6 | 45.7 | 19 | 8 | AZ466725 1M0277C09 |
| 10 | 9.6 | 45.7 | 19 | 8 | AZ858446 2M0163D08 |
| 11 | 9.6 | 45.7 | 20 | 1 | AL039677 DKFZp434H |
| 12 | 9.6 | 45.7 | 20 | 1 | AL043331 DKFZp434O |
| 13 | 9.6 | 45.7 | 20 | 1 | AL043349 DKFZp434P |
| 14 | 9.6 | 45.7 | 20 | 1 | AL045408 DKFZp434E |
| 15 | 9.6 | 45.7 | 21 | 8 | AZ794033 2M0047D12 |
| 16 | 9.4 | 44.8 | 17 | 9 | AJ589127 Arabidops |
| 17 | 9.4 | 44.8 | 20 | 8 | AZ827586 2M0104C08 |
| 18 | 9.4 | 44.8 | 21 | 7 | CO785256 BL283A A0 |
| 19 | 9.2 | 43.8 | 15 | 1 | AL039409 DKFZp434L |
| 20 | 9.2 | 43.8 | 21 | 9 | AG195343 Pan trogl |
| 21 | 9 | 42.9 | 18 | 6 | CA851577 D15C05 E1 |
| 22 | 9 | 42.9 | 20 | 8 | AZ318416 1M0037P19 |
| 23 | 9 | 42.9 | 21 | 7 | CO788185 NT003C A1 |
| 24 | 9 | 42.9 | 21 | 8 | AZ806008 2M0067I15 |

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|----|-----|------|----|---|----------|-----------|
| 25 | 8.8 | 41.9 | 20 | 5 | BX563610 | BX563610 |
| 26 | 8.8 | 41.9 | 20 | 8 | AZ309156 | 1M0013B09 |
| 27 | 8.8 | 41.9 | 20 | 8 | AZ386570 | 1M0145C08 |
| 28 | 8.8 | 41.9 | 20 | 8 | AZ823352 | 2M0097A22 |
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| 32 | 8.6 | 41.0 | 19 | 1 | AI049374 | ub33a03.r |
| 33 | 8.6 | 41.0 | 20 | 8 | AZ616822 | 1M0446L13 |
| 34 | 8.6 | 41.0 | 20 | 9 | AG204980 | Pan trogl |
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| 36 | 8.4 | 40.0 | 19 | 4 | BM399863 | 5009-0-62 |
| 37 | 8.4 | 40.0 | 20 | 8 | AZ309592 | 1M0016N09 |
| 38 | 8.4 | 40.0 | 20 | 8 | AZ803105 | 2M0063L17 |
| 39 | 8.4 | 40.0 | 21 | 5 | BQ593572 | E012766-0 |
| 40 | 8.4 | 40.0 | 21 | 8 | AZ665199 | 1M0546E01 |
| 41 | 8.2 | 39.0 | 13 | 1 | AL043127 | DKFZp434D |
| 42 | 8.2 | 39.0 | 14 | 1 | AL039339 | DKFZp434F |
| 43 | 8.2 | 39.0 | 15 | 1 | AL043135 | DKFZp434D |
| 44 | 8.2 | 39.0 | 15 | 1 | AL043264 | DKFZp434L |
| 45 | 8.2 | 39.0 | 15 | 1 | AL043298 | DKFZp434M |

ALIGNMENTS

RESULT 1
AZ763411
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ763411 19 bp DNA linear GSS 16-FEB-2001
1M0558B24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0558B24 R, genomic survey sequence.
AZ763411
AZ763411.1 GI:12874413
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0558 row: B column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0558B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

Fri Aug 19 08:52:57 2005

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 19;
Best Local Similarity 68.8%; Pred. No. 7.6e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CUGUCGGGAACUGGCT 20
|:|:|||||
Db 4 CTGTTGGGTACAGGCT 19

RESULT 2

AJ589126/c 17 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 545A02, genomic survey sequence.

ACCESSION AJ589126.1 GI:37938750
VERSION GSS; left border; T-DNA flanking sequence.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS 1
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.

TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

MEDLINE 22363535

PUBMED 12446565

REFERENCE 2 (bases 1 to 17)

AUTHORS Balzergue, S.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

COMMENT Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES

source

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/mol_type="genomic DNA"
/cultivar="Wassiljewskija"
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/clone="545A02"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature 1. .17

ORIGIN

Query Match 46.7%; Score 9.8; DB 9; Length 17;
Best Local Similarity 69.2%; Pred. No. 3.8e+06;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 UGCCUGUCGGGAA 14
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Db 17 TACCGGTCGGGAA 5

RESULT 3

AZ486389

LOCUS

DEFINITION

AZ486389 19 bp DNA linear GSS 05-OCT-2000
1M0314E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0314E21 F, genomic survey sequence.

ACCESSION AZ486389.1 GI:10653117

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0314 row: E column: 21

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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/db_xref="taxon:10090"

/clone="UUGC1M0314E21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 19;
Best Local Similarity 69.2%; Pred. No. 3.8e+06;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 UGCCUGUCGGGAA 14
|:|:| | | | | |
Db 4 TGCCTGATGGGAA 16

RESULT 4
AZ593689
LOCUS AZ593689 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0405C21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0405C21 F, genomic survey sequence.

ACCESSION AZ593689
VERSION AZ593689.1 GI:11715879
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0405 row: C column: 21
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0405C21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 20;
Best Local Similarity 61.5%; Pred. No. 3.9e+06;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUG 17
|:|:| | | | | |
Db 5 CTGTTGGTAACTG 17

RESULT 5
AL039794
LOCUS AL039794 16 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp434B1612_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1612, mRNA sequence.

ACCESSION AL039794
VERSION AL039794.1 GI:49682336
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 16)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

TITLE

EST (Duesterhoeft, et al.)

JOURNAL

COMMENT

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..16
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/db_xref="taxon:9606"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

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Best Local Similarity 56.2%; Pred. No. 4.8e+06;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACU 16
|:| | | | | | | |
Db 1 GTACCGGTCCGGAATT 16

RESULT 6

AL039892
LOCUS AL039892 18 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp434G1212_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434G1212, mRNA sequence.

ACCESSION AL039892
VERSION AL039892.1 GI:49682352
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 18)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS

JOURNAL

COMMENT

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 19;
Best Local Similarity 62.5%; Pred. No. 4.8e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
|:|:|||||||
Db 2 CTGTGGGAACCTACT 17

RESULT 10
AZ858446
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DEFINITION 2M0163D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0163D08 R, genomic survey sequence.

ACCESSION AZ858446
VERSION AZ858446.1 GI:13051622
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0163D08"

FEATURES

source
Location/Qualifiers
1. .19
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163D08"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 19;
Best Local Similarity 56.2%; Pred. No. 4.8e+06;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCUGUCGGGAACUGGC 19
|:|:|:|:|:|:|
Db 4 CCTGTAGGATCCTGGC 19

RESULT 11

AL039677
LOCUS
DEFINITION DKFZp434H0411_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0411, mRNA sequence.

ACCESSION AL039677
VERSION AL039677.1 GI:49682316
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

CONTACT: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1. .20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434H0411"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 45.7%; Score 9.6; DB 1; Length 20;
Best Local Similarity 56.2%; Pred. No. 4.9e+06;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACU 16
|:|:|:|:|:|:|
Db 5 GTACCGGTCCGGAAATT 20

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0047 row: D column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0047D12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 21;
Best Local Similarity 62.5%; Pred. No. 4.9e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCUGUCGGGACUGG 18
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Db 4 GGCTGGAGGGAGCTGG 19

Search completed: August 18, 2005, 07:56:22
Job time : 1773 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:53:53 ; Search time 1790 Seconds
(without alignments)
76.221 Million cell updates/sec

Title: US-10-774-721-37
Perfect score: 21
Sequence: 1 gugccugcggaacuggctt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 2032376

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10J_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 19 | 90.5 | 21 | 21 | US-10-774-721-38 |
| 3 | 18.4 | 87.6 | 20 | 21 | US-10-774-721-31 |
| 4 | 13.4 | 63.8 | 16 | 20 | US-10-451-805-6 |
| 5 | 13 | 61.9 | 21 | 20 | US-10-792-280-281 |
| 6 | 12.8 | 61.0 | 16 | 21 | US-10-776-934-100 |
| 7 | 12.8 | 61.0 | 16 | 21 | US-10-776-934-540 |
| | | | | | Sequence 37, Appl |
| | | | | | Sequence 38, Appl |
| | | | | | Sequence 31, Appl |
| | | | | | Sequence 6, Appl |
| | | | | | Sequence 281, App |
| | | | | | Sequence 100, App |
| | | | | | Sequence 540, App |

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| C 8 | 12.8 | 61.0 | 16 | 21 | US-10-776-934-541 | Sequence 541, App |
| C 9 | 12.8 | 61.0 | 16 | 21 | US-10-776-934-542 | Sequence 542, App |
| C 10 | 12.8 | 61.0 | 16 | 21 | US-10-776-934-543 | Sequence 543, App |
| C 11 | 12.8 | 61.0 | 21 | 20 | US-10-751-736-36589 | Sequence 36589, A |
| C 12 | 12.8 | 61.0 | 21 | 20 | US-10-751-736-37093 | Sequence 37093, A |
| C 13 | 12.8 | 61.0 | 21 | 22 | US-10-349-780A-195 | Sequence 195, App |
| C 14 | 12.6 | 60.0 | 21 | 22 | US-10-736-892-1 | Sequence 1, Appli |
| C 15 | 12.4 | 59.0 | 20 | 9 | US-09-800-631-126 | Sequence 126, App |
| C 16 | 12.4 | 59.0 | 20 | 15 | US-10-293-783-126 | Sequence 126, App |
| C 17 | 12.4 | 59.0 | 20 | 17 | US-10-388-263-778 | Sequence 778, App |
| C 18 | 12.2 | 58.1 | 20 | 17 | US-10-173-240-36 | Sequence 36, Appl |
| C 19 | 12.2 | 58.1 | 20 | 17 | US-10-173-240-70 | Sequence 70, Appl |
| C 20 | 12.2 | 58.1 | 20 | 19 | US-10-476-021-62 | Sequence 62, Appl |
| C 21 | 12.2 | 58.1 | 20 | 20 | US-10-695-568-104 | Sequence 104, App |
| C 22 | 12.2 | 58.1 | 20 | 20 | US-10-695-568-120 | Sequence 120, App |
| C 23 | 12.2 | 58.1 | 21 | 20 | US-10-751-736-46727 | Sequence 46727, A |
| C 24 | 12 | 57.1 | 21 | 20 | US-10-792-280-279 | Sequence 279, App |
| C 25 | 12 | 57.1 | 21 | 20 | US-10-751-736-25592 | Sequence 25592, A |
| C 26 | 11.8 | 56.2 | 17 | 16 | US-10-180-781-50 | Sequence 50, Appl |
| C 27 | 11.8 | 56.2 | 17 | 19 | US-10-712-672-1359 | Sequence 1359, Ap |
| C 28 | 11.8 | 56.2 | 17 | 19 | US-10-712-672-1360 | Sequence 1360, Ap |
| C 29 | 11.8 | 56.2 | 17 | 19 | US-10-712-672-1361 | Sequence 1361, Ap |
| C 30 | 11.8 | 56.2 | 20 | 16 | US-10-171-319-98 | Sequence 98, Appl |
| C 31 | 11.8 | 56.2 | 20 | 16 | US-10-171-319-100 | Sequence 100, App |
| C 32 | 11.8 | 56.2 | 20 | 17 | US-10-177-573-15 | Sequence 15, Appl |
| C 33 | 11.8 | 56.2 | 20 | 17 | US-10-210-479-26 | Sequence 26, Appl |
| C 34 | 11.8 | 56.2 | 20 | 17 | US-10-210-479-97 | Sequence 97, Appl |
| C 35 | 11.8 | 56.2 | 20 | 19 | US-10-619-739-1288 | Sequence 1288, Ap |
| C 36 | 11.8 | 56.2 | 21 | 9 | US-09-765-081-133 | Sequence 133, App |
| C 37 | 11.8 | 56.2 | 21 | 20 | US-10-751-736-37094 | Sequence 37094, A |
| C 38 | 11.8 | 56.2 | 21 | 21 | US-10-847-918-3427 | Sequence 3427, Ap |
| C 39 | 11.6 | 55.2 | 18 | 10 | US-09-093-972C-823 | Sequence 823, App |
| C 40 | 11.6 | 55.2 | 18 | 21 | US-10-758-451-823 | Sequence 823, App |
| C 41 | 11.6 | 55.2 | 19 | 9 | US-09-986-632-27 | Sequence 27, Appl |
| C 42 | 11.6 | 55.2 | 19 | 10 | US-09-093-972C-809 | Sequence 809, App |
| C 43 | 11.6 | 55.2 | 19 | 10 | US-09-093-972C-822 | Sequence 822, App |
| C 44 | 11.6 | 55.2 | 19 | 16 | US-10-251-117-189 | Sequence 189, App |
| C 45 | 11.6 | 55.2 | 19 | 16 | US-10-251-117-438 | Sequence 438, App |

ALIGNMENTS

RESULT 1

US-10-774-721-37
; Sequence 37, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-37

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3;

Fri Aug 19 08:52:57 2005

Best Local Similarity 75.0%; Pred. No. 26;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 UGCCUGUCGGGAACUGGCTT 21
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Db 20 TGCCTGTCTCGGAACTGGCAT 1

RESULT 4

US-10-451-805-6
; Sequence 6, Application US/10451805
; Publication No. US20040248099A1
; GENERAL INFORMATION:
; APPLICANT: Goppelt, Andreas
; APPLICANT: Alzheimer, Christian
; APPLICANT: Kogel, Heidi
; TITLE OF INVENTION: Use of Intermediate-Conductance
; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity
; FILE REFERENCE: 50125/080001
; CURRENT APPLICATION NUMBER: US/10/451,805
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/15317
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/277,453
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: DE 10065475.4
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-451-805-6

Query Match 63.8%; Score 13.4; DB 20; Length 16;
Best Local Similarity 80.0%; Pred. No. 8.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGC 19
|:|||||:|||||
Db 1 CTGCGGGAACTGGC 15

RESULT 5

US-10-792-280-281
; Sequence 281, Application US/10792280
; Publication No. US20040234517A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Bowman, Michael
; APPLICANT: Follettie, Maximillian
; APPLICANT: Chen, Heng
; APPLICANT: Williams, Cara
; APPLICANT: Ellis, Debra
; APPLICANT: Winkler, Aaron
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR
; TITLE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES
; FILE REFERENCE: AM101023-2
; CURRENT APPLICATION NUMBER: US/10/792,280
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 1535
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 281
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-792-280-281

Query Match 61.9%; Score 13; DB 20; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.3e+04;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACUGGCTT 21
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Db 1 GUGCCUGUCGGGAACUGGCTT 21

RESULT 2

US-10-774-721-38/c
; Sequence 38, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-38

Query Match 90.5%; Score 19; DB 21; Length 21;
Best Local Similarity 78.9%; Pred. No. 13;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACUGGC 19
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Db 19 GTGCCTGTCTCGGAACTGGC 1

RESULT 3

US-10-774-721-31/c
; Sequence 31, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS10
US-10-774-721-31

Query Match 87.6%; Score 18.4; DB 21; Length 20;

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Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GUGCCUGUCGGGAACUGGCTT 21
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Db 1 GUGGCUCUCUGGCACUUGCUU 21

RESULT 6
US-10-776-934-100/c
; Sequence 100, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-100

Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
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Db 16 CTGTGGGGGACTGGCT 1

RESULT 7
US-10-776-934-540/c
; Sequence 540, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 540
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-540
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; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorthioate linkage
US-10-776-934-540

Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
   ||: ||| ||: ||| |||
Db 16 CTGTGGGGGACTGGCT 1

RESULT 8
US-10-776-934-541/c
; Sequence 541, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 541
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-541

Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
   ||: ||| ||: ||| |||
Db 16 CTGTGGGGGACTGGCT 1

RESULT 9
US-10-776-934-542/c
; Sequence 542, Application US/10776934
; Publication No. US20050014712A1
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; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 542
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(13)
; OTHER INFORMATION: phosphorthioate linkage
; US-10-776-934-542
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Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 5 CUGUCGGGAACUGGCT 20
Db 16 CTGTGGGGGACTGGCT 1

RESULT 10
US-10-776-934-543/c
; Sequence 543, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 543
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorthioate linkage
; US-10-776-934-543

Query Match 61.0%; Score 12.8; DB 21; Length 16;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 CUGUCGGGAACUGGCT 20
Db 16 CTGTGGGGGACTGGCT 1

RESULT 11
US-10-751-736-36589/c
; Sequence 36589, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36589
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-751-736-36589

Query Match 61.0%; Score 12.8; DB 20; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 6 UGUCGGGAACUGGCTT 21
Db 16 TGTCGTGAAGTGGCTT 1

RESULT 12
US-10-751-736-37093/c
; Sequence 37093, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37093
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-751-736-37093

Query Match 61.0%; Score 12.8; DB 20; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY      6 UGUCGGGAACUGGCTT 21
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Db      17 TGTGCGTGAAGTGGCTT 2

RESULT 13
US-10-349-780A-195
; Sequence 195, Application US/10349780A
; Publication No. US20040146866A1
; GENERAL INFORMATION:
; APPLICANT: Fu, Guoliang
; TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
; FILE REFERENCE: patent1
; CURRENT APPLICATION NUMBER: US/10/349,780A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-780A-195

Query Match      61.0%; Score 12.8; DB 22; Length 21;
Best Local Similarity 68.8%; Pred. No. 1.7e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCCUGUCGGGAACUGG 18
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Db      1 GCCTGTGGGTAAC TGG 16

RESULT 14
US-10-736-892-1
; Sequence 1, Application US/10736892
; Publication No. US20050148505A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: JI, Tai
; APPLICANT: JI, Inhae
; TITLE OF INVENTION: GENES AND AGENTS TO REGULATE FOLLICULAR DEVELOPMENT, OVULATION
; TITLE OF INVENTION: CYCLE AND STERIOGENESIS
; FILE REFERENCE: 050229-0424
; CURRENT APPLICATION NUMBER: US/10/736,892
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: 60/437,729
; PRIOR FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-10-736-892-1

Query Match      60.0%; Score 12.6; DB 22; Length 21;
Best Local Similarity 63.2%; Pred. No. 2.1e+04;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 UGCCUGUCGGGAACUGGCT 20
      :|:|:| |||:|
Db      2 TGACTGGCGAGAACTGGAT 20

RESULT 15
US-09-800-631-126/c
; Sequence 126, Application US/09800631
; Patent No. US20020082228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
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; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPRESSION
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/09/800,631
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-800-631-126

Query Match      59.0%; Score 12.4; DB 9; Length 20;
Best Local Similarity 78.6%; Pred. No. 2.7e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      7 GUCGGGAACUGGCT 20
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Db      16 GTCGGGAAC TGCCT 3

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Job time : 1797 secs
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:53:53 ; Search time 1790 Seconds
(without alignments)
76.221 Million cell updates/sec

Title: US-10-774-721-38
Perfect score: 21
Sequence: 1 gccaguuccgacaggcactt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 2032376

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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| 8: | /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:* |
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| 10: | /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:* |
| 11: | /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:* |
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| 14: | /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:* |
| 15: | /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:* |
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| 17: | /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:* |
| 18: | /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:* |
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| 20: | /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:* |
| 21: | /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:* |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 21 | 100.0 | 21 | 21 | US-10-774-721-38 |
| 2 | 19 | 90.5 | 21 | 21 | US-10-774-721-37 |
| 3 | 18 | 85.7 | 20 | 21 | US-10-774-721-31 |
| 4 | 13.4 | 63.8 | 16 | 20 | US-10-451-805-6 |
| 5 | 13 | 61.9 | 21 | 20 | US-10-792-280-280 |
| 6 | 12.8 | 61.0 | 21 | 22 | US-10-349-780A-195 |
| 7 | 12.6 | 60.0 | 19 | 9 | US-09-986-632-27 |
| | | | | | Sequence 38, Appl |
| | | | | | Sequence 37, Appl |
| | | | | | Sequence 31, Appl |
| | | | | | Sequence 6, Appli |
| | | | | | Sequence 280, App |
| | | | | | Sequence 195, App |
| | | | | | Sequence 27, Appl |

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|----|------|------|----|----|---------------------|-------------------|
| 8 | 12.6 | 60.0 | 19 | 18 | US-10-189-359-16 | Sequence 16, Appl |
| 9 | 12.6 | 60.0 | 20 | 19 | US-10-688-706-1896 | Sequence 1896, Ap |
| 10 | 12.6 | 60.0 | 20 | 19 | US-10-688-706-2734 | Sequence 2734, Ap |
| 11 | 12.4 | 59.0 | 18 | 22 | US-10-499-544-15 | Sequence 15, Appl |
| 12 | 12.2 | 58.1 | 20 | 17 | US-10-173-240-36 | Sequence 36, Appl |
| 13 | 12.2 | 58.1 | 20 | 17 | US-10-173-240-70 | Sequence 70, Appl |
| 14 | 12.2 | 58.1 | 20 | 19 | US-10-671-395-382 | Sequence 382, App |
| 15 | 12.2 | 58.1 | 20 | 19 | US-10-671-395-455 | Sequence 455, App |
| 16 | 12.2 | 58.1 | 20 | 19 | US-10-671-395-537 | Sequence 537, App |
| 17 | 12.2 | 58.1 | 20 | 19 | US-10-671-395-730 | Sequence 730, App |
| 18 | 12.2 | 58.1 | 20 | 20 | US-10-695-568-104 | Sequence 104, App |
| 19 | 12.2 | 58.1 | 20 | 20 | US-10-695-568-120 | Sequence 120, App |
| 20 | 12.2 | 58.1 | 21 | 22 | US-10-736-892-1 | Sequence 1, Appli |
| 21 | 12 | 57.1 | 21 | 20 | US-10-751-736-14876 | Sequence 14876, A |
| 22 | 12 | 57.1 | 21 | 20 | US-10-751-736-25591 | Sequence 25591, A |
| 23 | 12 | 57.1 | 21 | 20 | US-10-751-736-39050 | Sequence 39050, A |
| 24 | 12 | 57.1 | 21 | 20 | US-10-751-736-39053 | Sequence 39053, A |
| 25 | 11.8 | 56.2 | 16 | 21 | US-10-776-934-100 | Sequence 100, App |
| 26 | 11.8 | 56.2 | 16 | 21 | US-10-776-934-540 | Sequence 540, App |
| 27 | 11.8 | 56.2 | 16 | 21 | US-10-776-934-541 | Sequence 541, App |
| 28 | 11.8 | 56.2 | 16 | 21 | US-10-776-934-542 | Sequence 542, App |
| 29 | 11.8 | 56.2 | 16 | 21 | US-10-776-934-543 | Sequence 543, App |
| 30 | 11.8 | 56.2 | 17 | 16 | US-10-180-781-50 | Sequence 50, Appl |
| 31 | 11.8 | 56.2 | 17 | 19 | US-10-712-672-1359 | Sequence 1359, Ap |
| 32 | 11.8 | 56.2 | 17 | 19 | US-10-712-672-1360 | Sequence 1360, Ap |
| 33 | 11.8 | 56.2 | 17 | 19 | US-10-712-672-1361 | Sequence 1361, Ap |
| 34 | 11.8 | 56.2 | 18 | 18 | US-10-280-183A-215 | Sequence 215, App |
| 35 | 11.8 | 56.2 | 20 | 16 | US-10-171-319-98 | Sequence 98, Appl |
| 36 | 11.8 | 56.2 | 20 | 16 | US-10-171-319-100 | Sequence 100, App |
| 37 | 11.8 | 56.2 | 20 | 17 | US-10-177-573-15 | Sequence 15, Appl |
| 38 | 11.8 | 56.2 | 20 | 17 | US-10-210-479-26 | Sequence 26, Appl |
| 39 | 11.8 | 56.2 | 20 | 17 | US-10-210-479-97 | Sequence 97, Appl |
| 40 | 11.8 | 56.2 | 20 | 19 | US-10-619-739-1288 | Sequence 1288, Ap |
| 41 | 11.8 | 56.2 | 20 | 19 | US-10-476-021-62 | Sequence 62, Appl |
| 42 | 11.8 | 56.2 | 21 | 9 | US-09-765-081-133 | Sequence 133, App |
| 43 | 11.8 | 56.2 | 21 | 21 | US-10-847-918-3427 | Sequence 3427, Ap |
| 44 | 11.6 | 55.2 | 19 | 16 | US-10-251-117-46 | Sequence 46, Appl |
| 45 | 11.6 | 55.2 | 19 | 16 | US-10-251-117-189 | Sequence 189, App |

ALIGNMENTS

RESULT 1
US-10-774-721-38
; Sequence 38, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774, 721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461, 005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-38

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2;

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| Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | Best Local Similarity 88.9%; Pred. No. 39; Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0; | |
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| Db | 1 GCCAGUUCGACAGGCACTT 21 | | 3 GCCAGTTCGACAGGCA 20 |
| RESULT 2 | | | |
| US-10-774-721-37/c | | | |
| ; Sequence 37, Application US/10774721 | | | |
| ; Publication No. US2005009042A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: JOCKERS, Ralf | | | |
| ; APPLICANT: COUTURIER, Cyril | | | |
| ; APPLICANT: UHLMANN, Eugen | | | |
| ; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein | | | |
| ; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction | | | |
| ; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor | | | |
| ; FILE REFERENCE: FRV2003/0005 US NP | | | |
| ; CURRENT APPLICATION NUMBER: US/10/774,721 | | | |
| ; CURRENT FILING DATE: 2004-02-09 | | | |
| ; PRIOR APPLICATION NUMBER: 60/461,005 | | | |
| ; PRIOR FILING DATE: 2003-04-07 | | | |
| ; PRIOR APPLICATION NUMBER: 0301543 | | | |
| ; PRIOR FILING DATE: 2003-02-10 | | | |
| ; NUMBER OF SEQ ID NOS: 47 | | | |
| ; SOFTWARE: PatentIn version 3.1 | | | |
| ; SEQ ID NO 37 | | | |
| ; LENGTH: 21 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Artificial Sequence | | | |
| ; FEATURE: | | | |
| ; OTHER INFORMATION: Artificial | | | |
| US-10-774-721-37 | | | |
| Query Match 90.5%; Score 19; DB 21; Length 21; | | Query Match 63.8%; Score 13.4; DB 20; Length 16; | |
| Best Local Similarity 89.5%; Pred. No. 12; | | Best Local Similarity 80.0%; Pred. No. 8.3e+03; | |
| Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0; | | Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0; | |
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| RESULT 3 | | | |
| US-10-774-721-31 | | | |
| ; Sequence 31, Application US/10774721 | | | |
| ; Publication No. US2005009042A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: JOCKERS, Ralf | | | |
| ; APPLICANT: COUTURIER, Cyril | | | |
| ; APPLICANT: UHLMANN, Eugen | | | |
| ; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein | | | |
| ; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction | | | |
| ; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor | | | |
| ; FILE REFERENCE: FRV2003/0005 US NP | | | |
| ; CURRENT APPLICATION NUMBER: US/10/774,721 | | | |
| ; CURRENT FILING DATE: 2004-02-09 | | | |
| ; PRIOR APPLICATION NUMBER: 60/461,005 | | | |
| ; PRIOR FILING DATE: 2003-04-07 | | | |
| ; PRIOR APPLICATION NUMBER: 0301543 | | | |
| ; PRIOR FILING DATE: 2003-02-10 | | | |
| ; NUMBER OF SEQ ID NOS: 47 | | | |
| ; SOFTWARE: PatentIn version 3.1 | | | |
| ; SEQ ID NO 31 | | | |
| ; LENGTH: 20 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Artificial Sequence | | | |
| ; FEATURE: | | | |
| ; OTHER INFORMATION: AS10 | | | |
| US-10-774-721-31 | | | |
| Query Match 85.7%; Score 18; DB 21; Length 20; | | Query Match 61.9%; Score 13; DB 20; Length 21; | |
| US-10-774-721-31 | | Best Local Similarity 66.7%; Pred. No. 1.3e+04; | |
| RESULT 4 | | RESULT 5 | |
| US-10-451-805-6/c | | US-10-792-280-280 | |
| ; Sequence 6, Application US/10451805 | | ; Sequence 280, Application US/10792280 | |
| ; Publication No. US20040248099A1 | | ; Publication No. US20040234517A1 | |
| ; GENERAL INFORMATION: | | ; GENERAL INFORMATION: | |
| ; APPLICANT: Goppelt, Andreas | | ; APPLICANT: Bowman, Michael | |
| ; APPLICANT: Alzheimer, Christian | | ; APPLICANT: Follettie, Maximillian | |
| ; APPLICANT: Kogel, Heidi | | ; APPLICANT: Chen, Heng | |
| ; TITLE OF INVENTION: Use of Intermediate-Conductance | | ; APPLICANT: Williams, Cara | |
| ; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and | | ; APPLICANT: Ellis, Debra | |
| ; TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity | | ; APPLICANT: Winkler, Aaron | |
| ; FILE REFERENCE: 50125/080001 | | ; APPLICANT: Liu, Wei | |
| ; CURRENT APPLICATION NUMBER: US/10/451,805 | | ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR | |
| ; CURRENT FILING DATE: 2003-06-25 | | ; TITLE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES | |
| ; PRIOR APPLICATION NUMBER: PCT/EP01/15317 | | ; FILE REFERENCE: AM101023-2 | |
| ; PRIOR FILING DATE: 2001-12-27 | | ; CURRENT APPLICATION NUMBER: US/10/792,280 | |
| ; PRIOR APPLICATION NUMBER: US 60/277,453 | | ; CURRENT FILING DATE: 2004-03-04 | |
| ; PRIOR FILING DATE: 2001-03-20 | | ; NUMBER OF SEQ ID NOS: 1535 | |
| ; PRIOR APPLICATION NUMBER: DE 10065475.4 | | ; SOFTWARE: PatentIn version 3.2 | |
| ; PRIOR FILING DATE: 2000-12-28 | | ; SEQ ID NO 280 | |
| ; NUMBER OF SEQ ID NOS: 13 | | ; LENGTH: 21 | |
| ; SOFTWARE: FastSEQ for Windows Version 4.0 | | ; TYPE: RNA | |
| ; SEQ ID NO 6 | | ; ORGANISM: RNAi-sense strand | |
| ; LENGTH: 16 | | US-10-792-280-280 | |
| ; TYPE: DNA | | Query Match 61.9%; Score 13; DB 20; Length 21; | |
| ; ORGANISM: Mus musculus | | Best Local Similarity 66.7%; Pred. No. 1.3e+04; | |
| ; OTHER INFORMATION: | | | |
| US-10-451-805-6 | | | |

| | Matches | 14; | Conservative | 2; | Mismatches | 5; | Indels | 0; | Gaps | 0; |
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| Db | 1 | GCAAGUGCCAGAGAGCCACUU | 21 | | | | | | | |

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RESULT 6
US-10-349-780A-195/c
; Sequence 195, Application US/10349780A
; Publication No. US20040146866A1
; GENERAL INFORMATION:
; APPLICANT: Fu, Guoliang
; TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
; FILE REFERENCE: patent1
; CURRENT APPLICATION NUMBER: US/10/349,780A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-780A-195

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RESULT 7
US-09-986-632-27/c
; Sequence 27, Application US/09986632
; Patent No. US20020119944A1
; GENERAL INFORMATION:
; APPLICANT: AGUERA, Michelle
; TITLE OF INVENTION: Modulation of Ulip/CRMP activity for the prevention of
; TITLE OF INVENTION: treatment of myelin disorders
; FILE REFERENCE: P06974US01/BAS
; CURRENT APPLICATION NUMBER: US/09/986,632
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/246,751
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-986-632-27

RESULT 8
US-10-189-359-16
; Sequence 16, Application US/10189359
; Publication No. US20040039187A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Annette
; APPLICANT: SANGAR, DAVID V

```

; APPLICANT: LEMON, STANLEY M.
; TITLE OF INVENTION: Chimeric GB Virus B (GBV-B)
; FILE REFERENCE: UTSG:258US
; CURRENT APPLICATION NUMBER: US/10/189,359
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 10/189,359
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-189-359-16

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RESULT 9
US-10-688-706-1896/c
; Sequence 1896, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1896
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-1896

RESULT 10
US-10-688-706-2734/c
; Sequence 2734, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071

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QY      1 GCCAGUCCCGACAGGC 17
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Db      3 GCCAGGGCCCGACCGGC 19

RESULT 13
US-10-173-240-70/c
; Sequence 70, Application US/10173240
; Publication No. US20030232436A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
; FILE REFERENCE: HTS-0021
; CURRENT APPLICATION NUMBER: US/10/173,240
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
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US-10-173-240-70

Query Match      58.1%; Score 12.2; DB 17; Length 20;
Best Local Similarity 82.4%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCCAGUCCCGACAGGC 17
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RESULT 14
US-10-671-395-382
; Sequence 382, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 382
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
;
US-10-671-395-382

Query Match      58.1%; Score 12.2; DB 19; Length 20;
Best Local Similarity 70.6%; Pred. No. 3.3e+04;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 GUUCCCGACAGCAGCTT 21
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Db      1 GTTCCCATCAGCCACTT 17

RESULT 15
US-10-671-395-455
; Sequence 455, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.

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; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 455
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-455

Query Match 58.1%; Score 12.2; DB 19; Length 20;
Best Local Similarity 70.6%; Pred. No. 3.3e+04;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GUUCCCGACAGGCACTT 21
|:| | | | | | | | | |
Db 3 GTTCCCATCAGGCACTT 19

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:17:36 ; Search time 1765 Seconds
(without alignments)
452.889 Million cell updates/sec

Title: US-10-774-721-38
Perfect score: 21
Sequence: 1 gccaguuccgacaggcactt 21
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 1 | 11.2 | 53.3 | 19 | 8 | AZ486389 | AZ486389 1M0314E21 |
| C 2 | 10.2 | 48.6 | 19 | 8 | AZ763411 | AZ763411 1M0558B24 |
| C 3 | 10 | 47.6 | 20 | 1 | AL039677 | AL039677 DKFZp434H |
| C 4 | 10 | 47.6 | 20 | 1 | AL045408 | AL045408 DKFZp434E |
| C 5 | 10 | 47.6 | 21 | 8 | AZ393800 | AZ393800 1M0157H04 |
| C 6 | 9.8 | 46.7 | 17 | 9 | AJ589126 | AJ589126 Arabidops |
| C 7 | 9.8 | 46.7 | 20 | 8 | AZ593689 | AZ593689 1M0405C21 |
| C 8 | 9.6 | 45.7 | 16 | 1 | AL039794 | AL039794 DKFZp434B |
| C 9 | 9.6 | 45.7 | 18 | 1 | AL039892 | AL039892 DKFZp434G |
| C 10 | 9.6 | 45.7 | 18 | 1 | AL043072 | AL043072 DKFZp434B |
| C 11 | 9.6 | 45.7 | 19 | 1 | AL042746 | AL042746 DKFZp434C |
| C 12 | 9.6 | 45.7 | 19 | 8 | AZ858446 | AZ858446 2M0163D08 |
| C 13 | 9.6 | 45.7 | 20 | 1 | AL043331 | AL043331 DKFZp434O |
| C 14 | 9.6 | 45.7 | 20 | 1 | AL043349 | AL043349 DKFZp434P |
| C 15 | 9.6 | 45.7 | 20 | 9 | AG204980 | AG204980 Pan trogl |
| C 16 | 9.6 | 45.7 | 21 | 8 | AZ794033 | AZ794033 2M0047D12 |
| C 17 | 9.4 | 44.8 | 17 | 9 | AJ589127 | AJ589127 Arabidops |
| C 18 | 9.4 | 44.8 | 19 | 8 | AZ466725 | AZ466725 1M0277C09 |
| C 19 | 9.4 | 44.8 | 20 | 8 | AZ495853 | AZ495853 1M0331O23 |
| C 20 | 9.4 | 44.8 | 21 | 7 | CO785256 | CO785256 BL283A A0 |
| C 21 | 9.4 | 44.8 | 21 | 8 | AZ806008 | AZ806008 2M0067I15 |
| C 22 | 9.2 | 43.8 | 15 | 1 | AL039409 | AL039409 DKFZp434L |
| C 23 | 9.2 | 43.8 | 21 | 5 | BX315383 | BX315383 BX315383 |
| C 24 | 9 | 42.9 | 20 | 1 | AU254152 | AU254152 AU254152 |

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|------|-----|------|----|---|----------|--------------------|
| C 25 | 9 | 42.9 | 20 | 8 | AZ318416 | AZ318416 1M0037P19 |
| C 26 | 9 | 42.9 | 21 | 7 | CO788185 | CO788185 NT003C A1 |
| C 27 | 8.8 | 41.9 | 20 | 8 | AZ309156 | AZ309156 1M0013B09 |
| C 28 | 8.8 | 41.9 | 20 | 8 | AZ386570 | AZ386570 1M0145C08 |
| C 29 | 8.8 | 41.9 | 20 | 8 | AZ823352 | AZ823352 2M0097A22 |
| C 30 | 8.8 | 41.9 | 21 | 1 | AL043263 | AL043263 DKFZp434L |
| C 31 | 8.6 | 41.0 | 19 | 1 | AI049374 | AI049374 ub33a03.r |
| C 32 | 8.6 | 41.0 | 20 | 8 | AZ616822 | AZ616822 1M0446L13 |
| C 33 | 8.6 | 41.0 | 20 | 8 | AZ789903 | AZ789903 2M0038F15 |
| C 34 | 8.4 | 40.0 | 19 | 8 | AZ514533 | AZ514533 1M0361H08 |
| C 35 | 8.4 | 40.0 | 20 | 8 | AZ309592 | AZ309592 1M0016N09 |
| C 36 | 8.4 | 40.0 | 20 | 8 | AZ325340 | AZ325340 1M0047M08 |
| C 37 | 8.4 | 40.0 | 21 | 5 | BQ593572 | BQ593572 E012766-0 |
| C 38 | 8.4 | 40.0 | 21 | 8 | AZ436036 | AZ436036 1M0233F03 |
| C 39 | 8.4 | 40.0 | 21 | 8 | AZ609424 | AZ609424 1M0434O16 |
| C 40 | 8.4 | 40.0 | 21 | 8 | AZ665199 | AZ665199 1M0546E01 |
| C 41 | 8.2 | 39.0 | 13 | 1 | AL043127 | AL043127 DKFZp434D |
| C 42 | 8.2 | 39.0 | 14 | 1 | AL039339 | AL039339 DKFZp434F |
| C 43 | 8.2 | 39.0 | 15 | 1 | AL043135 | AL043135 DKFZp434D |
| C 44 | 8.2 | 39.0 | 15 | 1 | AL043264 | AL043264 DKFZp434L |
| C 45 | 8.2 | 39.0 | 15 | 1 | AL043298 | AL043298 DKFZp434M |

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AZ486389 19 bp DNA linear GSS 05-OCT-2000
1M0314E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0314E21 F, genomic survey sequence.
ACCESSION
AZ486389
VERSION
AZ486389.1 GI:10653117
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0314 row: E column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0314E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.6%; Score 10.2; DB 8; Length 19;
Best Local Similarity 73.3%; Pred. No. 2.3e+06;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGUCCCGACAG 15
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Db 18 GCCTGTACCAACAG 4

RESULT 3

AL039677/c 20 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZp434H0411_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFZp434H0411, mRNA sequence.

ACCESSION AL039677 GI:49682316
VERSION AL039677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 20)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434H0411"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 47.6%; Score 10; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. No. 3e+06;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGUUCGACGACGACTT 21
|:| | | | | | | | | | | | |
Db 20 AATTCGGACCGGTACCT 3

RESULT 4

AL045408/c 20 bp mRNA linear EST 06-JUL-2004
LOCUS AL045408
DEFINITION DKFZp434E105_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434E105, mRNA sequence.

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 19;
Best Local Similarity 68.8%; Pred. No. 7.3e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 UUCCGACAGGCACTT 21
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Db 16 TTCCCATCAGGCATT 1

RESULT 2

AZ763411/c 19 bp DNA linear GSS 16-FEB-2001
LOCUS AZ763411 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION 1M0558B24R clone UUGC1M0558B24 R, genomic survey sequence.

ACCESSION AZ763411 GI:12874413
VERSION AZ763411
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH GENOME CENTER
UNIVERSITY OF UTAH
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0558 row: B column: 24
Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers
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/clone="UUGC1M0558B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

FEATURES
source

ACCESSION AL045408
VERSION AL045408.1 GI:49682595
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
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/mol_type="mRNA"
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/clone="DKFZp434E105"
/tissue type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: Sali"

ORIGIN
Query Match 47.6%; Score 10; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. NO. 3e+06;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGUUCGCGACAGGCACCTT 21
|::||| ||| ||| |||
Db 20 AATTCGCGACCGGTACCT 3

RESULT 5
AZ393800/c
LOCUS AZ393800 21 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0157H04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0157H04 F, genomic survey sequence.
ACCESSION AZ393800
VERSION AZ393800.1 GI:10508872
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: H column: 04
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 47.6%; Score 10; DB 8; Length 21;
Best Local Similarity 61.1%; Pred. NO. 3e+06;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGUUCGCGACAGGCACCTT 21
|::||| ||| ||| |||
Db 19 AGTTTTCAGCAGCACTT 2

RESULT 6
AJ589126
LOCUS AJ589126 17 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 545A02, genomic survey sequence.
ACCESSION AJ589126
VERSION AJ589126.1 GI:37938750
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 17)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics


```
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
FEATURES
    source
        1..17
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
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            /db_xref="taxon:3702"
            /clone="545A02"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        misc_feature
            1..17
                /note="T-DNA flanking sequence
                left border"
ORIGIN
    Query Match          46.7%;   Score 9.8;   DB 9;   Length 17;
    Best Local Similarity 69.2%;   Pred. No. 3.7e+06;
    Matches              9;   Conservative 2;   Mismatches 2;   Indels 0;   Gaps 0;
QY      6 UUUCCGACAGGCA 18
       |:|||||
Db      5 TTCCCGACCGGTA 17
RESULT 7
AZ593689/c
LOCUS
DEFINITION
    AZ593689
    1M0405C21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
    clone UUGC1M0405C21 F, genomic survey sequence.
ACCESSION
    AZ593689
VERSION
    AZ593689.1 GI:11715879
KEYWORDS
    GSS.
SOURCE
    Mus musculus (house mouse)
ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 20)
AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0405 row: C column: 21
    Seq primer: CGTTGTAAACGACGGCCAGT
    Class: plasmid ends
    High quality sequence stop: 20.
FEATURES
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            /db_xref="taxon:10090"
            /clone="UUGC1M0405C21"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
```

```
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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ORIGIN

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Query Match          46.7%;   Score 9.8;   DB 8;   Length 20;
Best Local Similarity 69.2%;   Pred. No. 3.7e+06;
Matches              9;   Conservative 2;   Mismatches 2;   Indels 0;   Gaps 0;
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QY      3 CAGUUCCGACAG 15
       |||::|||
Db      17 CAGTTACCAACAG 5
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RESULT 8

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AL039794/c
LOCUS
DEFINITION
    AL039794
    DKFZp434B1612_r1 434 (synonym: htes3) Homo sapiens cDNA clone
    DKFZp434B1612, mRNA sequence.
ACCESSION
    AL039794
VERSION
    AL039794.1 GI:49682336
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
```

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ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 16)
AUTHORS
    Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
    Wiemann,S.
    EST (Duesterhoeft, et al.)
    Unpublished (1999)
    Contact: MIPS
    MIPS
    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
    Location/Qualifiers
    source
        1..16
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp434B1612"
            /tissue_type="testis"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="434 (synonym: htes3)"
            /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
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ORIGIN

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Query Match          45.7%;   Score 9.6;   DB 1;   Length 16;
Best Local Similarity 62.5%;   Pred. No. 4.6e+06;
Matches             10;   Conservative 2;   Mismatches 4;   Indels 0;   Gaps 0;
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QY      4 AGUUCCGACAGGCAC 19
       |:|||||
Db      16 AATTCGGACCGGTAC 1
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RESULT 9

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AL039892/c
LOCUS
DEFINITION
    AL039892
    DKFZp434G1212_r1 434 (synonym: htes3) Homo sapiens cDNA clone
    DKFZp434G1212, mRNA sequence.
ACCESSION
    AL039892
VERSION
    AL039892.1 GI:49682352
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source Location/Qualifiers
1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434G1212"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 45.7%; Score 9.6; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 AGUUCCGACAGGCAC 19
| :||| ||| |||
Db 16 AATTCGGACCGGTAC 1
RESULT 10
AL043072/c
LOCUS
DEFINITION DKFZp434B1823_r1 434 (synonym: htes3) Homo sapiens cDNA clone
EST 18 bp mRNA linear EST 06-JUL-2004
ACCESSION DKFZp434B1823, mRNA sequence.
VERSION AL043072
KEYWORDS GI:49682480
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source Location/Qualifiers
1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="adult"
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/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 45.7%; Score 9.6; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 AGUUCCGACAGGCAC 19
| :||| ||| |||
Db 16 AATTCGGACCGGTAC 1
RESULT 10
AL043072/c
LOCUS
DEFINITION DKFZp434B1823_r1 434 (synonym: htes3) Homo sapiens cDNA clone
EST 18 bp mRNA linear EST 06-JUL-2004
ACCESSION DKFZp434B1823, mRNA sequence.
VERSION AL043072
KEYWORDS GI:49682480
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source Location/Qualifiers
1. .18
/organism="Homo sapiens"
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/clone="DKFZp434B1823"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 45.7%; Score 9.6; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 AGUUCCGACAGGCAC 19
| :||| ||| |||

Db 18 AATTCGGACCGGTAC 3
RESULT 11
AL042746/c
LOCUS
DEFINITION DKFZp434C1822_r1 434 (synonym: htes3) Homo sapiens cDNA clone
EST 19 bp mRNA linear EST 06-JUL-2004
ACCESSION DKFZp434C1822, mRNA sequence.
VERSION AL042746
KEYWORDS GI:49682451
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="DKFZp434C1822"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match 45.7%; Score 9.6; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 AGUUCCGACAGGCAC 19
| :||| ||| |||
Db 17 AATTCGGACCGGCGC 2
RESULT 12
AZ858446/c
LOCUS
DEFINITION 2M0163D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163D08 R, genomic survey sequence..
ACCESSION AZ858446
VERSION AZ858446.1 GI:13051622
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0163 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 4.7e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCAGUCCCGACAGG 16
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Db 19 GCCAGGATCCTACAGG 4

RESULT 13
AL043331/c
LOCUS
DEFINITION
AL043331 20 bp mRNA linear EST 06-JUL-2004
DKFZp43402323_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp43402323, mRNA sequence.
AL043331 1 GI:49682508
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Blum, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

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/clone_lib="434 (synonym: htes3)"

ORIGIN

Query Match 45.7%; Score 9.6; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGUUCGGACAGGCAC 19
| : | | | | | | | | | | | | | | | | | | | | | |
Db 18 AATTCGGACCGGGAC 3

RESULT 14

AL043349/c
LOCUS
DEFINITION
AL043349 20 bp mRNA linear EST 06-JUL-2004
DKFZp434P1923_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434P1923, mRNA sequence.
AL043349
AL043349.1 GI:49682510
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Blum, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
1. .20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434P1923"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

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Best Local Similarity 62.5%; Pred. No. 4.7e+06;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGUUCGGACAGGCAC 19
| : | | | | | | | | | | | | | | | | | | | | | |
Db 18 AATTCGGACCGGGAC 3

RESULT 15

AG204980/c
LOCUS
DEFINITION
AG204980 20 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-090P12.TJ, genomic survey
sequence.
AG204980
AG204980.1 GI:45237155
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
Unpublished
2 (bases 1 to 20)
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

REFERENCE

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.krribb.re.kr, URL:http://phs.grc.krribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-090P12.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match 45.7%; Score 9.6; DB 9; Length 20;
Best Local Similarity 68.8%; Pred. No. 4.7e+06;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 5 GUUCCCGACAGGCACT 20
| :||| | ||| |||
Db 17 GGTCCCCCAAGGAAGT 2

Search completed: August 18, 2005, 07:56:24
Job time : 1767 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 05:29:57 ; Search time 842 Seconds
(without alignments)
1208.503 Million cell updates/sec

Title: US-10-774-721-38
Perfect score: 21
Sequence: 1 gccaguucccgacaggcactt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 21 | 100.0 | 21 | 6 | CQ860126 Sequence |
| C 2 | 19 | 90.5 | 21 | 6 | CQ860125 Sequence |
| 3 | 18 | 85.7 | 20 | 6 | CQ860119 Sequence |
| C 4 | 13.4 | 63.8 | 16 | 6 | AX471987 Sequence |
| 5 | 13.2 | 62.9 | 21 | 6 | I25270 Sequence 57 |
| 6 | 12.8 | 61.0 | 19 | 6 | AR163030 Sequence |
| 7 | 12.8 | 61.0 | 19 | 6 | I24629 Sequence 13 |
| 8 | 12.8 | 61.0 | 19 | 6 | I25226 Sequence 13 |
| 9 | 12.8 | 61.0 | 20 | 6 | AR037349 Sequence |
| 10 | 12.8 | 61.0 | 20 | 6 | AR040632 Sequence |
| 11 | 12.8 | 61.0 | 20 | 6 | I19643 Sequence 24 |
| C 12 | 12.8 | 61.0 | 21 | 6 | CQ848735 Sequence |
| 13 | 12.4 | 59.0 | 18 | 6 | AX797219 Sequence |
| C 14 | 12.2 | 58.1 | 21 | 6 | AX614231 Sequence |
| 15 | 11.8 | 56.2 | 16 | 6 | CQ858638 Sequence |
| C 16 | 11.8 | 56.2 | 17 | 6 | AR240883 Sequence |
| C 17 | 11.8 | 56.2 | 18 | 6 | AX298581 Sequence |
| 18 | 11.8 | 56.2 | 20 | 6 | AR215747 Sequence |
| C 19 | 11.8 | 56.2 | 20 | 6 | AX708916 Sequence |

| | | | | | | |
|------|------|------|----|---|-----------|--------------------|
| 20 | 11.8 | 56.2 | 20 | 6 | AX708918 | AX708918 Sequence |
| 21 | 11.6 | 55.2 | 18 | 6 | AR075066 | AR075066 Sequence |
| 22 | 11.6 | 55.2 | 18 | 6 | AR141884 | AR141884 Sequence |
| C 23 | 11.6 | 55.2 | 18 | 6 | E15984 | E15984 Oligonucleo |
| C 24 | 11.6 | 55.2 | 21 | 8 | ZAMRRN04 | M82174 Zamia flori |
| C 25 | 11.6 | 55.2 | 21 | 8 | ZAMRRNA03 | M82055 Zamia Otton |
| 26 | 11.4 | 54.3 | 15 | 6 | AR176696 | AR176696 Sequence |
| 27 | 11.4 | 54.3 | 15 | 6 | BD260047 | BD260047 Hybridiza |
| 28 | 11.4 | 54.3 | 18 | 6 | AR111342 | AR111342 Sequence |
| 29 | 11.4 | 54.3 | 18 | 6 | BD225242 | BD225242 Pyrazolo[|
| C 30 | 11.4 | 54.3 | 18 | 6 | AR225855 | AR225855 Sequence |
| 31 | 11.4 | 54.3 | 18 | 6 | AR256566 | AR256566 Sequence |
| 32 | 11.4 | 54.3 | 20 | 6 | AR054621 | AR054621 Sequence |
| 33 | 11.4 | 54.3 | 20 | 6 | E35993 | E35993 Method for |
| 34 | 11.4 | 54.3 | 20 | 6 | AR271882 | AR271882 Sequence |
| C 35 | 11.4 | 54.3 | 20 | 6 | AX293210 | AX293210 Sequence |
| C 36 | 11.4 | 54.3 | 21 | 6 | AR009478 | AR009478 Sequence |
| C 37 | 11.4 | 54.3 | 21 | 6 | AR043544 | AR043544 Sequence |
| C 38 | 11.4 | 54.3 | 21 | 6 | AR064136 | AR064136 Sequence |
| 39 | 11.4 | 54.3 | 21 | 6 | CQ778155 | CQ778155 Sequence |
| 40 | 11.4 | 54.3 | 21 | 6 | CQ778156 | CQ778156 Sequence |
| C 41 | 11.4 | 54.3 | 21 | 6 | I35557 | I35557 Sequence 4 |
| 42 | 11.4 | 54.3 | 21 | 6 | I65324 | I65324 Sequence 46 |
| 43 | 11.4 | 54.3 | 21 | 6 | AR530445 | AR530445 Sequence |
| 44 | 11.4 | 54.3 | 21 | 6 | AX096470 | AX096470 Sequence |
| 45 | 11.2 | 53.3 | 17 | 6 | I87791 | I87791 Sequence 19 |

ALIGNMENTS

| | | | | | | |
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| RESULT 1 | CQ860126 | Sequence 38 from Patent WO2004072293. | 21 bp | DNA | linear | PAT 10-SEP-2004 |
| LOCUS | CQ860126 | | | | | |
| DEFINITION | CQ860126 | | | | | |
| ACCESSION | CQ860126.1 | GI:51982014 | | | | |
| VERSION | | | | | | |
| KEYWORDS | | | | | | |
| SOURCE | | synthetic construct | | | | |
| ORGANISM | | synthetic construct | | | | |
| REFERENCE | 1 | other sequences; artificial sequences. | | | | |
| AUTHORS | | Jockers,R., Couturier,C. and Uhlmann,E. | | | | |
| TITLE | | Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor | | | | |
| JOURNAL | | Patent: WO 2004072293-A 38 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR) | | | | |
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| ORIGIN | | | | | | |
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| Best Local Similarity | | 90.5%; Pred. No. 9.3; | | | | |
| Matches | 19; Conservative | 2; Mismatches | 0; Indels | 0; Gaps | 0; | |
| Qy | 1 | GCCAGUCCCCGACAGGCACCTT 21 | | | | |
| | | : | | | | |
| Db | 1 | GCCAGTTCCTCCGACAGGCACCTT 21 | | | | |
| | | : | | | | |
| RESULT 2 | CQ860125/c | Sequence 37 from Patent WO2004072293. | 21 bp | DNA | linear | PAT 10-SEP-2004 |
| LOCUS | CQ860125 | | | | | |
| DEFINITION | CQ860125 | | | | | |
| ACCESSION | CQ860125 | | | | | |

us-10-774-721-38.rge

Fri Aug 19 08:52:57 2005

ACCESSION AX471987 GI:22207038
VERSION AX471987.1
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 Alzheimer,C., Goppelt,A. and Koegel,H.
AUTHORS Use of intermediate-conductance potassium channels and modulators
TITLE for the diagnosis and treatment of illnesses having disturbed
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL Patent: WO 2004072293-A 37 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..21
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Artificiel"
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Query Match 90.5%; Score 19; DB 6; Length 21;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGUUCGCCGACAGGCAC 19
Db 19 GCCAGTTCGCCGACAGGCAC 1
RESULT 3
LOCUS CQ860119 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 31 from Patent WO2004072293.
ACCESSION CQ860119
VERSION CQ860119.1 GI:51982007
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Jockers,R., Couturier,C. and Uhlmann,E.
AUTHORS Oligonucleotides which inhibit the expression of the ob-rgrp
TITLE protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL Patent: WO 2004072293-A 31 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
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/mol_type="synthetic construct"
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/note="AS10"
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Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGUUCGCCGACAGGCA 18
Db 3 GCCAGTTCGCCGACAGGCA 20
RESULT 4
AX471987/c AX471987 16 bp DNA linear PAT 09-AUG-2002
LOCUS AX471987
DEFINITION Sequence 6 from Patent WO02053171.

ACCESSION AX471987 GI:22207038
VERSION AX471987.1
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 Alzheimer,C., Goppelt,A. and Koegel,H.
AUTHORS Use of intermediate-conductance potassium channels and modulators
TITLE for the diagnosis and treatment of illnesses having disturbed
keratinocyte activity
JOURNAL Patent: WO 02053171-A 6 11-JUL-2002;
LUDWIG MAXIMILIANS UNI (DE)
FEATURES Location/Qualifiers
source 1..16
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
/note="mIK1 Primer 1"
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Best Local Similarity 80.0%; Pred. No. 8.4e+04;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGUUCGCCGACAG 15
Db 15 GCCAGTTCGCCGCCAG 1
RESULT 5
LOCUS I25270 21 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 57 from patent US 5550020.
ACCESSION I25270
VERSION I25270.1 GI:1605140
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for
retinoblastoma
JOURNAL Patent: US 5550020-A 57 27-AUG-1996;
FEATURES Location/Qualifiers
source 1..21
/mol_type="unassigned DNA"
ORIGIN
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Best Local Similarity 72.2%; Pred. No. 1.1e+05;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 CCAGUUCGCCGACAGGCAC 19
Db 4 CCAGTTCGCCCAGACGC 21
RESULT 6
AR163030 19 bp DNA linear PAT 17-OCT-2001
LOCUS AR163030
DEFINITION Sequence 13 from patent US 6270963.
ACCESSION AR163030
VERSION AR163030.1 GI:16233504
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E.

TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 6270963-A 13 07-AUG-2001;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
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Query Match 61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCAGUUCGCCGACAGGC 17
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Db 4 CCAGTTCGCCACAGAC 19

RESULT 7
LOCUS I24629 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5545527.
ACCESSION I24629
VERSION I24629.1 GI:1604499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Stevens,J.K. and Dunn,J.M.
TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 5545527-A 13 13-AUG-1996;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
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ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 19;
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Db 4 CCAGTTCGCCACAGAC 19

RESULT 8
LOCUS I25226 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5550020.
ACCESSION I25226
VERSION I25226.1 GI:1605096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for retinoblastoma
JOURNAL Patent: US 5550020-A 13 27-AUG-1996;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCAGUUCGCCGACAGGC 17
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Db 4 CCAGTTCGCCACAGAC 19

RESULT 9
LOCUS AR037349 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5801154.
ACCESSION AR037349
VERSION AR037349.1 GI:5955205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini,E., Bennett,C.Frank. and Dean,N.M.
TITLE Antisense oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5801154-A 24 01-SEP-1998;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
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Qy 1 GCCAGUUCGCCGACAGG 16
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Db 5 GCCAGTTCGCCGACAGG 20

RESULT 10
LOCUS AR040632 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5807838.
ACCESSION AR040632
VERSION AR040632.1 GI:5959995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini,E. Jr. and Bennett,C.Frank.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5807838-A 24 15-SEP-1998;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
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Query Match 61.0%; Score 12.8; DB 6; Length 20;
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Db 5 GCCAGTTCGCCGACAGG 20

RESULT 11
LOCUS I19643 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 24 from patent US 5510239.
ACCESSION I19643
VERSION I19643.1 GI:1599998
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini,E. Jr. and Bennett,C.Frank.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5510239-A 24 07-OCT-1996;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

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Qy 1 GCCAGUUCGCCGACAGG 16
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Db 5 GCCAGTTCGCCGACAGG 20

RESULT 11
LOCUS I19643 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 24 from patent US 5510239.
ACCESSION I19643
VERSION I19643.1 GI:1599998
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini,E. Jr. and Bennett,C.Frank.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5510239-A 24 07-OCT-1996;
FEATURES Location/Qualifiers
source 1. .20
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/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCAGUUCGCCGACAGG 16
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Db 5 GCCAGTTCGCCGACAGG 20

REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini,E. Jr. and Bennett,C.F.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5510239-A 24 23-APR-1996;
FEATURES Location/Qualifiers
source 1..20
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ORIGIN

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Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 5 GCCAGTTCAGGCAGG 20

RESULT 12
CQ848735/c
LOCUS CQ848735 21 bp DNA linear PAT 19-AUG-2004
DEFINITION Sequence 195 from Patent WO2004065628.
ACCESSION CQ848735
VERSION CQ848735.1 GI:51470163
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Fu,G.
TITLE Quantitative multiplex detection of nucleic acids
JOURNAL Patent: WO 2004065628-A 195 05-AUG-2004;
Fu, Guoliang (GB)
FEATURES Location/Qualifiers
source 1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 61.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUCCCGACAGGC 17
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Db 16 CCAGTTACCCACAGGC 1

RESULT 13
AX797219
LOCUS AX797219 18 bp DNA linear PAT 04-OCT-2003
DEFINITION Sequence 15 from Patent WO03052143.
ACCESSION AX797219
VERSION AX797219.1 GI:37517872
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS angles D'Auriac,M.B. and Sirevaag,R.
TITLE New primers for the detection and identification of bacterial indicator groups and virulence factors
JOURNAL Patent: WO 03052143-A 15 26-JUN-2003;
Angles D'Auriac, Marc B. (NO)
FEATURES Location/Qualifiers
source 1..18
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

/note="Enterobacteriaceae family"

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Best Local Similarity 68.8%; Pred. No. 2.8e+05;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 UUCCCGACAGGCATT 21
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Db 1 TTCCCGYCAGGCRTTT 16

RESULT 14
AX614231/c
LOCUS AX614231 21 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 5256 from Patent WO02072882.
ACCESSION AX614231
VERSION AX614231.1 GI:28409660
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 5256 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES Location/Qualifiers
source 1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Db 17 CCAGTTCAGAGAGGGCA 1

RESULT 15
CQ858638
LOCUS CQ858638 16 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 100 from Patent WO2004069991.
ACCESSION CQ858638
VERSION CQ858638.1 GI:51852605
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hansen,B., Thruue,C.A., Petersen,K.D., Westergaard,M. and Wissenbach,M.
TITLE Oligomeric compounds for the modulation of survivin expression
JOURNAL Patent: WO 2004069991-A 100 19-AUG-2004;
Santaris Pharma A/S (DK)
FEATURES Location/Qualifiers
source 1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 04:18:21 ; Search time 229 Seconds
(without alignments)
542.858 Million cell updates/sec

Title: US-10-774-721-38
Perfect score: 21
Sequence: 1 gccaguucccgacaggcactt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 4 | 13.2 | 62.9 | 21 | 2 | AAT11420 |
| C 5 | 12.8 | 61.0 | 18 | 12 | ADP66743 |
| C 6 | 12.8 | 61.0 | 19 | 2 | AAT11532 |
| C 7 | 12.8 | 61.0 | 19 | 2 | AAT12851 |
| C 8 | 12.8 | 61.0 | 20 | 2 | AAQ86849 |
| C 9 | 12.8 | 61.0 | 20 | 2 | AAV53600 |
| C 10 | 12.8 | 61.0 | 21 | 13 | ADQ31737 |
| C 11 | 12.6 | 60.0 | 19 | 6 | ABK91203 |
| C 12 | 12.6 | 60.0 | 19 | 12 | ADJ56746 |
| C 13 | 12.6 | 60.0 | 19 | 12 | ADJ64258 |
| C 14 | 12.6 | 60.0 | 20 | 12 | ADK94393 |
| C 15 | 12.6 | 60.0 | 20 | 12 | ADP78935 |
| C 16 | 12.6 | 60.0 | 20 | 12 | ADP78097 |
| C 17 | 12.4 | 59.0 | 18 | 9 | ACF05415 |
| C 18 | 12.4 | 59.0 | 21 | 12 | ADH09468 |
| C 19 | 12.4 | 59.0 | 21 | 12 | ADP46888 |
| C 20 | 12.2 | 58.1 | 17 | 4 | AAH24024 |

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| C | 21 | 12.2 | 58.1 | 20 | 3 | AAZ95350 | Aaz95350 Human mtP |
| | 22 | 12.2 | 58.1 | 20 | 6 | ABL52426 | Ab152426 Human FLI |
| | 23 | 12.2 | 58.1 | 20 | 6 | ABL52442 | Ab152442 Human FLI |
| C | 24 | 12.2 | 58.1 | 20 | 12 | ADG72431 | Adg72431 Human E2- |
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| | 26 | 12.2 | 58.1 | 20 | 12 | ADM14350 | Adm14350 Human mPG |
| | 27 | 12.2 | 58.1 | 20 | 12 | ADM14543 | Adm14543 Human mPG |
| | 28 | 12.2 | 58.1 | 20 | 12 | ADM14195 | Adm14195 Human mPG |
| | 29 | 12.2 | 58.1 | 20 | 12 | ADM14268 | Adm14268 Human mPG |
| C | 30 | 12 | 57.1 | 20 | 3 | AAZ95324 | Aaz95324 Human mtP |
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| | 32 | 11.8 | 56.2 | 15 | 4 | AAF53027 | Aaf53027 IGF-I oli |
| | 33 | 11.8 | 56.2 | 16 | 13 | ADR70031 | Adr70031 Human sur |
| C | 34 | 11.8 | 56.2 | 18 | 6 | AAS97605 | Aas97605 Murine SA |
| C | 35 | 11.8 | 56.2 | 18 | 12 | ADM15945 | Adm15945 Murine SA |
| C | 36 | 11.8 | 56.2 | 20 | 2 | AAV28296 | Aav28296 Schizophy |
| | 37 | 11.8 | 56.2 | 20 | 6 | ABQ74812 | Abq74812 Human TNF |
| C | 38 | 11.8 | 56.2 | 20 | 10 | ADG32645 | Adg32645 Murine pr |
| | 39 | 11.8 | 56.2 | 20 | 10 | ADG32643 | Adg32643 PCR prime |
| | 40 | 11.8 | 56.2 | 20 | 12 | ADI27267 | Adi27267 Antisense |
| | 41 | 11.8 | 56.2 | 20 | 12 | ADJ86220 | Adj86220 Nucleic a |
| | 42 | 11.8 | 56.2 | 20 | 12 | ADJ53366 | Adj53366 Human G p |
| C | 43 | 11.8 | 56.2 | 20 | 12 | ADJ53437 | Adj53437 Human GPC |
| | 44 | 11.8 | 56.2 | 21 | 4 | AAF96883 | Aaf96883 Human gen |
| C | 45 | 11.8 | 56.2 | 21 | 6 | ABK65513 | Abk65513 Human sin |

ALIGNMENTS

RESULT 1

ADR27688

ID ADR27688 standard; DNA; 20 BP.

XX ADR27688;

AC ADR27688;

XX 04-NOV-2004 (first entry)

XX OB-RGRP antisense oligonucleotide, AS 10.

DE Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

XX Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

KW Leptin receptor related protein; OB-RGRP; leptin receptor;

KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;

KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;

KW thrombus formation; immunity; inflammation; fetal development; cancer;

KW antisense; ss.

XX Synthetic.

XX OS

XX Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "Optional thioester"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 20

FT /tag= d

FT /mod_base= OTHER

FT /note= "3' triethyleneglycol spacer"

XX FR2850971-A1.

XX 13-AUG-2004.

XX 10-FEB-2003; 2003FR-00001543.

PF

XX 10-FEB-2003; 2003FR-00001543.
XX (AVET) AVENTIS PHARMA SA.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
DR New oligonucleotides that inhibit expression of the leptin receptor;
XX related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX Example 6; Fig 1; 104pp; French.
PS The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
SQ Query Match 85.7%; Score 18; DB 13; Length 20;
Best Local Similarity 88.9%; Pred. No. 30;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGUUCGACAGGCA 18
Db 3 GCCAGTCCCGACAGGCA 20
RESULT 2
ABQ78935/c
ID ABQ78935 standard; DNA; 16 BP.
XX AC ABQ78935;
XX 04-NOV-2002 (first entry)
DT Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
XX Mouse; intermediate-conductance potassium channel; dermatological;
XX antiinflammatory; keratolytic; vulnery; antipsoriatic; atopic eczema;
KW contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose;
KW hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIK1;
KW PCR; primer; ss.
XX Mus musculus.
OS WO200253171-A2.
XX 11-JUL-2002.
XX 27-DEC-2001; 2001WO-EP015317.
XX

PR 28-DEC-2000; 2000DE-01065475.
PR 20-MAR-2001; 2001US-0277453P.
XX (SWIT-) SWITCH BIOTECH AG.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
XX Goppelt A, Alzheimer C, Koegel H;
PI WPI; 2002-643295/69.
DR Use of intermediate-conductance potassium channel proteins for the
XX diagnosis, prevention and treatment of disorders associated with
PT disturbed keratinocyte activity, especially psoriasis.
PT Example 3; Page 119; 121pp; German.
PS The invention relates to a novel use of intermediate-conductance
XX potassium channel proteins. The proteins of the invention have
CC dermatological, antiinflammatory, keratolytic, vulnery, and
CC antipsoriatic activity. The method is used especially in the field of
CC damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo,
CC hyperkeratosis, actinic keratosis, hypertrophic scars, keloids, lentigo,
CC aged skin, ulcers and especially psoriasis. The sequence represents a PCR
CC primer for the mouse potassium channel protein mIK1 of the invention
XX Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
SQ Query Match 63.8%; Score 13.4; DB 6; Length 16;
Best Local Similarity 80.0%; Pred. No. 6.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGUUCGACAG 15
Db 15 GCCAGTCCCGCAG 1
RESULT 3
AAQ88255/c
ID AAQ88255 standard; DNA; 19 BP.
XX AC AAQ88255;
XX 25-MAR-2003 (revised)
DT 07-DEC-1995 (first entry)
XX Neisseria pilC gene constant region probe TR60.
DE pilC protein; pilin; pathogenic type 4 pilus bacteria; vaccine;
XX detection; bacterial adhesin; phase variation; constant region; probe;
KW Neisseria gonorrhoeae; Neisseria meningitidis; Pseudomonas aeruginosa;
KW ss.
XX Synthetic.
OS DE4336530-C1.
XX 13-APR-1995.
PD 26-OCT-1993; 93DE-04336530.
XX 26-OCT-1993; 93DE-04336530.
PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Meyer TFF, Rudel T, Rylf RR, Scheuerpflug IB;
PI WPI; 1995-140328/19.
DR Recombinant PilC-proteins derived from Neisseria gonorrhoeae - and their
XX prodn. methods; useful for immunisation against pathogen type 4 pilus
PT carrying bacteria or their detection.
XX Claim 5; Page 12; 29pp; German.
PS

XX Sequences coding for pilin PilC proteins from Neisseria spp. have been
CC isolated (see AAQ88239-088241). The pilC1 and pilC2 genes from
CC N.gonorrhoeae have 84% identity. Probes were designed based on regions of
CC shared homology (see AAQ88242-88261) and these constant region probes
CC were used in Southern hybridisations to identify other pilC genes in
CC N.gonorrhoeae strain MS11 and N.meningitidis strain A1493. Also, the same
CC probes were used to screen a Pseudomonas aeruginosa strain and identified
CC a pilC-like sequence. Gene sequences which hybridise with any of the
CC constant region probes are claimed. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. No. 8.3e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGUUCGCCGACAGGCA 18
Db 19 GCCGTTCCCGACTGGCA 2

RESULT 4

AAT11420
ID AAT11420 standard; DNA; 21 BP.

AC AAT11420;

XX 09-SEP-1996 (first entry)

XX Retinoblastoma gene, RB1, exon 1 PCR 5' primer.

DE Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;
XX mutation; polymerase chain reaction; PCR; ss.

XX Synthetic.

XX WO9601908-A1.

XX 25-JAN-1996.

XX 07-JUL-1995; 95WO-US008604.

XX 08-JUL-1994; 94US-00271942.

XX (VISI-) VISIBLE GENETICS INC.
PA (HSCR-) HSC RES & DEV LP.

XX Gallie BL, Dunn JM, Stevens JK, Hui M;

PI WPI; 1996-097637/10.

XX Identifying mutation(s) in RB1 exons by quantitative amplification - and
PT by comparing length of amplification products and sequencing, for
PT diagnosis and genetic screening of retinoblastoma.

XX Claim 12; Page 22; 48pp; English.

XX AAT11420-T11473 are PCR amplification primers used for the amplification
CC of exons 1 to 27 and the promoter of the human retinoblastoma RB1 gene,
CC used to amplify RB1 exons for use in a method of diagnosing mutations in
CC the RB1 gene. By comparing the lengths of amplification products of RB
CC exons from a suspected RB patient with those of RB wild-type DNA,
CC patients can be diagnosed early which may avoid the need for
CC radiotherapy. Any difference in length of exons between a suspected RB
CC patient and those from wild-type RB1 indicates either a deletion or
CC insertion mutation. Further sequencing of suspect exons can pinpoint the
CC mutation. The method is directed to the diagnosis of and targeted genetic
CC screening for retinoblastoma in family members of a retinoblastoma
CC patient

XX Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 2; Length 21;
Best Local Similarity 72.2%; Pred. No. 8.4e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAGUUCGCCGACAGGCAC 19
Db 4 CCAGTTCCCGACAGACGC 21

RESULT 5

ADP66743/c

ID ADP66743 standard; cDNA; 18 BP.

XX ADP66743;

XX 09-SEP-2004 (first entry)

XX Mouse KIAA0377 forward primer.

XX ss; acid phosphatase; BT42-I; BT42; histidine acid phosphatase;
KW hydrolysis; phosphate ester; BT42-II; deletion; fasting;
KW genetically induced; obesity; isoform; metabolic disease; dysfunction;
KW metabolic syndrome; obesity; diabetes; eating disorder; cachexia;
KW hypertension; coronary heart disease; hypercholesterolaemia;
KW dyslipidemia; osteoarthritis; gallstone; liver fibrosis; primer.

XX Mus sp.

XX WO2004050007-A2.

XX 17-JUN-2004.

XX 01-DEC-2003; 2003WO-EP013521.

XX 29-NOV-2002; 2002EP-00026693.

XX (DEVE-) DEVELOGEN AG.

XX Schreiter K;

XX WPI; 2004-460971/43.

XX New pharmaceutical composition comprising a BT-42 homologous protein or
PT nucleic acid, and carriers, diluents or/and additives, useful for
PT treating obesity, hyperlipidemia, osteoarthritis, cell masses.

XX Example 4; Page 39; 79pp; English.

XX This sequence is a primer which was used in the amplification of the
CC mouse KIAA0377 coding sequence. KIAA0377 is homologous to human BT42.
CC BT42 contains the central signature of a histidine acid phosphatase,
CC which are known to hydrolyze phosphate ester at low pH and are able to
CC use a wide spectrum of substrates. The two BT42 isoforms of the
CC invention, BT42-I hypercholesterolaemia of 40 amino acids compared to
CC mouse BT42. Also BT42-II contains an additional exon of 40 amino acids.
CC BT42 is regulated by fasting and by genetically induced obesity. BT42,
CC and the disclosed isoforms, may be used for the manufacture of an agent
CC for detecting or/and verifying, for the treatment, alleviation and/or
CC prevention of metabolic diseases or dysfunctions, including metabolic
CC syndrome, obesity or/and diabetes, as well as related disorders such as
CC eating disorder, cachexia, hypertension, coronary heart disease, or liver
CC hypercholesterolaemia, dyslipidemia, osteoarthritis, gallstones, or liver
CC fibrosis, in cells, cell masses, organs and/or subjects in vivo or in
CC vitro . The BT42 nucleic acid molecule and polypeptide are useful for the
CC manufacture of a medicament for the treatment of obesity, diabetes, a
CC or/and metabolic syndrome for controlling the function of a gene or/and a
CC gene product, which is influenced or/and modified by a BT42 homologous
CC polypeptide, for identifying substances capable of interacting with a
CC BT42 homologous polypeptide, and for the production of a non-human
CC transgenic animal which over- or under-expresses the BT42.

XX Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;


```

XX AC
XX XX
DT DT
DE DE
XX XX
KW KW
KW KW
KW KW
XX XX
OS OS
XX XX
PN PN
XX XX
PD PD
XX XX
PF PF
XX XX
PR PR
XX XX
PA PA
XX XX
PI PI
XX XX
DR DR
XX XX
PT PT
PT PT
XX XX
PS PS
XX XX
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
CC CC
XX XX
SQ SQ

Query Match 61.0%; Score 12.8; DB 12; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAGG 16
Db 16 GCCAGTTCACAGG 1

RESULT 6
AAT11532
ID AAT11532 standard; DNA; 19 BP.
XX XX
AC AAT11532;
XX XX
DT 10-SEP-1996 (first entry)
XX XX
DE Retinoblastoma gene, RB1, exon 1 PCR 5' primer.
XX XX
KW Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;
KW mutation; polymerase chain reaction; PCR; ss.
XX XX
OS Synthetic.
XX XX
PN WO9601908-A1.
XX XX
PD 25-JAN-1996.
XX XX
PF 07-JUL-1995; 95WO-US008604.
XX XX
PR 08-JUL-1994; 94US-00271942.
XX XX
PA (VISI-) VISIBLE GENETICS INC.
PA (HSCR-) HSC RES & DEV LP.
XX XX
PI Gallie BL, Dunn JM, Stevens JK, Hui M;
XX XX
DR WPI; 1996-097637/10.
XX XX
PT Identifying mutation(s) in RB1 exons by quantitative amplification - and
PT by comparing length of amplification products and sequencing, for
PT diagnosis and genetic screening of retinoblastoma.
XX XX
PS Claim 12; Page 14; 48pp; English.
XX XX
CC AAT11532 is a PCR amplification primer used for the amplification of exon
CC 1 of the human retinoblastoma RB1 gene. This primer and many other
CC primers (see AAT11420-T11473) are used to amplify RB1 exons for use in a
CC method of diagnosing mutations in the RB1 gene. By comparing the lengths
CC of amplification products of RB exons from a suspected RB patient with
CC those of RB wild-type DNA, patients can be diagnosed early which may
CC avoid the need for radiotherapy. Any difference in length of exons
CC between a suspected RB patient and those from wild-type RB1 indicates
CC either a deletion or insertion mutation. Further sequencing of suspect
CC exons can pinpoint the mutation. The method is directed to the diagnosis
CC of and targeted genetic screening for retinoblastoma in family members of
CC a retinoblastoma patient
XX XX
SQ Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCGACAGGC 17
Db 4 CCAGTTCACAGAC 19

RESULT 7
AAT12851
ID AAT12851 standard; DNA; 19 BP.
```

```

XX AAT12851;
XX 22-OCT-1996 (first entry)
DT PCR 5' primer for exon 1 of human RB1 (retinoblastoma-1) gene.
DE PCR; polymerase chain reaction; retinoblastoma; tumour suppressor;
XX cancer; mutation; identification; diagnosis; cystic fibrosis;
KW hierarchy assay; method; specificity; ss.
KW Homo sapiens.
XX WO9607761-A2.
XX 14-MAR-1996.
XX 07-JUL-1995; 95WO-US008606.
XX 08-JUL-1994; 94US-00271946.
XX (VISI-) VISIBLE GENETICS INC.
XX Dunn JM, Stevens JK, Capatos D, Matthews DE;
PI WPI; 1996-171632/17.
DR Testing for a disease-associated mutation in a gene - using a hierarchy
XX of tests selected to optimise performance while minimising cost.
XX Example 1; Page 32; 63pp; English.
XX AAT12839-T12899 (excluding AAT12878) are PCR primers used to amplify
CC various regions of the RB-1 genome, including exons 1-27, the promoter
CC region and a control sequence unrelated to RB-1 from chromosome 15. The
CC primers are used in an example of a method for testing a disease-
CC associated mutation in a gene, the gene may not necessarily be a tumour
CC suppressor gene like the retinoblastoma gene another example is the
CC cystic fibrosis transmembrane conductance regulator (CFTR) gene which may
CC be analysed using the same method. The primers are used in various
CC groupings to produce a hierarchical assay useful to test a group of
CC patients suspected to have a genetic mutation. The method allows the
CC optimum (or near optimum) diagnostic algorithm by considering the cost
CC and the sensitivity and specificity of each test
XX Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 U; 0 Other;
SQ

Query Match 61.0%; Score 12.8; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCGACAGGC 17
Db 4 CCAGTTCACAGAC 19

RESULT 8
AAQ86849
ID AAQ86849 standard; DNA; 20 BP.
XX AAQ86849;
XX 13-DEC-1995 (first entry)
DT Antisense oligonucleotide ISIS 8363 hybridises to MRP gene.
XX Untranslated region; coding sequence; chemotherapeutic drug treatment;
KW antisense; modulation; multidrug resistance protein; drug; cancer; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_feature 1. .20
FT
```


FT /*tag= a
FT /note= "contains phosphorothioate internucleotide
XX linkages"
PN WO9510938-A1.
XX
PD 27-APR-1995.
XX
XX
PF 23-SEP-1994; 94WO-US010827.
XX
XX 18-OCT-1993; 93US-00136811.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Baracchini E, Bennett CF;
PI WPI; 1995-169974/22.
XX
XX New oligo:nucleotide cpds., esp. for cancer therapy - which are
PT specifically hybridisable with nucleic acid encoding multi:drug
PT resistance-associated protein.
XX
XX Claim 7; Page 11; 36pp; English.
XX
XX Oligonucleotides AAQ86826-50 are antisense oligonucleotides used to
CC modulate the expression of the multidrug resistance protein (MRP) by
CC hybridising with the multidrug resistance (MDR) gene or its RNA message.
CC This sequence is targeted to the 3' untranslated region (3'UTR) of the
CC MDR gene. The oligonucleotides can be used to improve the efficacy of
CC chemotherapeutic drug treatment of a disease such as cancer or to prevent
CC multidrug resistance developing during drug treatment of a disease
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCAGUUCGCCGACAGG 16
|||||:|||||
Db 5 GCCAGTTCAGGCAGG 20
RESULT 9
AAV53600
ID AAV53600 standard; DNA; 20 BP.
XX
AC AAV53600;
XX
DT 25-MAR-2003 (revised)
DT 20-NOV-1998 (first entry)
DE Nucleotide sequence of a phosphorothioate oligonucleotide 24.
XX
KW Phosphorothioate oligonucleotide; antisense; inhibition; cancer;
KW multidrug resistance; multi-resistant protein; MRP; chemotherapy; human;
KW leukotriene; inflammatory condition; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "phosphorothioate backbone"
XX
PN US5801154-A.
XX
PD 01-SEP-1998.
XX
XX
PF 08-APR-1997; 97US-00835770.
XX
XX 18-OCT-1993; 93US-00136811.

PR 16-APR-1996; 96US-00628731.
XX (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Baracchini E;
XX
XX WPI; 1998-494825/42.
XX
XX
PT Anti:sense oligo:nucleotide(s) inhibiting multi:drug resistance protein
PT expression - useful for increasing the efficacy of drugs that certain
PT conditions have become resistant to e.g. small cell lung cancer.
XX
XX Claim 11; Col 12; 29pp; English.
XX
XX This is the nucleotide sequence of the phosphorothioate oligonucleotide
CC used in the method of the invention, involving the use of antisense
CC oligonucleotides to inhibit multidrug resistance. The oligonucleotides
CC are used for the antisense inhibition of multi-resistant proteins (MRPs).
CC These proteins are commonly found in some cancers which initially respond
CC to chemotherapy, but overexpression of the protein leads to chemotherap
CC drug resistance. They are administered with the drugs to attempt to
CC enhance efficacy of the drugs. MRPs are also expressed in other ailments,
CC and as such, the oligonucleotides can be used to treat these conditions,
CC as well. The sequences are based on the human MRP and are used to treat
CC conditions such as cancers, especially small-cell lung cancer, prevention
CC of development of multidrug resistance during chemotherapy, and treatment
CC of conditions characterised by leukotriene production, especially
CC inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCAGUUCGCCGACAGG 16
|||||:|||||
Db 5 GCCAGTTCAGGCAGG 20
RESULT 10
ADQ31737/c
ID ADQ31737 standard; DNA; 21 BP.
XX
AC ADQ31737;
XX
DT 21-OCT-2004 (first entry)
XX
DE Multiplex amplification of human SNP fragments, primer #153.
XX
KW Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX US2004146866-A1.
XX
PD 29-JUL-2004.
XX
XX
PF 24-JAN-2003; 2003US-00349780.
XX
XX 24-JAN-2003; 2003US-00349780.
XX
XX (FUGG/) FU G.
XX
XX Fu G;
XX
XX WPI; 2004-552653/53.
XX
XX Analyzing multiple targets in polynucleotide, by providing multiple
PT primers with target nucleic acids, digesting nucleic acid products with
PT cognate restriction enzymes, amplifying digested products, and detecting

DR 03-JUL-2002; 2002US-00189359.
XX (TEXA) UNIV TEXAS SYSTEM.
PA (INSP) INST PASTEUR.
XX Martin A, Sangar DV, Lemon SM, Rijnbrand R;
PI WPI; 2004-091362/09.
XX
XX New chimeric GBV-B polynucleotide, useful as a model for hepatitis C
PT virus, for identifying compounds active against a viral infection, or for
PT developing hepatitis C virus preventive and therapeutic treatments.
XX
PS Example 24; SEQ ID NO 16; 108pp; English.
XX
CC This invention relates to novel isolated chimeric GB virus B (GBV-B)/HCV
CC polynucleotides. Specifically, it refers to using the hepatotropic
CC flavivirus GBV-B that has a unique phylogenetic relationship to the human
CC hepatitis C virus (HCV) and can serve as a surrogate virus in drug
CC discovery efforts related to antiviral drug development. The present
CC invention describes the construction of an infectious molecular clone
CC using the newly determined 3' terminal sequence of GBV-B. Furthermore,
CC the GBV-B/HCV chimeras exhibit liver-specific expression and express HCV
CC envelope proteins such that they can have utility as a vaccine immunogen
CC for hepatitis C. In addition, they can be used for screening compounds
CC active against viral infection, as well as for developing HCV
CC preventative and therapeutic treatments. Accordingly, these compositions
CC exhibit virucidal, antiinflammatory and hepatotropic activities. This
CC oligonucleotide sequence is a PCR primer used to amplify the GBV-B NS5A
CC gene sequence of the invention. NOTE: This sequence is given as SeqID 16
CC in the sequence listing but is referred to as SeqID 15 in example 24.
XX
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 12; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.7e+04;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUUCGCCGACAGGCACT 20
|||:|||||
Db 1 CCAGTTCGGGCAAGAACT 19

RESULT 13
ADJ64258
ID ADJ64258 standard; DNA; 19 BP.
XX
AC ADJ64258;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hepatitis GB virus B nucleic acid detection primer seqid 16.
XX
KW antiinflammatory; hepatotropic; virucide; GB virus B; GBV-B;
KW hepatitis C virus; HCV; 3' terminal; hepatitis C virus; HCV; primer; ss;
KW PCR.
XX
OS Hepatitis GB virus B.
XX
XX US2004039187-A1.
PN
XX
PD 26-FEB-2004.
XX
PF 03-JUL-2002; 2002US-00189359.
XX
PR 04-JUN-1999; 99US-0137665P.
PR 05-JUN-2000; 2000US-00587653..
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA (INSP) INST PASTEUR.
XX
PI Martin A, Sangar DV, Lemon SM, Rijnbrand R;
XX

DR WPI; 2004-203294/19.
XX
PT New GB virus B and/or hepatitis C virus (HCV) sequences, useful in
PT diagnosing and in treating HCV and in investigating the mechanisms for
PT the different biological properties of the viruses.
XX
XX Example 24; SEQ ID NO 16; 58pp; English.
XX
CC The invention describes a new isolated polynucleotide (I) encoding a 3'
CC sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric
CC GBV-B genome, where at least part, but not all of a 5' nontranslated
CC region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR.
CC (I) is a GB virus B and/or hepatitis C virus polynucleotide comprising a
CC fully defined of 260 or 9399 bp (SEQ ID NOS: 1 or 2). The polynucleotides
CC or chimaeras are useful diagnosing or treating hepatitis C virus (HCV)
CC and in investigating the mechanisms for the different biological
CC properties of the viruses. This sequence represents a primer used to
CC detect a chimeric virus comprising domain III of the 5'NTR of HCV (IRES)
CC within a genetic background of GBV-B.
XX
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 12; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.7e+04;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCAGUUCGCCGACAGGCACT 20
|||:|||||
Db 1 CCAGTTCGGGCAAGAACT 19

RESULT 14
ADK94393/c
ID ADK94393 standard; DNA; 20 BP.
XX
AC ADK94393;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #113.
XX
KW human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS Synthetic.
XX
PN JP2003259875-A.
XX
PD 16-SEP-2003.
XX
PF 08-MAR-2002; 2002JP-00064373.
XX
PR 08-MAR-2002; 2002JP-00064373.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2004-093977/10.
DR
XX
PT Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
PS Claim 2; SEQ ID NO 3422; 2627pp; Japanese.
XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 12; Length 20;
Best Local Similarity 73.7%; Pred. No. 1.7e+04;

us-10-774-721-38.rng

Fri Aug 19 08:52:58 2005

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CCAGUUCGACAGGCACT 20
Db 20 CCGATCCCGCCAGCCACT 2
Search completed: August 18, 2005, 06:25:08
Job time : 231 secs

RESULT 15
ADP78935/c
ID ADP78935 standard; DNA; 20 BP.
XX
AC ADP78935;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2734.
XX
DE GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..4 /*tag= a
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT modified_base 17..20 /*tag= b
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT
FT
XX WO2004035763-A2.
XX
XX 29-APR-2004.
PD
XX
XX 02-OCT-2003; 2003WO-US033332.
PF
XX
XX 17-OCT-2002; 2002US-0419268P.
PR
XX (PHAA) PHARMACIA CORP.
XX
XX Broschat KO, Crosby SD;
PI
XX WPI; 2004-348453/32.
DR
XX
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
PT ischemia/reperfusion injury.
XX
PS Claim 4; SEQ ID NO 2734; 175pp; English.
XX
XX The present invention relates to a compound which specifically hybridizes
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of
CC modulating the expression of GFAT, and which comprise any of the 3063
CC sequences of 20 base pairs, given in the specification. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.
CC They are also useful in research and diagnostics for modulating the
CC expression of GFAT. The present sequence represents a chimeric
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
CC oligonucleotides inhibit human GFAT expression.
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 12; Length 20;
Best Local Similarity 73.7%; Pred. NO. 1.7e+04;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:25:21 ; Search time 72.5 Seconds
(without alignments)
473.956 Million cell updates/sec

Title: US-10-774-721-38
Perfect score: 21
Sequence: 1 gccaguuccgacaggcactt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

. Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
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| C 1 | 13.2 | 62.9 | 19 | 3 | US-08-637-732A-26 |
| 2 | 13.2 | 62.9 | 21 | 1 | US-08-271-942A-57 |
| 3 | 13.2 | 62.9 | 21 | 3 | US-08-779-916A-57 |
| 4 | 13.2 | 62.9 | 21 | 5 | PCT-US95-08604-57 |
| 5 | 12.8 | 61.0 | 19 | 1 | US-08-271-946A-13 |
| 6 | 12.8 | 61.0 | 19 | 1 | US-08-271-942A-13 |
| 7 | 12.8 | 61.0 | 19 | 3 | US-08-779-916A-13 |
| 8 | 12.8 | 61.0 | 19 | 3 | US-08-750-232-13 |
| 9 | 12.8 | 61.0 | 19 | 5 | PCT-US95-08604-13 |
| 10 | 12.8 | 61.0 | 19 | 5 | PCT-US95-08606-13 |
| 11 | 12.8 | 61.0 | 20 | 1 | US-08-136-811-24 |
| 12 | 12.8 | 61.0 | 20 | 1 | US-08-835-770-24 |
| 13 | 12.8 | 61.0 | 20 | 1 | US-08-628-731-24 |
| 14 | 12.2 | 58.1 | 17 | 3 | US-09-275-680-7 |
| C 15 | 12.2 | 58.1 | 20 | 3 | US-09-366-257-38 |
| C 16 | 12 | 57.1 | 20 | 3 | US-09-366-257-12 |
| C 17 | 11.8 | 56.2 | 17 | 3 | US-09-375-318-50 |
| 18 | 11.8 | 56.2 | 20 | 3 | US-09-844-634-62 |
| 19 | 11.8 | 56.2 | 20 | 4 | US-10-177-573-15 |
| 20 | 11.6 | 55.2 | 18 | 2 | US-08-897-340-26 |
| 21 | 11.6 | 55.2 | 18 | 3 | US-09-252-329-26 |
| 22 | 11.6 | 55.2 | 20 | 3 | US-09-418-641-23 |
| 23 | 11.6 | 55.2 | 21 | 4 | US-09-693-205A-34 |
| 24 | 11.4 | 54.3 | 15 | 3 | US-09-054-832-27 |
| 25 | 11.4 | 54.3 | 15 | 4 | US-09-640-953-27 |
| 26 | 11.4 | 54.3 | 18 | 3 | US-09-054-830-17 |
| C 27 | 11.4 | 54.3 | 18 | 3 | US-09-658-679A-5 |

| | | | | | | |
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| 28 | 11.4 | 54.3 | 18 | 4 | US-09-431-385-17 | Sequence 17, Appl |
| 29 | 11.4 | 54.3 | 20 | 2 | US-08-229-528-42 | Sequence 42, Appl |
| 30 | 11.4 | 54.3 | 20 | 4 | US-09-657-346A-126 | Sequence 126, App |
| C 31 | 11.4 | 54.3 | 21 | 1 | US-08-116-389-4 | Sequence 4, Appli |
| 32 | 11.4 | 54.3 | 21 | 1 | US-08-066-325-46 | Sequence 46, Appl |
| C 33 | 11.4 | 54.3 | 21 | 1 | US-08-708-431-4 | Sequence 4, Appli |
| C 34 | 11.4 | 54.3 | 21 | 1 | US-08-912-976-3 | Sequence 3, Appli |
| C 35 | 11.4 | 54.3 | 21 | 2 | US-08-880-830-4 | Sequence 4, Appli |
| 36 | 11.4 | 54.3 | 21 | 4 | US-09-657-472-1648 | Sequence 1648, Ap |
| C 37 | 11.4 | 54.3 | 21 | 5 | PCT-US94-13895-4 | Sequence 4, Appli |
| 38 | 11.2 | 53.3 | 17 | 1 | US-08-369-796-19 | Sequence 19, Appl |
| 39 | 11.2 | 53.3 | 17 | 2 | US-08-852-091-19 | Sequence 19, Appl |
| 40 | 11.2 | 53.3 | 17 | 5 | PCT-US95-17025-19 | Sequence 19, Appl |
| 41 | 11.2 | 53.3 | 18 | 1 | US-08-484-816-23 | Sequence 23, Appl |
| 42 | 11.2 | 53.3 | 18 | 1 | US-08-476-625-23 | Sequence 23, Appl |
| 43 | 11.2 | 53.3 | 18 | 2 | US-08-949-076-23 | Sequence 23, Appl |
| 44 | 11.2 | 53.3 | 18 | 2 | US-08-484-519-23 | Sequence 23, Appl |
| 45 | 11.2 | 53.3 | 20 | 2 | US-08-651-692-19 | Sequence 19, Appl |

ALIGNMENTS

RESULT 1
US-08-637-732A-26/c
; Sequence 26, Application US/08637732A
; Patent No. 6268171
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas F.F.
; APPLICANT: Rudel, Thomas
; APPLICANT: Ryll, Roland R.
; APPLICANT: Scheuerfleug, Ina B.
; TITLE OF INVENTION: Recombinant Pilc Proteins, Process for
; TITLE OF INVENTION: Producing Them and Their Use
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,732A
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 147-155P(PCT)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer T60"
US-08-637-732A-26

Query Match 62.9%; Score 13.2; DB 3; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCAGUCCCCGACAGGCA 18


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; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08604
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
; PCT-US95-08604-57

Query Match 62.9%; Score 13.2; DB 5; Length 21;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCAGUUCGCGACAGGC 19
Db 4 CCAGTCCCCACAGCG 21

RESULT 5
US-08-271-946A-13
; Sequence 13, Application US/08271946A
; Patent No. 5545527
; GENERAL INFORMATION:
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
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; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
; US-08-271-946A-13

Query Match 61.0%; Score 12.8; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCGCGACAGGC 17
Db 4 CCAGTCCCCACAGAC 19

RESULT 6
US-08-271-942A-13
; Sequence 13, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
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; APPLICATION NUMBER: US/08/271,942A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
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US-08-750-232-13

Query Match 61.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCCGACAGGC 17
||||:|||||
Db 4 CCAGTCCCCACAGAC 19

RESULT 9
PCT-US95-08604-13
; Sequence 13, Application PC/TUS9508604
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: HSC Research and Development Limited Partnership
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08604
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,942
; APPLICATION NUMBER: 08-JUL-1994
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
; PCT-US95-08604-13

Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCCGACAGGC 17
||||:|||||
Db 4 CCAGTCCCCACAGAC 19

RESULT 10
PCT-US95-08606-13
; Sequence 13, Application PC/TUS9508606
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/271,946
; APPLICATION NUMBER: 08-JUL-1994
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
; PCT-US95-08606-13

Query Match 61.0%; Score 12.8; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAGUUCCGACAGGC 17
||||:|||||
Db 4 CCAGTCCCCACAGAC 19

RESULT 11
US-08-136-811-24
; Sequence 24, Application US/08136811
; Patent No. 5510239
; GENERAL INFORMATION:
; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
; APPLICANT: Clarence Frank

Fri Aug 19 08:52:58 2005

; TITLE OF INVENTION: Oligonucleotide Interference with
; TITLE OF INVENTION: Multidrug Resistance
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,811
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-136-811-24

Query Match 61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAGG 16
|||||:| | | |
Db 5 GCCAGTTCGAGCAGG 20

RESULT 12
US-08-835-770-24
; Sequence 24, Application US/08835770
; Patent No. 5801154
; GENERAL INFORMATION:
; APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett
; APPLICANT: and Nicholas M. Dean
; TITLE OF INVENTION: Oligonucleotide Modulation of Multidrug
; TITLE OF INVENTION: Resistance-Associated Protein
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,770
; FILING DATE: Herewith
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,811
; FILING DATE: 10/18/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/628,731
; FILING DATE: 04/16/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-835-770-24

Query Match 61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGUUCGACAGG 16
|||||:| | | |
Db 5 GCCAGTTCGAGCAGG 20

RESULT 13
US-08-628-731-24
; Sequence 24, Application US/08628731
; Patent No. 5807838
; GENERAL INFORMATION:
; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
; APPLICANT: Clarence Frank
; TITLE OF INVENTION: Oligonucleotide Interference with
; TITLE OF INVENTION: Multidrug Resistance
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,731
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,811
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear


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; ANTI-SENSE: Yes
US-08-628-731-24

Query Match      61.0%; Score 12.8; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCCAGUUCGCCGACAGG 16
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Db      5 GCCAGTTCCAGGCAGG 20

RESULT 14
US-09-275-680-7/c
; Sequence 7, Application US/09275680
; Patent No. 6221630
; GENERAL INFORMATION:
; APPLICANT: Hopper, James E
; TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
; TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
; TITLE OF INVENTION: Yeast
; FILE REFERENCE: 98428
; CURRENT APPLICATION NUMBER: US/09/275,680
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7

Query Match      58.1%; Score 12.2; DB 3; Length 17;
Best Local Similarity 70.6%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db      17 GCCAGTTGTCAACAGGC 1

RESULT 15
US-09-366-257-38/c
; Sequence 38, Application US/09366257
; Patent No. 6030837
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-MITOCHONDRIAL EXPRESSION
; FILE REFERENCE: RTS-0073
; CURRENT APPLICATION NUMBER: US/09/366,257
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-366-257-38

Query Match      58.1%; Score 12.2; DB 3; Length 20;
Best Local Similarity 76.5%; Pred. No. 5.6e+03;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db      20 CAGTGCCCGAGAGACAC 4

Search completed: August 18, 2005, 07:58:56
Job time : 74.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 00:02:48 ; Search time 852 Seconds
(without alignments)
8494.798 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctgcttgccaggctgc.....gttacctgctcatttgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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| 2: | /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:* |
| 3: | /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* |
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| 15: | /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:* |
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| 19: | /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:* |
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| 24: | /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:* |
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| 26: | /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1114 | 100.0 | 1114 | 21 | US-10-956-157-2162 |
| 3 | 1111.6 | 99.8 | 2732 | 9 | US-09-925-302-178 |
| 4 | 1111.6 | 99.8 | 2732 | 10 | US-09-925-302-178 |
| 5 | 1077 | 96.7 | 1156 | 17 | US-10-115-831-161 |
| 6 | 869.6 | 78.1 | 874 | 10 | US-09-993-756A-2 |
| 7 | 768.4 | 69.0 | 207542 | 22 | US-10-893-315-148 |
| | | | | | Sequence 21, Appl |
| | | | | | Sequence 2162, Ap |
| | | | | | Sequence 178, App |
| | | | | | Sequence 178, App |
| | | | | | Sequence 161, App |
| | | | | | Sequence 2, Appli |
| | | | | | Sequence 148, App |

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| 8 | 768.4 | 69.0 | 207557 | 22 | US-10-893-315-134 | Sequence 134, App |
| 9 | 648 | 58.2 | 648 | 21 | US-10-774-721-1 | Sequence 1, Appli |
| 10 | 600 | 53.9 | 600 | 21 | US-10-956-157-7397 | Sequence 7397, Ap |
| 11 | 599.6 | 53.8 | 601 | 22 | US-10-893-315-733 | Sequence 733, App |
| 12 | 577.4 | 51.8 | 647 | 19 | US-10-283-975A-466 | Sequence 466, App |
| 13 | 396 | 35.5 | 396 | 14 | US-10-038-010-23 | Sequence 23, Appli |
| 14 | 396 | 35.5 | 396 | 21 | US-10-774-721-3 | Sequence 3, Appli |
| 15 | 393 | 35.3 | 1128 | 21 | US-10-774-721-7 | Sequence 7, Appli |
| 16 | 393 | 35.3 | 1359 | 21 | US-10-774-721-5 | Sequence 5, Appli |
| 17 | 349.6 | 31.4 | 384 | 17 | US-10-242-535A-41292 | Sequence 41292, A |
| 18 | 349.6 | 31.4 | 384 | 18 | US-10-085-783A-41292 | Sequence 41292, A |
| 19 | 174.6 | 15.7 | 664 | 20 | US-10-842-740-56 | Sequence 56, Appl |
| 20 | 174.6 | 15.7 | 770 | 9 | US-09-984-245-82 | Sequence 82, Appl |
| 21 | 174.6 | 15.7 | 770 | 10 | US-09-966-262-82 | Sequence 82, Appl |
| 22 | 174.6 | 15.7 | 770 | 10 | US-09-983-966-82 | Sequence 82, Appl |
| 23 | 174.6 | 15.7 | 770 | 14 | US-10-059-395-82 | Sequence 82, Appl |
| 24 | 174.6 | 15.7 | 770 | 14 | US-10-143-090-82 | Sequence 82, Appl |
| 25 | 174.6 | 15.7 | 770 | 17 | US-10-264-237-552 | Sequence 552, App |
| 26 | 174.6 | 15.7 | 770 | 21 | US-10-960-251-82 | Sequence 82, Appl |
| 27 | 174.6 | 15.7 | 2694 | 9 | US-09-989-722-275 | Sequence 275, App |
| 28 | 174.6 | 15.7 | 2694 | 9 | US-09-989-723-275 | Sequence 275, App |
| 29 | 174.6 | 15.7 | 2694 | 9 | US-09-989-279-275 | Sequence 275, App |
| 30 | 174.6 | 15.7 | 2694 | 9 | US-09-989-727-275 | Sequence 275, App |
| 31 | 174.6 | 15.7 | 2694 | 9 | US-09-989-731-275 | Sequence 275, App |
| 32 | 174.6 | 15.7 | 2694 | 9 | US-09-989-732-275 | Sequence 275, App |
| 33 | 174.6 | 15.7 | 2694 | 9 | US-09-991-073-275 | Sequence 275, App |
| 34 | 174.6 | 15.7 | 2694 | 9 | US-09-990-442-275 | Sequence 275, App |
| 35 | 174.6 | 15.7 | 2694 | 9 | US-09-991-163-275 | Sequence 275, App |
| 36 | 174.6 | 15.7 | 2694 | 9 | US-09-993-604-275 | Sequence 275, App |
| 37 | 174.6 | 15.7 | 2694 | 9 | US-09-990-456-275 | Sequence 275, App |
| 38 | 174.6 | 15.7 | 2694 | 9 | US-09-989-721-275 | Sequence 275, App |
| 39 | 174.6 | 15.7 | 2694 | 9 | US-09-992-598-275 | Sequence 275, App |
| 40 | 174.6 | 15.7 | 2694 | 9 | US-09-989-293A-275 | Sequence 275, App |
| 41 | 174.6 | 15.7 | 2694 | 9 | US-09-989-735-275 | Sequence 275, App |
| 42 | 174.6 | 15.7 | 2694 | 9 | US-09-990-444-275 | Sequence 275, App |
| 43 | 174.6 | 15.7 | 2694 | 9 | US-09-991-181-275 | Sequence 275, App |
| 44 | 174.6 | 15.7 | 2694 | 9 | US-09-989-730-275 | Sequence 275, App |
| 45 | 174.6 | 15.7 | 2694 | 9 | US-09-990-436-275 | Sequence 275, App |

ALIGNMENTS

RESULT 1
US-10-774-721-21
; Sequence 21, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-774-721-21

Query Match 100.0%; Score 1114; DB 21; Length 1114;
Best Local Similarity 100.0%; Pred. No. 2.6e-309;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 61 | TTCCGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATATCCTTCAGTGGGCTATTGG | 120 |
| Db | 61 | | |
| QY | 121 | ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATATGGCGTTTACTGGCCCTTATT | 180 |
| Db | 121 | | |
| QY | 181 | CGTCCCTGATTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTA | 240 |
| Db | 181 | | |
| QY | 241 | TGACTCAGATGCAACCAAGTAGTGCCTGTCGGAACTGGCATATTTCTTCACTACTGGAAT | 300 |
| Db | 241 | | |
| QY | 301 | TGTTGTTTCTGCCTTTGGATTTCCGTCTGCTGGCTGTGATCAAAATGGG | 360 |
| Db | 301 | | |
| QY | 361 | AGCCTGCGGCCCTTGTGTTGGCAGGCAATGCGATCATTTTCCITTACAATTCGAAGGTTTTT | 420 |
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| QY | 421 | CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTCCTGAT | 480 |
| Db | 421 | | |
| QY | 481 | TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 540 |
| Db | 481 | | |
| QY | 541 | TTACTATGAAATTTAATATGCTGGTTTTTAATACCTTTATATATCATGTTCACTTTAA | 600 |
| Db | 541 | | |
| QY | 601 | GAAAGACTTCATAAGTAGGAGATGAGTTTTATCTCAGCAAATAGACCTGTCAAATTTAG | 660 |
| Db | 601 | | |
| QY | 661 | ATTATGTTACTCAAATFATGTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTCTCAGA | 720 |
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| QY | 721 | AAATATATTAACGCAGTCTTTAGGCAGCTGCCACCCTTATGCAGTGCAATCGAAACCTTTT | 780 |
| Db | 721 | | |
| QY | 781 | GCTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA | 840 |
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| QY | 841 | GGCCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAGTGTGGCCCAACAGAC | 900 |
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| QY | 901 | CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAAATCTGAAACCCCACTCTG | 960 |
| Db | 901 | | |
| QY | 961 | GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCATGAAAGTTTGAGAAGCA | 1020 |
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| QY | 1021 | TCATCATAGAGAAGTAAACATCACACCCCACTTCTTATCTTTCCAGTGGCTAAACCACT | 1080 |
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| QY | 1081 | TAACCTCTCTGGGTGTACCTGCTCATTTTGTTTA | 1114 |
| Db | 1081 | | |

| | | | |
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| Db | 1081 | TAACCTCTCTGGGTGTACCTGCTCATTTTGTTTA | 1114 |
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| QY | 61 | TTCCGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATATCCTTCAGTGGGCTATTGG | 120 |
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| QY | 121 | ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATATGGCGTTTACTGGCCCTTATT | 180 |
| Db | 121 | | |
| QY | 181 | CGTCCCTGATTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTA | 240 |
| Db | 181 | | |
| QY | 241 | TGACTCAGATGCAACCAAGTAGTGCCTGTGGGAACTGGCATATTTCTTCACTACTGGAAT | 300 |
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| QY | 301 | TGTTGTTTCTGCCTTTGGATTTCTGTATTCTTGCTGTGGCTGTGATCAAATGGG | 360 |
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| QY | 361 | AGCCTGCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCGAAGGTTTTT | 420 |
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| QY | 481 | TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 540 |
| Db | 481 | | |
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| QY | 601 | GAAAGACTTCATAAGTAGGAGATGAGTTTTATCTCAGCAAATAGACCTGTCAAATTTAG | 660 |
| Db | 601 | | |
| QY | 661 | ATTATGTTACTCAAATFATGTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTCTCAGA | 720 |
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RESULT 2
US-10-956-157-2162
; Sequence 2162, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2162
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-2162

Query Match 100.0%; Score 1114; DB 21; Length 1114;
Best Local Similarity 100.0%; Pred. No. 2.6e-309;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 61 | | |
| QY | 121 | ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATATGGCGTTTACTGGCCCTTATT | 180 |
| Db | 121 | | |
| QY | 181 | CGTCCCTGATTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTA | 240 |
| Db | 181 | | |
| QY | 241 | TGACTCAGATGCAACCAAGTAGTGCCTGTGGGAACTGGCATATTTCTTCACTACTGGAAT | 300 |
| Db | 241 | | |
| QY | 301 | TGTTGTTTCTGCCTTTGGATTTCTGTATTCTTGCTGTGGCTGTGATCAAATGGG | 360 |
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| QY | 361 | AGCCTGCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCGAAGGTTTTT | 420 |
| Db | 361 | | |
| QY | 421 | CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTCCTGAT | 480 |
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| QY | 481 | TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 540 |
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| QY | 541 | TTACTATGAAATTTAATATGCTGGTTTTTAATACCTTTATATATCATGTTCACTTTAA | 600 |
| Db | 541 | | |
| QY | 601 | GAAAGACTTCATAAGTAGGAGATGAGTTTTATCTCAGCAAATAGACCTGTCAAATTTAG | 660 |
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| QY | 661 | ATTATGTTACTCAAATFATGTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTCTCAGA | 720 |
| Db | 661 | | |

Db 661 ATTATGTTACTCAAAATTATGTTACTTGTGTCGTTCATGTAATCAGGTGCTCTCAGA 720
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Qy 781 GCTTGGGGATGTCTTGGAGAGGCAGATAAACGCTGAAGCAGGCCTCTCATGACCCAGGAA 840
Db 781 GCTTGGGGATGTCTTGGAGAGGCAGATAAACGCTGAAGCAGGCCTCTCATGACCCAGGAA 840
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Db 841 GGCCGGGGTGGATCCCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCACAGAC 900
Qy 901 CAAGAGCCTCAACATTTCCCTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCCACTCTG 960
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Qy 961 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1020
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Db 1021 TCATCATAGAGAAATGTAACATCACACCCAACTTCCCTATCTTTCCAGTGGCTFAAACCACT 1080
Qy 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114
Db 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114

RESULT 3

US-09-925-302-178
; Sequence 178, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1653)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2664)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2699)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-178
Query Match 99.8%; Score 1111.6; DB 9; Length 2732;
Best Local Similarity 99.7%; Pred. No. 2.2e-308;
Matches 1111; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Db 78 CTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 137
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Qy 181 CGTCTGTATTTTCCACGCCCATCTCCCCCATCCCCCATTTCAATTGCCAAAAGAGTCACCTA 240
Db 198 CGTCTGTATTTTCCACGCCCATCTCCCCCATCCCCCATTTCAATTGCCAAAAGAGTCACCTA 257
Qy 241 TGACTCAGATGCAACCCAGTAGTGCCCTGTCCGGAACCTGGCATAATTCTTCACTACTGGAAT 300
Db 258 TGACTCAGATGCAACCCAGTAGTGCCCTGTCCGGAACCTGGCATAATTCTTCACTACTGGAAT 317
Qy 301 TGTTGTTTCTGCCCTTTGGATTTCCTGTTATTCTTGCTCGTGTGGCTGTGATCAAAATGGGG 360
Db 318 TGTTGTTTCTGCCCTTTGGATTTCCTGTTATTCTTGCTCGTGTGGCTGTGATCAAAATGGGG 377
Qy 361 AGCCTGGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCAAGGGTTTTT 420
Db 378 AGCCTGGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCAAGGGTTTTT 437
Qy 421 CCTTATATTTGGAAGAGGAGATGATTTTAGTGGGAGCAGTGGTAGCACTTTATTCTTGAT 480
Db 438 CCTTATATTTGGAAGAGGAGATGATTTTAGTGGGAGCAGTGGTAGCACTTTATTCTTGAT 497
Qy 481 TACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGGCGCATT 540
Db 498 TACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGGCGCATT 557
Qy 541 TTACTATGAAATTTAATATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACTTTAA 600
Db 558 TTACTATGAAATTTAATATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACTTTAA 617
Qy 601 GAAAGACTTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAAATAGACCTGTCAAATTTAG 660
Db 618 GAAAGACTTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAAATAGACCTGTCAAATTTAG 677
Qy 661 ATTATGTTACTCAAATTTATGTTACTTGTGTTGGCTGTTCATGTAGTCACGGTGTCTCAGA 720
Db 678 ATTATGTTACTCAAATTTATGTTACTTGTGTTGGTGTTCATGTAGTCACGGTGTCTCAGA 737
Qy 721 AAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780
Db 738 AAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 797
Qy 781 GCTTGGGGATGTCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA 840
Db 798 GCTTGGGGATGTCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA 857
Qy 841 GGCCGGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCACAGAC 900
Db 858 GGCCGGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCACAGAC 917
Qy 901 CAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCACTCTG 960
Db 918 CAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCACTCTG 977
Qy 961 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1020
Db 978 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1037
Qy 1021 TCATCATAGAGAAATGTAACATCACACCCAACTTCCCTATCTTTCCAGTGGCTFAAACCACT 1080
Db 1038 TCATCATAGAGAAATGTAACATCACACCCAACTTCCCTATCTTTCCAGTGGCTFAAACCACT 1097
Qy 1081 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114
Db 1098 TAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1131

QY 10 GGGCAGGCTGCCCGGCGCTGGGAGGAGCCGGAAGCAGCCGCGGCCCGAGTTCGGGAGA 69
Db 34 GGGCAGGCTGCCCGGCGCTGGGAGGAGCCGGAAGCAGCCGCGGCCCGAGTTCGGGAGA 93
QY 70 CATGGCGGGCGTTAAAGCTTCGTGGCATTTATCCCTCAGTGGGCTATTGGACTGACTTT 129
Db 94 CATGGCGGGCGTTAAAGCTTCGTGGCATTTATCCCTCAGTGGGCTATTGGACTGACTTT 153
QY 130 TCTTATGCTGGGATGTCCTTAGAGGATTATG-----GCCTTACTG 171
Db 154 TCTTATGCTGGGATGTCCTTAGAGGATTATGGCCCTGGGTCCAACCTGACAGCGTTTACTG 213
QY 172 GCCCTTATTCGTCCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAG 231
Db 214 GCCCTTATTCGTCCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAG 273
QY 232 AGTCACCTATGACTCAGATGCAACCAAGTAGTGCCCTGCGGGAAGTGGCATATTTCTTCAC 291
Db 274 AGTCACCTATGACTCAGATGCAACCAAGTAGTGCCCTGCGGGAAGTGGCATATTTCTTCAC 333
QY 292 TACTGGAATTGTTGTTCTGCCCTTTGGATTTCTGTTATTCTTGCTCGTGGCTGTGAT 351
Db 334 TACTGGAATTGTTGTTCTGCCCTTTGGATTTCTGTTATTCTTGCTCGTGGCTGTGAT 393
QY 352 CAAATGGGAGCCTCGCGCCTTGTTGGCAGGCAATGCAGTCATTTTCCCTACAAATTC 411
Db 394 CAAATGGGAGCCTCGCGCCTTGTTGGCAGGCAATGCAGTCATTTTCCCTACAAATTC 453
QY 412 AGGGTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTT 471
Db 454 AGGGTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTT 513
QY 472 TATTCTGATTACAGTGCATTTGAATTTCTTAGAATCATACTATCTGTATACATGTCACA 531
Db 514 TATTCTGATTACAGTGCATTTGAATTTCTTAGAATCATACTATCTGTATACATGTCACA 573
QY 532 TCGGCAATTTTACTATGAATTTAATAATGCTGGGTTTTTAATACCTTTATATATCATGT 591
Db 574 TCGGCAATTTTACTATGAATTTAATAATGCTGGGTTTTTAATACCTTTATATATCATGT 633
QY 592 TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAATAGACCTGT 651
Db 634 TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAATAGACCTGT 693
QY 652 CAAATTTAGATTATGTTACTCAAATTAATGTTACTGTTGGCTGTTTATGATGATCAGGT 711
Db 694 CAAATTTAGATTATGTTACTCAAATTAATGTTACTGTTGGCTGTTTATGATGATCAGGT 753
QY 712 GCTCTCAGAAAATATATTAACGCAGTCTTGTAGGAGCTGCCACCTTATGAGTGCATCG 771
Db 754 GCTCTCAGAAAATATATTAACGCAGTCTTGTAGGAGCTGCCACCTTATGAGTGCATCG 813
QY 772 AAACCTTTTGCTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCATG 831
Db 814 AAACCTTTTGCTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCATG 873
QY 832 ACCCAGGAAGCGCGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTAAAAAGTGTGG 891
Db 874 ACCCAGGAAGCGCGGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTAAAAAGTGTGG 933
QY 892 CCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAAATGCAGAAATCTGAAGC 951
Db 934 CCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAAATGCAGAAATCTGAAGC 993
QY 952 CCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCATGAAAGTT 1011
Db 994 CCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCATGAAAGTT 1053
QY 1012 TGAGAAGCATCATCATAGAGAAGTAAACATCACACCCAACTTCCTTATCTTCCAGTGGC 1071
Db 1054 TGAGAAGCATCATCATAGAGAAGTAAACATCACACCCAACTTCCTTATCTTCCAGTGGC 1113
QY 1072 TAAACCACTTAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114

Db 1114 TAAACCACTTAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1156
RESULT 6
US-09-993-756A-2
; Sequence 2, Application US/09993756A
; Publication No. US20030166847A1
; GENERAL INFORMATION:
; APPLICANT: Akerblom, Ingrid E.
; TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR
; GENE-RELATED PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,756A
; FILING DATE: 05-No. US20030166847A1-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/212,153
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/843,370
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/691,071
; FILING DATE: August 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0111-1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 874 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: HNT2NOT01
; CLONE: 492703
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-993-756A-2

Query Match 78.1%; Score 869.6; DB 10; Length 874;
Best Local Similarity 99.4%; Pred. No. 4.6e-239;
Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTCTGGCTTGGCAGGCTGCCGGGCGCTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 60
Db 1 GTCTGGCTTGGCAGGCTGCCGGGCGCTGGCAGGAAGCSGGAAGCAGCCGCGGCCCCAG 60
QY 61 TTCGGGAGACATGCGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
Db 61 TTCGGGAGACATGCGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
QY 121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGATTATGGCGTTTACTGGCCCTATT 180
Db 121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGATTATGGCGTTTACTGGCCCTATT 180
QY 181 CGTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTCGCAAAAGAGTCACCTA 240

Db 181 CGTCCTGATTTTCCACGGCATCTCCCCCATCCCCCATTTTCATTGCCAAAAAGAGTCACTCA 240

QY 241 TGA CT CAGATGCAACCAAGTAGTGCCCTGTGCGGAACTGGCATATTTCTTCACTACTGGAAT 300

Db 241 TGA CT CAGATGCAACCAAGTAGTGCCCTGTGCGGAACTGGCATATTTCTTCACTACTGGAAT 300

QY 301 TGTGTGTTCTGCCCTTTGGATTCCCTGTTATTTCTTGCTCGTGTGGCTGTGATCAAAATGGGG 360

Db 301 TGTGTGTTCTGCCCTTTGGATTCCCTGTTATTTCTTGCTCGTGTGGCTGTGATCAAAATGGGG 360

QY 361 AGCCTGGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCAGAGGTTT 420

Db 361 AGCCTGGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCAGAGGTTT 420

QY 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATCTGAT 480

Db 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATCTGAT 480

QY 481 TACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 540

Db 481 TACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 540

QY 541 TTACTATGAATTTAATATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600

Db 541 TTACTATGAATTTAATATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600

QY 601 GAAAGACTTCATRAAGTAGGAGATGAGTTTATTTCTCAGCAATFAGACCTGTCAAATTTAG 660

Db 601 GAAAGACTTCATRAAGTAGGAGATGAGTTTATTTCTCAGCAATFAGACCTGTCAAATTTAG 660

QY 661 ATTATGTTACTCAAATTTATGTTACTTGTGCTGTTCAATGATGACGGTGCTCTCAGA 720

Db 661 ATTATGTTACTCAAATTTATGTTACTTGTGCTGTTCAATGATGACGGTGCTCTCAGA 720

QY 721 AAATATATTAACGCAGTCTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780

Db 721 AAATATATTAACGCAGTCTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780

QY 781 GCCTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA 840

Db 781 GCCTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA 840

QY 841 GGCCGGGGTGGATCCCTCTTTGTGTTGTAGTCCA 874

Db 841 GGCCGGGGTGGWTCCCTCTTTKTTTGTAGTCCA 874

RESULT 7

US-10-893-315-148

; Sequence 148, Application US/10893315

; Publication No. US20050147987A1

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL000786

; CURRENT APPLICATION NUMBER: US/10/893,315

; CURRENT FILING DATE: 2004-07-19

; PRIOR APPLICATION NUMBER: 60/231,397

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 2172

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 148

; LENGTH: 207542

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(207542)

; OTHER INFORMATION: n = A,T,C or G

US-10-893-315-148

Query Match 69.0%; Score 768.4; DB 22; Length 207542;

Best Local Similarity 99.2%; Pred. No. 1.5e-208;

Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAAATGGGAGCCCTGCGGCCCTTGTGTTGGCAGCAATGCAGTCAT 396

Db 13025 TCTTGTCTTTCAGATCAAAATGGGAGCCCTGCGGCCCTTGTGTTGGCAGCAATGCAGTCAT 13084

QY 397 TTTCCTTACAATTCAGGGTTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGA 456

Db 13085 TTTCCTTACAATTCAGGGTTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGA 13144

QY 457 GCAGTGGTAGCACCTTTATTTCTGATTACAGTGCAATGAAATTTCTTAGAACTCATACTATCT 516

Db 13145 GCAGTGGTAGCACCTTTATTTCTGATTACAGTGCAATGAAATTTCTTAGAACTCATACTATCT 13204

QY 517 GTATACATGTGCACATGCGSCATTTTACTATGAAATTTAAATATGCTGGGTTTTTAAATAC 576

Db 13205 GTATACATGTGCACATGCGSCATTTTACTATGAAATTTAAATATGCTGGGTTTTTAAATAC 13264

QY 577 CTTTATATATCATGTTTCACTTTTAAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTC 636

Db 13265 CTTTATATATCATGTTTCACTTTTAAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTC 13324

QY 637 AGCAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTGTTTGGCTGT 696

Db 13325 AGCAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTGTTTGGCTGT 13384

QY 697 TCATGTAGTCACGGTGCTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACC 756

Db 13385 TCATGTAGTCACGGTGCTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACC 13444

QY 757 TTATGCAGTGCAATCGAAACCTTTTGTGGGATGTGCTTGGAGAGGCAGATAACGCTGA 816

Db 13445 TTATGCAGTGCAATCGAAACCTTTTGTGGGATGTGCTTGGAGAGGCAGATAACGCTGA 13504

QY 817 AGCAGGCCTCTCATGACCCAGGAAGGCCGGGTGGATCCCTCTTTTGTGTTGTAGTCCATG 876

Db 13505 AGCAGGCCTCTCATGACCCAGGAAGGCCGGGTGGATCCCTCTTTTGTGTTGTAGTCCATG 13564

QY 877 CTATTAAAAAGTGTGGCCACAGACCACAGAGCCCTCAACATTTCTTAGAGCCTTATTAGAAA 936

Db 13565 CTATTAAAAAGTGTGGCCACAGACCACAGAGCCCTCAACATTTCTTAGAGCCTTATTAGAAA 13624

QY 937 TGCAGAAATCTGAAGCCCACTCTGGACCCAGGACATTTTGTAGATCCAAAGGAGTTGT 996

Db 13625 TGCAGAAATCTGAAGCCCACTCTGGACCCAGGACATTTTGTAGATCCAAAGGAGTTGT 13684

QY 997 ATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAAGTAAACATCACACCCCACTTCT 1056

Db 13685 ATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAAGTAAACATCACACCCCACTTCT 13744

QY 1057 TATCTTTCCAGTGGCTAAACCCTTAAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114

Db 13745 TATCTTTCCAGTGGCTAAACCCTTAAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 13802

RESULT 8

US-10-893-315-134

; Sequence 134, Application US/10893315

; Publication No. US20050147987A1

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL000786

; CURRENT APPLICATION NUMBER: US/10/893,315

; CURRENT FILING DATE: 2004-07-19

; PRIOR APPLICATION NUMBER: 60/231,397

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 2172

; SOFTWARE: FastSeq for Windows Version 4.0


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; SEQ ID NO 134
; LENGTH: 207557
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)_(207557)
; OTHER INFORMATION: n = A,T,C or G
US-10-893-315-134
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Query Match 69.0%; Score 768.4; DB 22; Length 207557;
Best Local Similarity 99.2%; Pred. No. 1.5e-208;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 337 TCGTGTGGCTGTGATCAAAATGGGGAGCCTGCGGCCTTGTGTTGGCAGGCAATGCAGTCAT 396
   |||||
Db 13025 TCTTGTCTTTCAGATCAAAATGGGGAGCCTGCGGCCTTGTGTTGGCAGGCAATGCAGTCAT 13084

QY 397 TTTCTTTACAATTCAGGGTTTTTCTTTATATTTTGGAAAGAGAGATGATTTTAGCTGGGA 456
   |||||
Db 13085 TTTCTTTACAATTCAGGGTTTTTCTTTATATTTTGGAAAGAGAGATGATTTTAGCTGGGA 13144

QY 457 GCAGTGGTAGCATTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCT 516
   |||||
Db 13145 GCAGTGGTAGCATTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCT 13204

QY 517 GTATACATGTGCACATGCGGCATTTTACTATGAATTTAATATGCTGGGTTTTTAAATAC 576
   |||||
Db 13205 GTATACATGTGCACATGCGGCATTTTACTATGAATTTAATATGCTGGGTTTTTAAATAC 13264

QY 577 CTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTC 636
   |||||
Db 13265 CTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTC 13324

QY 637 AGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGGCTGT 696
   |||||
Db 13325 AGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGGCTGT 13384

QY 697 TCATGTAGTCACGGTGCTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACC 756
   |||||
Db 13385 TCATGTAGTCACGGTGCTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACC 13444

QY 757 TTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCTGA 816
   |||||
Db 13445 TTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCTGA 13504

QY 817 AGCAGGCCTCTCATGACCCAGGAAGGCCGGGTGGATCCCTCTTTGTGTTGPAGTCCATG 876
   |||||
Db 13505 AGCAGGCCTCTCATGACCCAGGAAGGCCGGGTGGATCCCTCTTTGTGTTGPAGTCCATG 13564

QY 877 CTATTAAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAA 936
   |||||
Db 13565 CTATTAAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAA 13624

QY 937 TGCAGAACTCTGAAGCCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGT 996
   |||||
Db 13625 TGCAGAACTCTGAAGCCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGT 13684

QY 997 ATGCACATGAAAGTTTGAGAAAGCATCATATAGAGAAGTAAACATCACACCAACTTCCT 1056
   |||||
Db 13685 ATGCACATGAAAGTTTGAGAAAGCATCATATAGAGAAGTAAACATCACACCAACTTCCT 13744

QY 1057 TATCTTTCCAGTGGCTAAACCACTTAAACCTCTCTGGGTGTACCTGCTCAATTGTTTA 1114
   |||||
Db 13745 TATCTTTCCAGTGGCTAAACCACTTAAACCTCTCTGGGTGTACCTGCTCAATTGTTTA 13802
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RESULT 9
US-10-774-721-1
; Sequence 1, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf

```
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-774-721-1
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Query Match 58.2%; Score 648; DB 21; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 467 CACTTTATTCGTATTACAGTGCATTGAAATTTCTTAGAACTCATACTATCTGTATACATGT 526
   |||||
Db 1 CACTTTATTCGTATTACAGTGCATTGAAATTTCTTAGAACTCATACTATCTGTATACATGT 60

QY 527 GCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATAT 586
   |||||
Db 61 GCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATAT 120

QY 587 CATGTTCACTTTAAGAAAAGACTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAATAGA 646
   |||||
Db 121 CATGTTCACTTTAAGAAAAGACTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAATAGA 180

QY 647 CCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGGCTGTTTCATGTAGTC 706
   |||||
Db 181 CCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGGCTGTTTCATGTAGTC 240

QY 707 ACGGTGCTCTCAGAAAATATATTAACGCAGTCTGTAGGCAGCTGCCACCTTATGCAGTG 766
   |||||
Db 241 ACGGTGCTCTCAGAAAATATATTAACGCAGTCTGTAGGCAGCTGCCACCTTATGCAGTG 300

QY 767 CATCGAAACCTTTTGTCTGGGATGTGCTTGGAGGCAGATAACGCTGAAGCAGGCCTC 826
   |||||
Db 301 CATCGAAACCTTTTGTCTGGGATGTGCTTGGAGGCAGATAACGCTGAAGCAGGCCTC 360

QY 827 TCATGACCCAGGAAGGCCGGGTGGATCCCTCTTGTGTTGTAGTCCATGCTATTAAAAAG 886
   |||||
Db 361 TCATGACCCAGGAAGGCCGGGTGGATCCCTCTTGTGTTGTAGTCCATGCTATTAAAAAG 420

QY 887 TGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTCT 946
   |||||
Db 421 TGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTCT 480

QY 947 GAAGCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGA 1006
   |||||
Db 481 GAAGCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGA 540

QY 1007 AAGTTTGAGAGCATCATATAGAGAAGTAAACATCACACCAACTTCCTTATCTTTCCA 1066
   |||||
Db 541 AAGTTTGAGAGCATCATATAGAGAAGTAAACATCACACCAACTTCCTTATCTTTCCA 600

QY 1067 GTGGCTAAACCACTTAAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 1114
   |||||
Db 601 GTGGCTAAACCACTTAAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 648
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RESULT 10
US-10-956-157-7397
; Sequence 7397, Application US/10956157
; Publication No. US20050118625A1

```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7397
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-7397

Query Match      53.9%; Score 600; DB 21; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      515 CTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTTAAAT 574
Db      1 CTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTTAAAT 60

QY      575 ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATTC 634
Db      61 ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATTC 120

QY      635 TCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAAATATGTTACTTGTTTGGCT 694
Db      121 TCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAAATATGTTACTTGTTTGGCT 180

QY      695 GTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAACGCAGTCTTGAGGCAGCTGCCA 754
Db      181 GTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAACGCAGTCTTGAGGCAGCTGCCA 240

QY      755 CCTTATGCAGTGCATCGAAACCTTTTGCTTGGGGANGTGCTTGGAGAGGCAGATAACGCT 814
Db      241 CCTTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCT 300

QY      815 GAAGCAGGCTCTCATGACCCAGGAAGGCCGGGGTGATCCCTCTTTGTGTGTAGTCCA 874
Db      301 GAAGCAGGCTCTCATGACCCAGGAAGGCCGGGGTGATCCCTCTTTGTGTGTAGTCCA 360

QY      875 TGCTATTAAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA 934
Db      361 TGCTATTAAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA 420

QY      935 AATGCAGATCTGAAGCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAGTT 994
Db      421 AATGCAGATCTGAAGCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAGTT 480

QY      995 GTATGCATGAAAGTTTGAGAAGCATCATAGAGAAGTAAACATCACACCCCACTTC 1054
Db      481 GTATGCATGAAAGTTTGAGAAGCATCATAGAGAAGTAAACATCACACCCCACTTC 540

QY      1055 CTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGIGTTACTGCTCATTTGTTTA 1114
Db      541 CTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGIGTTACTGCTCATTTGTTTA 600

RESULT 11
US-10-893-315-733
; Sequence 733, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19

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; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 733
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-733

Query Match      53.8%; Score 599.6; DB 22; Length 601;
Best Local Similarity 99.8%; Pred. No. 1.7e-161;
Matches 599; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      515 CTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTTAAAT 574
Db      1 CTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTTAAAT 60

QY      575 ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATTC 634
Db      61 ACCTTTATATATCATGTTTCACCTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATTC 120

QY      635 TCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAAATATGTTACTTGTTTGGCT 694
Db      121 TCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAAATATGTTACTTGTTTGGCT 180

QY      695 GTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAACGCAGTCTTGAGGCAGCTGCCA 754
Db      181 GTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAACGCAGTCTTGAGGCAGCTGCCA 240

QY      755 CCTTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCT 814
Db      241 CCTTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCT 300

QY      815 GAAGCAGGCTCTCATGACCCAGGAAGGCCGGGGTGATCCCTCTTTGTGTGTAGTCCA 874
Db      301 RAAGCAGGCTCTCATGACCCAGGAAGGCCGGGGTGATCCCTCTTTGTGTGTAGTCCA 360

QY      875 TGCTATTAAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA 934
Db      361 TGCTATTAAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGA 420

QY      935 AATGCAGAAATCTGAAGCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAGTT 994
Db      421 AATGCAGAAATCTGAAGCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAGTT 480

QY      995 GTATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCCACTTC 1054
Db      481 GTATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCCACTTC 540

QY      1055 CTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGIGTTACCTGCTCATTTGTTTA 1114
Db      541 CTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGIGTTACCTGCTCATTTGTTTA 600

RESULT 12
US-10-283-975A-466
; Sequence 466, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30

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; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 466
; LENGTH: 647
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(647)
; OTHER INFORMATION: N=any base
US-10-283-975A-466

Query Match 51.8%; Score 577.4; DB 19; Length 647;
Best Local Similarity 98.6%; Pred. No. 4.4e-155;
Matches 644; Conservative 0; Mismatches 3; Indels 6; Gaps 6;

QY 352 CAAATGGGAGCGCTGTGTGGCAGGCAATGCAGTCATTTTCCTTACAATTCA 411
Db 1 CAAATGGGAGCGCTGC-GCCTTGTGTGGCAGGCAATGCAGTCATTTTCCTTACAATTCA 59

QY 412 AGGGTTTTTCCTTATATTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGTAGCACTT 471
Db 60 AGGGTTTTTCCTTATATTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGTAGCACTT 119

QY 472 TATTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACA 531
Db 120 TATTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACA 179

QY 532 TCGGGCATTTTACTATGAAATTTAATAATAGCTGGGTTTTTAAATACCTTTATATATCATGT 591
Db 180 TCGGGCATTTTACTATGAAATTTAATAATAGCTGGGTTTTTAAATACCTTTATATATCATGT 239

QY 592 TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAATPAGACCTGT 651
Db 240 TCACCTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAATPAGACCTGT 299

QY 652 CAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTATGCTAGTCACGGT 711
Db 300 CAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTATGCTAGTCACGGT 359

QY 712 GCTCTCAGAAAAATATATTAAAGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCG 771
Db 360 GCTCTCAGAAAAATATATTAAACAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCG 419

QY 772 AAACCTTTTGTCTGGGATGTGCTTGGAGAGGAGATAACGCTGAAGCAGGCCTCTCATG 831
Db 420 AAACCTTTTGTCTGGGATGTGCTTGGAGAGGAGATAACGCTGAAGCAGGCCTCTCATG 479

QY 832 ACCCAGGAAGCCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAAAGTGTGG 891
Db 480 ACCCAGGAAGCCGGGTGGATCCCT-TTTGTGTGTAGTCCATGC-ATTAAAAAGTGTGG 537

QY 892 CCCACAGACCAAGAGCGCTCAACATTTTCTAGAGCCTTATTAGAAATGCAGAACTGGAAGC 951
Db 538 CCCACAGACCAAGAGCGCTCAACATTTTCTAGAGCCTTATTAGAAATGCAGAACTGGAAG- 596

QY 952 CCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACAT 1004
Db 597 CCCACTCTGGACCCAGGACA-TTTGATGAGATCC-AAAGAGTTGTATGCNCAT 647

RESULT 13
US-10-038-010-23
; Sequence 23, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377

; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(396)
; OTHER INFORMATION: Human OBRGRP
US-10-038-010-23

Query Match 35.5%; Score 396; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 130
Db 1 ATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 60

QY 131 CTTATGCTGGATGTGCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATT 190
Db 61 CTTATGCTGGATGTGCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATT 120

QY 191 TTCCACGCCATCTCCCCCATCCCCCATTTCAFTGCCAAAAAGAGTCACCTATGACTCAGAT 250
Db 121 TTCCACGCCATCTCCCCCATCCCCCATTTCAFTGCCAAAAAGAGTCACCTATGACTCAGAT 180

QY 251 GCAACCAAGTAGTGCCTGTGGGAACCTGGCATATTTCTTCACTACTGGAATTTGTTTCT 310
Db 181 GCAACCAAGTAGTGCCTGTGGGAACCTGGCATATTTCTTCACTACTGGAATTTGTTTCT 240

QY 311 GCCTTTGGATTTCTGTATTCTTGTCTCGTGTGCTGTGATCAAATGGGGAGCCCTGCGGC 370
Db 241 GCCTTTGGATTTCTGTATTCTTGTCTCGTGTGCTGTGATCAAATGGGGAGCCCTGCGGC 300

QY 371 CTTGTGTTGGCAGGCAATGCAGTCATTTTCCITTACAATTCAGGGTTTTTCCTTATATTT 430
Db 301 CTTGTGTTGGCAGGCAATGCAGTCATTTTCCITTACAATTCAGGGTTTTTCCTTATATTT 360

QY 431 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAG 466
Db 361 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAG 396

RESULT 14
US-10-774-721-3
; Sequence 3, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(396)

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; OTHER INFORMATION:
US-10-774-721-3
Query Match          35.5%; Score 396; DB 21; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ATGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 130
Db 1 ATGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 60

QY 131 CTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATT 190
Db 61 CTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATT 120

QY 191 TTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTATGACTCAGAT 250
Db 121 TTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTATGACTCAGAT 180

QY 251 GCAACCACTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 310
Db 181 GCAACCACTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 240

QY 311 GCCTTTGGATTTCCTGTTATTTCTTGCTCGTGTGGTGTGATCAAATGGGAGCCCTGCGGC 370
Db 241 GCCTTTGGATTTCCTGTTATTTCTTGCTCGTGTGGTGTGATCAAATGGGAGCCCTGCGGC 300

QY 371 CTTGTGTTGGCAGGCAATGCAGTCAATTTTCCTTACAATTCAGGGTTTTTCCTTATATTT 430
Db 301 CTTGTGTTGGCAGGCAATGCAGTCAATTTTCCTTACAATTCAGGGTTTTTCCTTATATTT 360

QY 431 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAG 466
Db 361 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAG 396

RESULT 15
US-10-774-721-7
; Sequence 7, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OB RGRP YFP
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: OB RGRP YFP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1128)
; OTHER INFORMATION:
US-10-774-721-7
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Query Match 35.3%; Score 393; DB 21; Length 1128;
Best Local Similarity 100.0%; Pred. No. 6.8e-102;

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Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ATGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 130
Db 1 ATGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 60

QY 131 CTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATT 190
Db 61 CTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATT 120

QY 191 TTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTATGACTCAGAT 250
Db 121 TTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTATGACTCAGAT 180

QY 251 GCAACCACTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 310
Db 181 GCAACCACTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACTACTGGAATTGTTTCT 240

QY 311 GCCTTTGGATTTCCTGTTATTTCTTGCTCGTGTGGTGTGATCAAATGGGAGCCCTGCGGC 370
Db 241 GCCTTTGGATTTCCTGTTATTTCTTGCTCGTGTGGTGTGATCAAATGGGAGCCCTGCGGC 300

QY 371 CTTGTGTTGGCAGGCAATGCAGTCAATTTTCCTTACAATTCAGGGTTTTTCCTTATATTT 430
Db 301 CTTGTGTTGGCAGGCAATGCAGTCAATTTTCCTTACAATTCAGGGTTTTTCCTTATATTT 360

QY 431 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGG 463
Db 361 GGAAGAGGAGATGATTTTAGCTGGGAGCAGTGG 393
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Job time : 860 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | |
|------------|--------|--------------------------|--------------------|
| Result No. | Score | Query Match Length DB ID | Description |
| 1 | 1114 | 100.0 1114 6 CQ716942 | CQ716942 Sequence |
| 2 | 1114 | 100.0 1114 6 CQ860109 | CQ860109 Sequence |
| 3 | 1114 | 100.0 1114 6 CQ878351 | CQ878351 Sequence |
| 4 | 1114 | 100.0 1114 9 HSOBRGRP | Y12670 Homo sapien |
| 5 | 1069 | 96.0 1080 6 CQ783702 | CQ783702 Sequence |
| 6 | 1069 | 96.0 1080 6 BD127789 | BD127789 Primer fo |
| 7 | 1067 | 96.0 1080 9 AK074841 | AK074841 Homo sapi |
| 8 | 1067 | 95.8 2388 6 AX779959 | AX779959 Sequence |
| 9 | 1057.6 | 94.9 1092 9 BC056250 | BC056250 Homo sapi |
| 10 | 1023.4 | 91.9 1056 9 BC011027 | BC011027 Homo sapi |
| 11 | 869.6 | 78.1 874 6 AR020775 | AR020775 Sequence |
| 12 | 869.6 | 78.1 874 6 BD132522 | BD132522 A novel h |
| 13 | 768.4 | 69.0 161112 9 AC119800 | AC119800 Homo sapi |
| 14 | 765.8 | 68.7 1614 9 AK130096 | AK130096 Homo sapi |
| 15 | 648 | 58.2 648 6 CQ860089 | CQ860089 Sequence |
| 16 | 588.4 | 52.8 629 6 CQ780218 | CQ780218 Sequence |
| 17 | 588.4 | 52.8 629 6 CQ781626 | CQ781626 Sequence |
| 18 | 588.4 | 52.8 629 6 BD124927 | BD124927 Primer fo |
| 19 | 588.4 | 52.8 629 6 BD126335 | BD126335 Primer fo |

| | | | | | | |
|----|-------|------|--------|----|-----------|--------------------|
| 20 | 577.4 | 51.8 | 647 | 6 | AX775150 | AX775150 Sequence |
| 21 | 533.2 | 47.9 | 647 | 11 | BV208716 | BV208716 OBRGRP_23 |
| c | 498.4 | 44.7 | 546 | 6 | CQ780977 | CQ780977 Sequence |
| c | 498.4 | 44.7 | 546 | 6 | BD125686 | BD125686 Primer fo |
| 24 | 399.8 | 35.9 | 1966 | 10 | BC062003 | BC062003 Rattus no |
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| 26 | 396 | 35.5 | 396 | 9 | CR541737 | CR541737 Homo sapi |
| 27 | 393 | 35.3 | 393 | 9 | CR541647 | CR541647 Homo sapi |
| 28 | 393 | 35.3 | 1128 | 6 | CQ860095 | CQ860095 Sequence |
| 29 | 393 | 35.3 | 1359 | 6 | CQ860093 | CQ860093 Sequence |
| 30 | 387.6 | 34.8 | 1859 | 10 | BC004744 | BC004744 Mus muscu |
| 31 | 365.2 | 32.8 | 635 | 10 | MMAJ11565 | AJ011565 Mus muscu |
| 32 | 357.4 | 32.1 | 447 | 10 | AF139209 | AF139209 Rattus no |
| 33 | 349.6 | 31.4 | 384 | 6 | CQ696366 | CQ696366 Sequence |
| c | 330.4 | 29.7 | 153350 | 2 | AC108402 | AC108402 Mus muscu |
| c | 330.4 | 29.7 | 187184 | 10 | AC121826 | AC121826 Mus muscu |
| 36 | 275.6 | 24.7 | 3641 | 5 | AJ720495 | AJ720495 Gallus ga |
| 37 | 246.6 | 22.1 | 1815 | 10 | BC010289 | BC010289 Mus muscu |
| 38 | 246 | 22.1 | 246 | 6 | AX677228 | AX677228 Sequence |
| 39 | 245 | 22.0 | 1012 | 5 | CR761280 | CR761280 Xenopus t |
| 40 | 241.8 | 21.7 | 1019 | 5 | BC053822 | BC053822 Xenopus 1 |
| 41 | 238.6 | 21.4 | 1032 | 5 | BC078594 | BC078594 Xenopus 1 |
| 42 | 190.8 | 17.1 | 505 | 11 | G26889 | G26889 human STS S |
| 43 | 185.8 | 16.7 | 2609 | 10 | BC004677 | BC004677 Mus muscu |
| 44 | 184.2 | 16.5 | 3327 | 5 | BC043984 | BC043984 Xenopus 1 |
| 45 | 179.8 | 16.1 | 1167 | 5 | CR385373 | CR385373 Gallus ga |

ALIGNMENTS

RESULT 1
CQ716942
LOCUS CQ716942 1114 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 2876 from Patent WO02068579.
ACCESSION CQ716942
VERSION CQ716942.1 GI:42277799
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 2876 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1..1114
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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|---|-----|--|-----|
| ORIGIN | | | |
| Query Match 100.0%; Score 1114; DB 6; Length 1114; | | | |
| Best Local Similarity 100.0%; Pred. No. 2.4e-290; | | | |
| Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 1 | GTCTGGCTTGGCAGGCTGCCGGCCGTGGCAGGAGCCGGAAGCAGCCGCGGCCCCAG | 60 |
| Db | 1 | GTCTGGCTTGGCAGGCTGCCGGCCGTGGCAGGAGCCGGAAGCAGCCGCGGCCCCAG | 60 |
| QY | 61 | TTCTGGGAGACATGGCGGCGGTTAAAGCTCTCGTGCATTATCTTTCAGTGGGCTATTGG | 120 |
| Db | 61 | TTCTGGGAGACATGGCGGCGGTTAAAGCTCTCGTGCATTATCTTTCAGTGGGCTATTGG | 120 |
| QY | 121 | ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTACTGGCCCTATT | 180 |
| Db | 121 | ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTACTGGCCCTATT | 180 |
| QY | 181 | CGTCTGTATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTTGCCAAAAGATCACCTA | 240 |

Db 721 AAATATATTAAACGAGTCTTGTTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780

Qy 781 GCTTGGGGATGTCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA 840

Db 781 GCTTGGGGATGTCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTCTCATGACCCAGGAA 840

Qy 841 GGCCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAGTGTGGCCCCACAGAC 900

Db 841 GGCCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAGTGTGGCCCCACAGAC 900

Qy 901 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTGGAAGCCCCACTCTG 960

Db 901 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTGGAAGCCCCACTCTG 960

Qy 961 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTGAGAAGCA 1020

Db 961 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTGAGAAGCA 1020

Qy 1021 TCATCATAGAGAACTAAACATCACACCCCACTTCCTTATCTTTCCAGTGGCTAAACCACT 1080

Db 1021 TCATCATAGAGAACTAAACATCACACCCCACTTCCTTATCTTTCCAGTGGCTAAACCACT 1080

Qy 1081 TAACCTCTCTGGGTGTACCTGCTCATTTTGTTTA 1114

Db 1081 TAACCTCTCTGGGTGTACCTGCTCATTTTGTTTA 1114

RESULT 3

CQ878351

LOCUS CQ878351 1114 bp DNA linear PAT 04-OCT-2004

DEFINITION Sequence 4 from Patent WO2004080272.

ACCESSION CQ878351

VERSION CQ878351.1 GI:53790910

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Bailleul,B., Rouille,Y., Seron,K. and Belouzard,S.

TITLE Use of the genes leptotl1 and ob-rgrp for the screening of active compounds for weight gain or loss or diabetes in human or animal subjects

JOURNAL Patent: WO 2004080272-A 4 23-SEP-2004;

FEATURES

source Location/Qualifiers

1. .1114

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/note="unnamed protein product; Cadre de lecture codant la OB-RGRP humaine"

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ORIGIN

Query Match 100.0%; Score 1114; DB 6; Length 1114;

Best Local Similarity 100.0%; Pred. No. 2.4e-290;

Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTCTGGCTTGGCAGGCTGCCCGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGCCCCCAG 60

Qy 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120

Db 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120

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Db 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180

Qy 181 CGTCTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTGCCCCAAAAGAGTCACCTA 240

Db 181 CGTCTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTGCCCCAAAAGAGTCACCTA 240

Qy 241 TGACTCAGATGCAACACAGTAGTGCCTGTGCGGGAACTGGCATATTTCTTTCACACTACTGGAAT 300

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Db 361 AGCCTGCGGCTTGTGTTGGCAGGCAATGTCAGTCAATTTCTTTACAATTCAGGGGTTTTT 420

Qy 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480

Db 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480

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Db 901 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAACTGGAAGCCCCACTCTG 960

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Qy 1021 TCATCATAGAGAACTAAACATCACACCCCACTTCCTTATCTTTCCAGTGGCTAAACCACT 1080

Db 1021 TCATCATAGAGAACTAAACATCACACCCCACTTCCTTATCTTTCCAGTGGCTAAACCACT 1080

Qy 1081 TAACCTCTCTGGGTGTACCTGCTCATTTTGTTTA 1114

Db 1081 TAACCTCTCTGGGTGTACCTGCTCATTTTGTTTA 1114

| | | | | | |
|----------------------------|--|------------|------|--------|-----------------|
| LOCUS | HSOBRGRP | 1114 bp | mRNA | linear | PRI 09-SEP-2004 |
| DEFINITION | Homo sapiens mRNA for leptin receptor gene-related protein. | | | | |
| ACCESSION | Y12670 | | | | |
| VERSION | Y12670.1 | GI:2266637 | | | |
| KEYWORDS | leptin receptor gene-related protein; OB-R gene related protein; OB-RGRP. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| REFERENCE | 1 Bailleul,B., Akerblom,I. and Strosberg,A.D. | | | | |
| AUTHORS | The leptin receptor promoter controls expression of a second | | | | |
| TITLE | distinct protein | | | | |
| JOURNAL | Nucleic Acids Res. 25 (14), 2752-2758 (1997) | | | | |
| MEDLINE | 97351143 | | | | |
| PUBMED | 9207021 | | | | |
| REFERENCE | 2 (bases 1 to 1114) | | | | |
| AUTHORS | Bailleul,B.R.P. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (17-APR-1997) B.R.P. Bailleul, UPR 0415 CNRS, 22 Rue | | | | |
| | Mechain, 75014 Paris, FRANCE | | | | |
| COMMENT | This is a splice variant from the leptin receptor locus but this variant encodes for a unrelated leptin receptor protein transcribed from one promoter of the leptin receptor locus. | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| | /number=1 | | | | |
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| exon | 87..162 | | | | |
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| Query Match | 100.0%; Score 1114; DB 9; Length 1114; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 2.4e-290; | | | | |
| Matches 1114; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
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| | | | | | |
| Db | 1 GTCTGGCTTGGCAGGCTGCCCGGCGGTGGCAGGAGCCGGAAGCAGCGCGGCCCCAG 60 | | | | |
| | | | | | |
| Qy | 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTTATCCTTCAGTGGGGCTATTGG 120 | | | | |
| | | | | | |
| Db | 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTTATCCTTCAGTGGGGCTATTGG 120 | | | | |
| | | | | | |

| | | | | |
|----|------|---------|--|------|
| Qy | 121 | ACTGAC | TTTCTTATGCTGGGATGCGCTTAGAGGATTATGGCCTTACTGGCCCTTATT | 180 |
| Db | 121 | ACTGAC | TTTCTTATGCTGGGATGCGCTTAGAGGATTATGGCCTTACTGGCCCTTATT | 180 |
| Qy | 181 | CGTCCT | GATTTTCACGCCATCTCCCCATCCCATTTTCATTGCAAAAGAGTCACCTA | 240 |
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| Qy | 241 | TGACTC | AGATGCAACCAAGTAGTGCCCTGCGGAACTGGCATATTTCTTCACTACTGGAAT | 300 |
| Db | 241 | TGACTC | AGATGCAACCAAGTAGTGCCCTGCGGAACTGGCATATTTCTTCACTACTGGAAT | 300 |
| Qy | 301 | TGTTGTT | CTGCGCTTTGGATTTCTGTTATTTCTGCTCGTGGTGTGATCAAAATGGGG | 360 |
| Db | 301 | TGTTGTT | CTGCGCTTTGGATTTCTGTTATTTCTGCTCGTGGTGTGATCAAAATGGGG | 360 |
| Qy | 361 | AGCCTG | CGGCTTGTGTTGGCAGGCAATGCAGTCATTTCTTACAATTCAGGGTTTT | 420 |
| Db | 361 | AGCCTG | CGGCTTGTGTTGGCAGGCAATGCAGTCATTTCTTACAATTCAGGGTTTT | 420 |
| Qy | 421 | CCTTAT | ATTTGGAAGAGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTTCTGAT | 480 |
| Db | 421 | CCTTAT | ATTTGGAAGAGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTTCTGAT | 480 |
| Qy | 481 | TACAGT | GCATTTCTTAGAATCATACTATCTGTATACATGTGCACATGCGGCATT | 540 |
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| Qy | 541 | TTACTA | TGAAATTAATAGCTGGGTTTTTAATACCTTTATATATCATGTTCACTTTAA | 600 |
| Db | 541 | TTACTA | TGAAATTAATAGCTGGGTTTTTAATACCTTTATATATCATGTTCACTTTAA | 600 |
| Qy | 601 | GAAAGAC | TTCAAGTAGGAGATGAGTTTATTTCTCAGCAATAGACCTGTCAAATTTAG | 660 |
| Db | 601 | GAAAGAC | TTCAAGTAGGAGATGAGTTTATTTCTCAGCAATAGACCTGTCAAATTTAG | 660 |
| Qy | 661 | ATTATG | TTACTCAAATTTACTTTGTTGGCTGTTTATGAGTGTGCTCTCAGA | 720 |
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| Qy | 721 | AAATAT | ATTAAACGAGCTTTGAGGAGTGCACCTTATGAGTGTGATGCAACCTTTT | 780 |
| Db | 721 | AAATAT | ATTAAACGAGCTTTGAGGAGTGCACCTTATGAGTGTGATGCAACCTTTT | 780 |
| Qy | 781 | GCTTGG | GGGATGTGCTTGGAGAGGCAGATAACCGTGAAGCAGGCCTCTCATGACCCAGGA | 840 |
| Db | 781 | GCTTGG | GGGATGTGCTTGGAGAGGCAGATAACCGTGAAGCAGGCCTCTCATGACCCAGGA | 840 |
| Qy | 841 | GGCCGG | GGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTAAGTGTGGCCACAGAC | 900 |
| Db | 841 | GGCCGG | GGTGGATCCCTCTTTGTTGTTAGTCCATGCTATTAAGTGTGGCCACAGAC | 900 |
| Qy | 901 | CAAGAG | CCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCACTCTG | 960 |
| Db | 901 | CAAGAG | CCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCACTCTG | 960 |
| Qy | 961 | GACCCG | AGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAAGTTTGAGAGCA | 1020 |
| Db | 961 | GACCCG | AGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAAGTTTGAGAGCA | 1020 |
| Qy | 1021 | TCATCA | TAGAGAAATCAATCACACCCCACTTCTTATCTTTCCAGTGGCTAAACCACT | 1080 |
| Db | 1021 | TCATCA | TAGAGAAATCAATCACACCCCACTTCTTATCTTTCCAGTGGCTAAACCACT | 1080 |
| Qy | 1081 | TAACTC | CTCTGGGTACCTGCTCATTTGTTTA | 1114 |
| Db | 1081 | TAACTC | CTCTGGGTACCTGCTCATTTGTTTA | 1114 |

RESULT 5
CQ783702
LOCUS

CQ783702 1080 bp DNA linear PAT 17-MAR-2004

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| Best Local Similarity | | 99.9%; | | Pred. No. 3.6e-278; | | | |
| Matches 1080; | | Conservative 0; | | Mismatches 0; | | Indels 1; Gaps 1; | |
| QY | 33 | AGGAAGCCGGAAGCAGCGCGCGCCCCAGTTTCGGGAGACATGGCGGGCGTTAAAGCTCTCG | 92 | | | | |
| Db | 1 | AGGAAGCCGGAAGCAGCGCGCGCCCCAGTTTCGGGAGACATGGCGGGCGTTAAAGCTCTCG | 60 | | | | |
| QY | 93 | TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCCCTTAG | 152 | | | | |
| Db | 61 | TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCCCTTAG | 120 | | | | |
| QY | 153 | AGGATTATGGCGTTTACTGGCCCTTATTGTCCTGATTTTCCACGCCATCTCCCCCATCC | 212 | | | | |
| Db | 121 | AGGATTATGGCGTTTACTGGCCCTTATTGTCCTGATTTTCCACGCCATCTCCCCCATCC | 180 | | | | |
| QY | 213 | CCCAATTTCATGGCCAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCCGG | 272 | | | | |
| Db | 181 | CCCAATTTCATGGCCAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCCGG | 240 | | | | |
| QY | 273 | AACTGGCATAATTTCTTCACTACTGGAATTGTTGTTTCTGCTTTGGATTTCCTGTTATTC | 332 | | | | |
| Db | 241 | AACTGGCATAATTTCTTCACTACTGGAATTGTTGTTTCTGCTTTGGATTTCCTGTTATTC | 300 | | | | |
| QY | 333 | TTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCTGCGGCCCTTGTTGTGGCAGGCAATGCAG | 392 | | | | |
| Db | 301 | TTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCTGCGGCCCTTGTTGTGGCAGGCAATGCAG | 360 | | | | |
| QY | 393 | TCATTTTCTTACAATTCAAGGGTTTTTCTTATATTTGGGAAGAGAGATGATTTTAGCT | 452 | | | | |
| Db | 361 | TCATTTTCTTACAATTCAAGGGTTTTTCTTATATTTGGGAAGAGAGATGATTTTAGCT | 420 | | | | |
| QY | 453 | GGGAGCAGTGGTAGCATTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACT | 512 | | | | |
| Db | 421 | GGGAGCAGTGGTAGCATTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACT | 480 | | | | |
| QY | 513 | ATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA | 572 | | | | |
| Db | 481 | ATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA | 540 | | | | |
| QY | 573 | ATACCTTTATATATCATGTTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTAT | 632 | | | | |
| Db | 541 | ATACCTTTATATATCATGTTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTAT | 600 | | | | |
| QY | 633 | TCTCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTG | 692 | | | | |
| Db | 601 | TCTCAGC-AAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTG | 659 | | | | |
| QY | 693 | CTGTTTCATGTAGTCACGGTGTCTCTCAGAAAAATATATTAAACGAGTCTTGTAGGCAGTGC | 752 | | | | |
| Db | 660 | CTGTTTCATGTAGTCACGGTGTCTCTCAGAAAAATATATTAAACGAGTCTTGTAGGCAGTGC | 719 | | | | |
| QY | 753 | CACCTTATGCAGTGCATCGAAACCTTTTGTGTTGGGATGTGCTTGGAGAGGCAGATAACG | 812 | | | | |
| Db | 720 | CACCTTATGCAGTGCATCGAAACCTTTTGTGTTGGGATGTGCTTGGAGAGGCAGATAACG | 779 | | | | |
| QY | 813 | CTGAAGCAGGCCCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTTAGTC | 872 | | | | |
| Db | 780 | CTGAAGCAGGCCCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTTAGTC | 839 | | | | |
| QY | 873 | CATGCTATTAAAGTGTGGCCCAACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTA | 932 | | | | |
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| QY | 933 | GAAATGCAGAAATCTGAAGCCCCCCTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAG | 992 | | | | |
| Db | 900 | GAAATGCAGAAATCTGAAGCCCCCCTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAG | 959 | | | | |

| | | | | | | | |
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| QY | 993 | TTGTATGCACATGAAAGTTTGGAGAGCATCATATAGAGAGTAAACATCACACCCAACT | 1052 | | | | |
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| QY | 1053 | TCCTTATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTACCTGCTCATTTGTT | 1112 | | | | |
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| Homo sapiens cDNA FLJ90360 fis, clone NT2RP2003664, highly similar to Homo sapiens mRNA for leptin receptor gene. | | | | | | | |
| ACCESSION | | | | | | | |
| VERSION | | | | | | | |
| KEYWORDS | | | | | | | |
| SOURCE | | | | | | | |
| ORGANISM | | | | | | | |
| REFERENCE | | | | | | | |
| AUTHORS | | | | | | | |
| 1 | | | | | | | |
| Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K. | | | | | | | |
| NEDO human cDNA sequencing project | | | | | | | |
| Unpublished | | | | | | | |
| 2 (bases 1 to 1080) | | | | | | | |
| Isogai, T. and Otsuki, T. | | | | | | | |
| Direct Submission | | | | | | | |
| Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) | | | | | | | |
| NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.). | | | | | | | |
| FEATURES | | | | | | | |
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| Query Match | | | | 96.0%; Score 1069; DB 9; Length 1080; | | | |
| Best Local Similarity | | | | 99.9%; Pred. No. 3.6e-278; | | | |
| Matches 1080; | | | | Conservative 0; Mismatches 0; Indels 1; Gaps 1; | | | |
| QY | 33 | AGGAAGCCGGAAGCAGCGCGCCCCAGTTTCGGGAGACATGGCGGGCGTTAAAGCTCTCG | 92 | | | | |
| Db | 1 | AGGAAGCCGGAAGCAGCGCGCGCCCCAGTTTCGGGAGACATGGCGGGCGTTAAAGCTCTCG | 60 | | | | |
| QY | 93 | TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCCCTTAG | 152 | | | | |
| Db | 61 | TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCCCTTAG | 120 | | | | |
| QY | 153 | AGGATTATGGCGTTTACTGGCCCTTATTGTCCTGATTTTCCACGCCATCTCCCCCATCC | 212 | | | | |
| Db | 121 | AGGATTATGGCGTTTACTGGCCCTTATTGTCCTGATTTTCCACGCCATCTCCCCCATCC | 180 | | | | |
| QY | 213 | CCCAATTTCATGGCCAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCCGG | 272 | | | | |
| Db | 181 | CCCAATTTCATGGCCAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCCGG | 240 | | | | |
| QY | 273 | AACTGGCATAATTTCTTCACTACTGGAATTGTTGTTTCTGCTTTGGATTTCCTGTTATTC | 332 | | | | |
| Db | 241 | AACTGGCATAATTTCTTCACTACTGGAATTGTTGTTTCTGCTTTGGATTTCCTGTTATTC | 300 | | | | |
| QY | 333 | TTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCTGCGGCCCTTGTTGTGGCAGGCAATGCAG | 392 | | | | |
| Db | 301 | TTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCTGCGGCCCTTGTTGTGGCAGGCAATGCAG | 360 | | | | |
| QY | 393 | TCATTTTCTTACAATTCAAGGGTTTTTCTTATATTTGGGAAGAGAGATGATTTTAGCT | 452 | | | | |
| Db | 361 | TCATTTTCTTACAATTCAAGGGTTTTTCTTATATTTGGGAAGAGAGATGATTTTAGCT | 420 | | | | |
| QY | 453 | GGGAGCAGTGGTAGCATTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACT | 512 | | | | |
| Db | 421 | GGGAGCAGTGGTAGCATTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACT | 480 | | | | |
| QY | 513 | ATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA | 572 | | | | |
| Db | 481 | ATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA | 540 | | | | |
| QY | 573 | ATACCTTTATATATCATGTTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTAT | 632 | | | | |
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| QY | 633 | TCTCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTG | 692 | | | | |
| Db | 601 | TCTCAGC-AAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTG | 659 | | | | |
| QY | 693 | CTGTTTCATGTAGTCACGGTGTCTCTCAGAAAAATATATTAAACGAGTCTTGTAGGCAGTGC | 752 | | | | |
| Db | 660 | CTGTTTCATGTAGTCACGGTGTCTCTCAGAAAAATATATTAAACGAGTCTTGTAGGCAGTGC | 719 | | | | |
| QY | 753 | CACCTTATGCAGTGCATCGAAACCTTTTGTGTTGGGATGTGCTTGGAGAGGCAGATAACG | 812 | | | | |
| Db | 720 | CACCTTATGCAGTGCATCGAAACCTTTTGTGTTGGGATGTGCTTGGAGAGGCAGATAACG | 779 | | | | |
| QY | 813 | CTGAAGCAGGCCCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTTAGTC | 872 | | | | |
| Db | 780 | CTGAAGCAGGCCCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTTAGTC | 839 | | | | |
| QY | 873 | CATGCTATTAAAGTGTGGCCCAACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTA | 932 | | | | |
| Db | 840 | CATGCTATTAAAGTGTGGCCCAACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTA | 899 | | | | |
| QY | 933 | GAAATGCAGAAATCTGAAGCCCCCCTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAG | 992 | | | | |
| Db | 900 | GAAATGCAGAAATCTGAAGCCCCCCTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAG | 959 | | | | |

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| QY | 993 | TTGTATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCAACT | 1052 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| QY | 153 | AGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATTTTCCACGCCATCTCCCCATCC | 212 |
| Db | 121 | AGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATTTTCCACGCCATCTCCCCATCC | 180 |
| QY | 213 | CCCATTTTCATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTCTGGG | 272 |
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| QY | 273 | AACTGGCATAATTTCTTCACTACTGGAATTTGTTTCTGCTTCTGCTTCTGGATTTCCGTATTTC | 332 |
| Db | 241 | AACTGGCATAATTTCTTCACTACTGGAATTTGTTTCTGCTTCTGCTTCTGGATTTCCGTATTTC | 300 |
| QY | 333 | TTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCCTGGGCCCTTGTGTTGGCAGGCAATGCAG | 392 |
| Db | 301 | TTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCCTGGGCCCTTGTGTTGGCAGGCAATGCAG | 360 |
| QY | 393 | TCATTTTCCTTACAATTCAAGGGTTTTTCCCTTATATTGGGAAGAGGAGATGATTTTAGCT | 452 |
| Db | 361 | TCATTTTCCTTACAATTCAAGGGTTTTTCCCTTATATTGGGAAGAGGAGATGATTTTAGCT | 420 |
| QY | 453 | GGGAGCAGTGGTAGCACTTTATTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACT | 512 |
| Db | 421 | GGGAGCAGTGGTAGCACTTTATTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACT | 480 |
| QY | 513 | ATCTGTATACATGTGCATGCGGCATTTTACTATGAAATTTAAATATGCTGGGTTTTTA | 572 |
| Db | 481 | ATCTGTATACATGTGCATGCGGCATTTTACTATGAAATTTAAATATGCTGGGTTTTTA | 540 |
| QY | 573 | ATACCTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTAT | 632 |
| Db | 541 | ATACCTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTAT | 600 |
| QY | 633 | TCTCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGTTGG | 692 |
| Db | 601 | TCTCAGC-AATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGTTGG | 659 |
| QY | 693 | CTGTTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAACGCAGTCTTGTAGGCAGCTGC | 752 |
| Db | 660 | CTGTTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAACGCAGTCTTGTAGGCAGCTGC | 719 |
| QY | 753 | CACCTTATGCAGTGCATCGAAACCTTTTGCTTGGGATGTGCTTGGAGAGGCAGATAACG | 812 |
| Db | 720 | CACCTTATGCAGTGCATCGAAACCTTTTGCTTGGGATGTGCTTGGAGAGGCAGATAACG | 779 |
| QY | 813 | CTGAAGCAGGCCCTCTCATGACCCAGGAAGCCGGGTGGATCCCTCTTTGTGTTGTAGTC | 872 |
| Db | 780 | CTGAAGCAGGCCCTCTCATGACCCAGGAAGCCGGGTGGATCCCTCTTTGTGTTGTAGTC | 839 |
| QY | 873 | CATGCTATTAAAGTGTGGCCCAACAGACCAAGAGCCTCAACATTTCCCTAGAGCCTTATTA | 932 |
| Db | 840 | CATGCTATTAAAGTGTGGCCCAACAGACCAAGAGCCTCAACATTTCCCTAGAGCCTTATTA | 899 |
| QY | 933 | GAAATGCAGAAATCTGAAGCCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAG | 992 |
| Db | 900 | GAAATGCAGAAATCTGAAGCCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAG | 959 |
| QY | 993 | TTGTATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCCAACT | 1052 |
| Db | 960 | TTGTATGCACATGAAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCCAACT | 1019 |
| QY | 1053 | TCCTTATCTTTCCAGTGGTAAACCCTTAACCTCTCTGGGTGTTACCTGCTCATTTGTT | 1112 |
| Db | 1020 | TCCTTATCTTTCCAGTGGTAAACCCTTAACCTCTCTGGGTGTTACCTGCTCATTTGTT | 1079 |
| QY | 1113 | T 1113 | |
| Db | 1080 | T 1080 | |

RESULT 8
AX779959
LOCUS

AX779959 2388 bp DNA linear PAT 14-JUL-2003

| | |
|----------------------------|---|
| DEFINITION | Sequence 2116 from Patent WO03039443. |
| ACCESSION | AX779959 |
| VERSION | AX779959.1 GI:32696953 |
| KEYWORDS | |
| SOURCE | Homo sapiens (human). |
| ORGANISM | Homo sapiens |
| REFERENCE | 1 |
| AUTHORS | Haerlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S., Dugas, M., Bils, R., Brors, B. and Mergenthaler, S. |
| TITLE | Novel genetic markers for leukemias |
| JOURNAL | Patent: WO 03039443-A 2116 15-MAY-2003; Deutsches Krebsforschungszentrum (DE); Ludwig-Maximilian-Universitaet Muenchen (DE); PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE) |
| FEATURES | Location/Qualifiers |
| source | 1..2388 |
| | /organism="Homo sapiens" |
| | /mol_type="unassigned DNA" |
| | /db_xref="taxon:9606" |
| ORIGIN | |
| Query Match | 95.8%; Score 1067; DB 6; Length 2388; |
| Best Local Similarity | 99.4%; Pred. No. 1.4e-277; |
| Matches 1111; Conservative | 0; Mismatches 3; Indels 4; Gaps 4; |
| QY | 1 GTCTGGCTTGGCAGGCTGCCGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCA- 59 |
| Db | 1 GTCTGGCTTGGCAGGCTGCCGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCAN 60 |
| QY | 60 GTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTG 119 |
| Db | 61 GNTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTG 120 |
| QY | 120 GACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTAT 179 |
| Db | 121 GACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTAT 180 |
| QY | 180 TCGTCCCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTCGCAAAAGAGTCACCT 239 |
| Db | 181 TCGTCCCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTTCATTCGCAAAAGAGTCACCT 240 |
| QY | 240 ATGACTCAGATGCAACCAAGTAGTGCCCTGTCGGGAACCTGGCATATTTCTTCACCTACTGGAA 299 |
| Db | 241 ATGACTCAGATGCAACCAAGTAGTGCCCTGTCGGGAACCTGGCATATTTCTTCACCTACTGGAA 300 |
| QY | 300 TTGTTGTTT-CTGCCTTTGGATT-TCCCTGTTATTCTTCTGCTCGTGGCTGTGATC-AAAT 356 |
| Db | 301 TTGTTGTTTNCCTTGCCCTTTGGATTNTCCTGTTATTCTTGTCTGCTGTGGCTGTGATCNAAT 360 |
| QY | 357 GGGAGCCCTGCGGCTTGTGTTGGCAGGCAATGCAGTCATTTTCCCTTACAATTCAGGGGT 416 |
| Db | 361 GGGAGCCCTGCGGCTTGTGTTGGCAGGCAATGCAGTCATTTTCCCTTACAATTCAGGGGT 420 |
| QY | 417 TTTTCCCTTATATTTGGAAGAGGAGATGATTTTGTAGCTGGGAGCAGTGGTAGCACTTTATTC 476 |
| Db | 421 TTTTCCCTTATATTTGGAAGAGGAGATGATTTTGTAGCTGGGAGCAGTGGTAGCACTTTATTC 480 |
| QY | 477 TGATTACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGG 536 |
| Db | 481 TGATTACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGG 540 |
| QY | 537 CATTTTACTATGAATTTAATATGCTGGGTTTTTAAATACCTTTTATATATCATGTTCACCT 596 |
| Db | 541 CATTTTACTATGAATTTAATATGCTGGGTTTTTAAATACCTTTTATATATCATGTTCACCT 600 |
| QY | 597 TTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTTATTTCTCAGCAAAATAGACCTGTCAAAAT 656 |
| Db | 601 TTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTTATTTCTCAGCAAAATAGACCTGTCAAAAT 660 |
| QY | 657 TTAGATTATGTTACTCAAATTTATGTTACTTTGGCTGTTTCATGTAGTCACGGTGCTCT 716 |

| | | | | | |
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| Db | 661 | TTAGATTATGTTACTCAAATTATGTTACTTGTGCTGTTTCATGCTAGTCACGGTGCTCT | 720 | REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov |
| | | | | COMMENT | Contact: MGC help desk |
| QY | 717 | CAGAAAAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTCATCGAAACC | 776 | | Email: cgapbs-r@mail.nih.gov |
| Db | 721 | CAGAAAAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTCATCGAAACC | 780 | | Tissue Procurement: CLONTECH |
| QY | 777 | TTTTGCTTGGGATGTGCTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCA | 836 | | cDNA Library Preparation: CLONTECH Laboratories, Inc. |
| Db | 781 | TTTTGCTTGGGATGTGCTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCA | 840 | | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) |
| QY | 837 | GGAAGCCGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCAC | 896 | | DNA Sequencing by: National Institutes of Health Intramural |
| Db | 841 | GGAAGCCNGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCAC | 900 | | Sequencing Center (NISC), |
| QY | 897 | AGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAACTCTGAAGCCCCAC | 956 | | Gaithersburg, Maryland; |
| Db | 901 | AGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAACTCTGAAGCCCCAC | 960 | | Web site: http://www.nisc.nih.gov/ |
| QY | 957 | TCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTGAGA | 1016 | | Contact: nisc_mgc@nhgri.nih.gov |
| Db | 961 | TCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTGAGA | 1020 | | Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., |
| QY | 1017 | AGCATCATCATAGAGAAGTAAACATCACACCCAACTTCCTTATCTTTCCAGTGGCTAAAC | 1076 | | Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., |
| Db | 1021 | AGCATCATCATAGAGAAGTAAACATCACACCCAACTTCCTTATCTTTCCAGTGGCTAAAC | 1080 | | Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., |
| QY | 1077 | CACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTA | 1114 | | Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., |
| Db | 1081 | CACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTA | 1118 | | Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., |
| RESULT 9 | BC056250 | 1092 bp | linear | PRI 30-JUN-2004 | McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., |
| LOCUS | Homo sapiens | leptin receptor gene-related protein, mRNA | (cDNA clone | | Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., |
| DEFINITION | MGC:61988 IMAGE:4328021), complete cds. | | | | Young,A., Zhang,L.-H. and Green,E.D. |
| ACCESSION | BC056250 | | | | Clone distribution: MGC clone distribution information can be found |
| VERSION | BC056250.1 | GI:33990029 | | | through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov |
| KEYWORDS | MGC. | | | | Series: IRAL Plate: 48 Row: c Column: 17 |
| SOURCE | Homo sapiens (human) | | | | This clone was selected for full length sequencing because it |
| ORGANISM | Homo sapiens | | | | passed the following selection criteria: matched mRNA gi: 4504978. |
| REFERENCE | 1 (bases 1 to 1092) | | | | Location/Qualifiers |
| AUTHORS | Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., | | | | 1. .1092 |
| | Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., | | | | /organism="Homo sapiens" |
| | Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., | | | | /mol_type="mRNA" |
| | Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., | | | | /db_xref="taxon:9606" |
| | Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., | | | | /clone="MGC:61988 IMAGE:4328021" |
| | Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., | | | | /tissue_type="Skeletal Muscle" |
| | Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., | | | | /clone_lib="NIH_MGC_81" |
| | Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., | | | | /lab_host="DH10B" |
| | Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., | | | | /note="Vector: pDNR-LIB" |
| | McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., | | | | 1. .1092 |
| | Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., | | | | /gene="OBRGRP" |
| | Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., | | | | /db_xref="LocusID:54741" |
| | Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., | | | | 23. .418 |
| | Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., | | | | /gene="OBRGRP" |
| | Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., | | | | /codon_start=1 |
| | Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., | | | | /product="leptin receptor gene-related protein" |
| | Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalrus,D.E., | | | | /protein_id="AAH56250.1" |
| | Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. | | | | /db_xref="GI:33990030" |
| | Generation and initial analysis of more than 15,000 full-length | | | | /db_xref="LocusID:54741" |
| | human and mouse cDNA sequences | | | | /translation="MAGVKALVALSFSGAIGLTFMLGCALEDYGVVWPLFVLIFHAI |
| | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | | | | SPIPHFIKRVTYDSDATSSACRELAYFFTTGIVVSAFGFPVILARVAVIKMGACGLV |
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| PUBMED | 2 (bases 1 to 1092) | | | | Query Match 94.9%; Score 1057.6; DB 9; Length 1092; |
| REFERENCE | Homo sapiens | | | | Best Local Similarity 99.6%; Pred. No. 4.4e-275; |
| AUTHORS | Strausberg,R. | | | | Matches 1060; Conservative 0; Mismatches 4; Indels 0; Gaps 0; |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (11-AUG-2003) National Institutes of Health, Mammalian | | | | 51 GCGGCCCCAGTTCGGGAGACATGGCGGCGGTTAAAGCTCTCGTGGCATTATCCTTCAGTG 110 |
| | Gene Collection (MGC), Cancer Genomics Office, National Cancer | | | | |
| | Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, | | | | 3 GGGGCCCCAGCTCGGAGACATGGCGGCGGTTAAAGCTCTCGTGGCATTATCCTTCAGTG 62 |
| | USA | | | | |
| | | | | | 111 GGGCTATTGGACTGACATTTTCTTATGCTGGGATGTCCTTAGAGGATTATGGCGTTTACT 170 |
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| | | | | | 231 GAGTCACCTATGACTCAGATGCAACACAGTAGTGCCTGTCGGGAACCTGGCATATTTCTTCA 290 |
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| | | | | | 183 GAGTCACCTATGACTCAGATGCAACACAGTAGTGCCTGTCGGGAACCTGGCATATTTCTTCA 242 |
| | | | | | |
| | | | | | 291 CTACTGGAATTGTTGTTTCTGCCTTTGGATTTTCCCTGTTATTCTTGCTCGTGGCTGTGA 350 |
| | | | | | |
| | | | | | 243 CTACTGGAATTGTTGTTTCTGCCTTTGGATTTTCCCTGTTATTCTTGCTCGTGGCTGTGA 302 |
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ORIGIN

Query Match 91.9%; Score 1023.4; DB 9; Length 1056;
Best Local Similarity 99.9%; Pred. No. 8.le-266;
Matches 1024; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 86 GCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGT 145
D 1 GCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGT 60
QY 146 GCCTTAGAGGATTATGGCGTTTACTTGGCCCTTATTCTGCTCCTGATTTTCCAGCCCATCTCC 205
D 61 GCCTTAGAGGATTATGGCGTTTACTTGGCCCTTATTCTGCTCCTGATTTTCCAGCCCATCTCC 120
QY 206 CCCATCCCCCATTTTCAATGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCC 265
D 121 CCCATCCCCCATTTTCAATGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCC 180
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D 181 TGTGCGGAACCTGGGCATATTCTTCACTACTGGAATTGTTGTTTCTGCTTTTGGATTTCTT 240
QY 326 GTTATTCTTGCTGCTGGCTGTGATCAAATGGGAGCCCTGCGGCCCTTGTTGGCAGGC 385
D 241 GTTATTCTTGCTGCTGGCTGTGATCAAATGGGAGCCCTGCGGCCCTTGTTGGCAGGC 300
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D 301 AATGCAGTCATTTTCCCTTACAATTTCAAGGGTTTTTCTTATATTGGAAAGAGGAGATGAT 360
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D 781 TGTAATCCATGCTATTAAAGTGTGGCCCAAGCAAGAGCCCTCAACATTTCTTAGAGC 840
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961 CCCAACTTCCCTTATCTTTCCAGTGGCTAAACCACCTTAACCTCTCTGGGTGTTACCTGCTC 1020
QY 1106 ATTTG 1110
D 1021 ATTTG 1025
RESULT 11
AR020775 AR020775 874 bp DNA linear PAT 05-DEC-1998
LOCUS Sequence 2 from patent US 5789198.
DEFINITION AR020775
ACCESSION AR020775
VERSION AR020775.1 GI:3975390
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 874)
AUTHORS Akerblom,I.E.
TITLE Human leptin receptor-related protein
JOURNAL Patent: US 5789198-A 2 04-AUG-1998;
FEATURES Location/Qualifiers
source
1..874
/organism="unknown"
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Query Match 78.1%; Score 869.6; DB 6; Length 874;
Best Local Similarity 99.4%; Pred. No. 3.5e-224;
Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 61 TTCGGGAGACATGCGGGCGGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
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D 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180
QY 181 CGTCCTGATTTTCCACGGCAATCTCCCCCATCCCCCATTTTCAATGCCAAAAGAGTCACCTA 240
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QY 481 TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATCGCGCAT 540
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RESULT 12
BD132522
LOCUS BD132522 874 bp DNA linear PAT 18-SEP-2002
DEFINITION A novel human leptin receptor gene-related protein.
ACCESSION BD132522
VERSION BD132522.1 GI:23227467
KEYWORDS JP 2002509427-A/1.
SOURCE synthetic construct
ORGANISM INCYTE PHARMACEUTICALS INC
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 874)
AUTHORS Akerblom,I.E.
TITLE A novel human leptin receptor gene-related protein
JOURNAL Patent: JP 2002509427-A 1 26-MAR-2002;
INCYTE PHARMACEUTICALS INC
COMMENT PN JP 2002509427-A/1
PD 26-MAR-2002
PF 25-JUL-1997 JP 1998508261
PR 01-AUG-1996 US 08/691071,15-APR-1997 US 08/843370 PI
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PC C12P7/40,C12M1/00
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ORIGIN
Query Match 78.1%; Score 869.6; DB 6; Length 874;
Best Local Similarity 99.4%; Pred. No. 3.5e-224;
Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 301 TGTGTTTTCTGCCCTTGGATTTCTGTATTCTTGTCTGTGGCTGTGATCAAATGGGG 360
DB 301 TGTGTTTTCTGCCCTTGGATTTCTGTATTCTTGTCTGTGGCTGTGATCAAATGGGG 360
QY 361 AGCCTGCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCAGAGGTTTTT 420
DB 361 AGCCTGCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATTCAGAGGTTTTT 420
QY 421 CCTTATATTGGAAGAGAGATGATTTTAGCTGGAGCAGTGGTAGCATTATTCTGTAT 480
DB 421 CCTTATATTGGAAGAGAGATGATTTTAGCTGGAGCAGTGGTAGCATTATTCTGTAT 480
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QY 781 GCTTGGGGATGTGCTTGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAA 840
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DB 841 GGCCGGGGTGGTCCCTCTTTKTTTGTAGTCCA 874

RESULT 13
AC119800
LOCUS AC119800 161112 bp DNA linear PRI 28-NOV-2002
DEFINITION Homo sapiens chromosome 1 clone RP4-630A11, complete sequence.
ACCESSION AC119800 AL157946
VERSION AC119800.2 GI:25815349
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 161112)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 161112)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (02-MAY-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 161112)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
COMMENT On Nov 28, 2002 this sequence version replaced gi:20389314.
----- Genome Center

Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwgchgs@u.washington.edu
Drafting Center: SC

----- Project Information

Center project name: chr-1
Center clone name: RP4-630A11 (sc0810)

----- Summary Statistics

Sequencing vector: plasmid; 68% of reads
Sequencing vector: plasmid; 108752; 32% of reads
Chemistry: Dye-terminator ET; 25% of reads
Chemistry: Dye-terminator Big Dye; 75% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160526 bases at least Q40
Consensus quality: 161073 bases at least Q30
Consensus quality: 161107 bases at least Q20
Insert size: 161112; sum-of-contigs
Quality coverage: 8.8x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': Mapping in progress
3': RPI1-430H12 (UWGC:sc0702) AC097063, 50135-bp overlap

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

| EcoRI | | BglII | | HindIII | |
|-----------|----------|-----------|----------|-----------|----------|
| SeqDerMap | FngrPrnt | SeqDerMap | FngrPrnt | SeqDerMap | FngrPrnt |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 5331 | 5304 | 7924 | 7908 | 2518 | 2492 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 2184 | 2158 | 5671 | 5808 | 449 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 8065 | 8117 | 3403 | 3485 | 512 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 486 | <800 | 10596 | 10659 | 2814 | 2807 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 106 | <800 | 5998 | 5808 | 1247 | 1212 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3938 | 3930 | 5361 | 5256 | 4695 | 4701 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4702 | 4497 | 9738 | 9982 | 3373 | 3402 |
| ----- | ----- | ----- | ----- | ----- | ----- |

| | | | | | |
|-------|-------|-------|-------|-------|-------|
| 454 | <800 | 677 | <800 | 2017 | 2035 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 565 | <800 | 3989 | 3959 | 1891 | 1878 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4116 | 4117 | 4018 | 3959 | 6353 | 6156 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3908 | 3930 | 9627 | 9385 | 1594 | 1588 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 12984 | 12767 | 792 | 800 | 3180 | 3218 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 2691 | 2561 | 2720 | 2682 | 727 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 1353 | 1330 | 2477 | 2477 | 1891 | 1878 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 130 | <800 | 2529 | 2477 | 6622 | 6531 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3743 | 3611 | 3828 | 3959 | 855 | 869 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 2498 | 2561 | 3173 | 3194 | 451 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 7241 | 7277 | 267 | <800 | 5443 | 5392 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3987 | 3930 | 799 | 800 | 10983 | 10933 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 2101 | 2063 | 884 | 899 | 655 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4560 | 4497 | 1272 | 1247 | 3427 | 3402 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 1266 | 1225 | 4968 | 4959 | 430 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3624 | 3611 | 1616 | 1588 | 1339 | 1318 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 1719 | 1676 | 186 | <800 | 3903 | 3862 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 225 | <800 | 9748 | 9982 | 1055 | 1081 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 23802 | 23955 | 5416 | 5448 | 7669 | 7660 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 9969 | 9806 | 5849 | 5808 | 7048 | 7002 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 6234 | 6179 | 7584 | 7591 | 4279 | 4362 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 760 | 796 | 2653 | 2682 | 653 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 78 | <800 | 1506 | 1451 | 2761 | 2807 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 5563 | 5491 | 6689 | 6748 | 7140 | 7002 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4515 | 4497 | 799 | 800 | 95 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3618 | 3611 | 10232 | 9982 | 15 | <800 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3628 | 3611 | 2996 | 3022 | 7722 | 7660 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4092 | 4117 | 3925 | 3959 | 6160 | 6156 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 9965 | 9806 | 911 | 899 | 1068 | 1081 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 2577 | 2561 | 2408 | 2477 | 1120 | 1081 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4216 | 4497 | 1486 | 1451 | 1889 | 1878 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 2874 | 2886 | 5192 | 4959 | 4812 | 4701 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 811 | 796 | 1847 | 1838 | 6934 | 7002 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 538 | <800 | 232 | <800 | 4398 | 4362 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 240 | <800 | 584 | <800 | 3834 | 3862 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 4811 | 4810 | 2262 | 2262 | 1608 | 1588 |
| ----- | ----- | ----- | ----- | ----- | ----- |
| 3434 | 3396 | 234 | <800 | 3928 | 3862 |

[illegible]

| | | | |
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| QY | 997 | ATGCACATGAAAGTTTGAGAAGCATCATCATAGAGAAGTAAACATCACACCAACTTCCT | 1056 |
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| QY | 1057 | TATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA | 1114 |
| Db | 30705 | TATCTTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA | 30762 |
| RESULT 14 | | | |
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| LOCUS | AK130096 | 1614 bp | linear |
| DEFINITION | Homo sapiens cDNA FLJ26586 fis, clone LNF07412. | | PRI 10-SEP-2003 |
| ACCESSION | AK130096 | | |
| VERSION | AK130096.1 | GI:34526837 | |
| KEYWORDS | oligo capping; fis (full insert sequence). | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| | 1 | | |
| | Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S. | | |
| TITLE | NEDO human cDNA sequencing project | | |
| JOURNAL | Unpublished | | |
| REFERENCE | 2 (bases 1 to 1614) | | |
| AUTHORS | Sugano, S. and Suzuki, Y. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flcdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416) | | |
| COMMENT | NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute. | | |
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| Best Local Similarity | 99.1%; | Pred. No. 5e-196; | |
| Matches | 770; Conservative | 0; Mismatches | 7; Indels 0; Gaps 0; |
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| QY | 397 | TTTCCTTACAATTCAAGGGTTTTTCCTTATATTTTGGAGAGGAGATGATTTTAGCTGGGA | 456 |
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RESULT 15
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LOCUS Sequence 1 from Patent WO2004072293.
DEFINITION CQ860089
ACCESSION CQ860089.1 GI:51981977
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL Patent: WO 2004072293-A 1 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES
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ORIGIN

Query Match 58.2%; Score 648; DB 6; Length 648;

Best Local Similarity 100.0%; Pred. No. 3.4e-164;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 601 GTGGCTAAACCACTTAACTCTCTGGGTGTTACCTGCTCATTTGTTTA 648

Search completed: August 18, 2005, 01:39:47
Job time : 5157 secs

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Db 841 GGCCGGGGTGGWTCCCTCTTTKTTTGTAGTCCA 874

RESULT 2
US-08-843-370-2
; Sequence 2, Application US/08843370
; Patent No. 5874535
; GENERAL INFORMATION:
; APPLICANT: Akerblom, Ingrid E.
; TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR
; TITLE OF INVENTION: GENE-RELATED PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,370
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/691,071
; FILING DATE: August 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0111-1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 874 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: HNT2NOT01
; CLONE: 492703
; US-08-843-370-2

Query Match 78.1%; Score 869.6; DB 2; Length 874;
Best Local Similarity 99.4%; Pred. No. 4.5e-270;
Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGSCAGGCTGCCGGGCGTGGGAGGAGCCGGAAGCAGCCGCGGCCCCAG 60
Db 1 GTCTGGCTTGGSCAGGCTGCCGGGCGTGGGAGGAGCCGGAAGCAGCCGCGGCCCCAG 60
QY 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCACTGGGGCTATTGG 120
Db 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCACTGGGGCTATTGG 120
QY 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180
Db 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180
QY 181 CGTCTGATTTTCCACGGCATCTCCCCCATCCCCCATTTCAATGCCAAAAGAGTCACCTA 240
Db 181 CGTCTGATTTTCCACGGCATCTCCCCCATCCCCCATTTCAATGCCAAAAGAGTCACCTA 240
QY 241 TGACTCAGATGCAACCCAGTAGTGCCTGTGGGAACTGGCATATTTCTTCACTACTGGAAT 300
Db 241 TGACTCAGATGCAACCCAGTAGTGCCTGTGGGAACTGGCATATTTCTTCACTACTGGAAT 300
QY 301 TGTGTTTCTGCCTTTGGATTTCCTGTTATTCTTGCTCGTGGCTGTGATCAAAATGGGG 360
Db 301 TGTGTTTCTGCCTTTGGATTTCCTGTTATTCTTGCTCGTGGCTGTGATCAAAATGGGG 360
QY 361 AGCCTGGCGCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCCTTACAATTCGAAGGTTT 420
Db 361 AGCCTGGCGCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCCTTACAATTCGAAGGTTT 420
QY 421 CCTTATATTGGAAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480
Db 421 CCTTATATTGGAAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGAT 480
QY 481 TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATCGCGCAAT 540
Db 481 TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATCGCGCAAT 540
QY 541 TTACTATGAAATTTAATATGCTGGGTTTTTAACTACCTTTTATATATCATGTTTCACTTTAA 600

Db 541 TTACTATGAAATTTAATATGCTGGGTTTTTAATACCTTTATATATCATGTTCACTTTAA 600
Qy 601 GAAAGACTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAATTTAG 660
Db 601 GAAAGACTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAATTTAG 660
Qy 661 ATTATGTTACTCAAATTATGTTACTTTGTTGGCTGTTTCATGTAGTCACGGTGTCTCAGA 720
Db 661 ATTATGTTACTCAAATTATGTTACTTTGTTGGCTGTTTCATGTAGTCACGGTGTCTCAGA 720
Qy 721 AAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780
Db 721 AAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780
Qy 781 GCTTGGGATGTCTTGAGAGGCAGATACGCTGAAGCAGGCGCTCTCATGACCCAGGAA 840
Db 781 GCTTGGGATGTCTTGAGAGGCAGATACGCTGAAGCAGGCGCTCTCATGACCCAGGAA 840
Qy 841 GGCCGGGTGGATCCCTCTTGTGTGTGTAGTCCA 874
Db 841 GGCCGGGTGGTCCCTCTTGTGTGTGTAGTCCA 874
RESULT 3
US-09-839-709-1
; Sequence 1, Application US/09839709
; Patent No. 6517489
; GENERAL INFORMATION:
; APPLICANT: Mao, Yumin
; APPLICANT: Xie, Yi
; APPLICANT: Huang, Yan
; TITLE OF INVENTION: NEW PROTEIN ASSOCIATED WITH LEPTIN RECEPTOR FOR OBESITY AND THE
; TITLE OF INVENTION: ENCODING SEQUENCE THEREOF AND THE METHODS FOR PRODUCING SAME AND
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 9548.60USWO
; CURRENT APPLICATION NUMBER: US/09/839,709
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/CN99/00167
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: CN 98121474.6
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-839-709-1

Query Match 15.7%; Score 174.6; DB 4; Length 2701;
Best Local Similarity 65.0%; Pred. No. 3.1e-45;
Matches 258; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
Qy 68 GACATGGCGGGCGTTAAAGCTCTCGTGGCAATTATCCTTCAGTGGGGCTAFTGGACTGACT 127
Db 82 GCCATGGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATG 141
Qy 128 TTTCTTATGCTGGGATGTGCCCTTAGAGGATTAATGGCGTTTACTGGCCCTTATTCGTCTCTG 187
Db 142 TTTTGTATGCTTGGATGTGCCCTTCCAATATACAAATACTTGCCCTCTTGTGTTCTA 201
Qy 188 ATTTTCCACGCCCATCTCCCCCATCCCCATTTTCATTGCCAAAGAGTCACTATGACTCA 247
Db 202 TTTTTTTACATCCTTTTACCTATTCCATCTGATAGCAAGAAGATTAGTGATGATACA 261
Qy 248 GATGCAACCAAGTAGTGCCTGTGCGGAACCTGGCATATTTCTTCACTACTGGAATTGTTGT 307
Db 262 GATGCTATGAGTAACGCTTGTAAGGAACCTTGCCATCTTTCTTACAACGGGCATGTGCGTG 321
Qy 308 TCTGCCCTTTGGATTTCTGTGTTATTTCTTGCTCGTGTGGCTGTGATCAAATGGGAGCCTGC 367
Db 322 TCAGCTTTTGGACTCCCTATTGTATTGTTGCCAGAGCACATCTGATTGATGGGGAGCTTGT 381

Qy 368 GGCCTTGTCTGGCAGGCAATGCAGTCATTTTCTTACAATCAAGGTTTTTCTTATA 427
Db 382 GCACCTTGTCTCACAGGAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTC 441
Qy 428 TTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGT 464
Db 442 TTTGGAAGCAAGGACGACTTCAGCTGGCAGCAGTGGT 478
RESULT 4
US-09-023-655-885
; Sequence 885, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 885:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1139594
US-09-023-655-885
Query Match 14.5%; Score 162; DB 4; Length 3800;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCTGGCTTGGCAGGCTGCCCGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGCCCCAG 60
Db 12 GTCTGGCTTGGCAGGCTGCCCGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGCCCCAG 71
Qy 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 131
Qy 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGG 173

db
132 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG 173

RESULT 5
US-08-599-455B-3
; Sequence 3, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

| | Query Match | 14.5%; | Score 162; | DB 2; | Length 3871; |
|----|-----------------------|---|--------------------|-----------|--------------|
| | Best Local Similarity | 100.0%; | Pred. No. 4.6e-41; | | |
| | Matches 162; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | GTCTGGCTTGGGCAGGCTGCGCCGCGGCCGTGGCAGGAAGCCGGAAAGCAGCCGCGGCCCCAG | 60 | | |
| | | | | | |
| | | | | | |
| Db | 12 | GTCTGGCTTGGGCAGGCTGCGCCGCGGCCGTGGCAGGAAGCCGGAAAGCAGCCGCGGCCCCAG | 71 | | |
| | | | | | |
| | | | | | |
| QY | 61 | TTCTGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCTTCAGTGGGGCTATTGG | 120 | | |
| | | | | | |
| | | | | | |
| Db | 72 | TTCTGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCTTCAGTGGGGCTATTGG | 131 | | |
| | | | | | |
| | | | | | |
| QY | 121 | ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG | 162 | | |
| | | | | | |
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```

RESULT 6
US-09-069-781B-3
; Sequence 3, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,781B
; FILING DATE: 29-APRIL-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
;
US-09-069-781B-3

```

5

| | | | |
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| Qy | 1 | GTCTGGCTTGGGCAGGCTGCCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG | 60 |
| Db | 12 | GTCTGGCTTGGGCAGGCTGCCCGGGCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG | 71 |
| Qy | 61 | TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG | 120 |
| Db | 72 | TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG | 131 |
| Qy | 121 | ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG | 162 |
| Db | 132 | ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGG | 173 |

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; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194....3688
US-09-137-132-3

Query Match      14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCTGGCTTGGCAGCGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 60
Db      12  GTCTGGCTTGGCAGCGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG 71

QY      61  TTCGGGAGACATGCGCGGCGCTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db      72  TTCGGGAGACATGCGCGGCGCTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131

QY      121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGATTATGG 162
Db      132 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGATTATGG 173

RESULT 8
US-08-864-564A-3
; Sequence 3, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,564A
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283

```


Fri Aug 19 08:52:54 2005

REFERENCE/DOCKET NUMBER: 07334/019002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 194...3688
US-08-864-564A-3
Query Match 14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCTGGCTTGGGCAGGCTGCCCGGCGGTGAGGAGCGGAGCGCGGCCCCCAG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
12 GTCTGGCTTGGGCAGGCTGCCCGGCGGTGAGGAGCGGAGCGCGGCCCCCAG 71
QY 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
72 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131
QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 9
US-09-094-410-3
Sequence 3, Application US/09094410
Patent No. 6403552
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,410
FILING DATE: 09-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 194...3688
US-09-094-410-3
Query Match 14.5%; Score 162; DB 3; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCTGGCTTGGGCAGGCTGCCCGGCGGTGAGGAGCGGAGCGCGGCCCCCAG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
12 GTCTGGCTTGGGCAGGCTGCCCGGCGGTGAGGAGCGGAGCGCGGCCCCCAG 71
QY 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
72 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131
QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 10
US-08-708-123D-3
Sequence 3, Application US/08708123D
Patent No. 6482927
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
FILING DATE: 03-SEP-1996

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
US-08-708-123D-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGGTCGCCGGCCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 60
Db 12 GTCTGGCTTGGCAGGTCGCCGGCCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 71

QY 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 131

QY 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGG 173

RESULT 11
US-08-583-153A-3
; Sequence 3, Application US/08583153A
; Patent No. 6506877
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153A
; FILING DATE: 28-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
US-08-583-153A-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGGTCGCCGGCCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 60
Db 12 GTCTGGCTTGGCAGGTCGCCGGCCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 71

QY 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 131

QY 121 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTGCCCTTAGAGGATTATGG 173

RESULT 12
US-08-570-142D-3
; Sequence 3, Application US/08570142D
; Patent No. 6509189
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,142D
; FILING DATE: 11-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
;
US-08-570-142D-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGGCTGCCCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 12 GTCTGGCTTGGCAGGCTGCCCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131

QY 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131

QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 13
US-08-638-524B-3
; Sequence 3, Application US/08638524B
; Patent No. 6548269
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB
; TITLE OF INVENTION: CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,524B
; FILING DATE: 26-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
;
US-08-638-524B-3

Query Match 14.5%; Score 162; DB 4; Length 3871;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGGCTGCCCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 60
Db 12 GTCTGGCTTGGCAGGCTGCCCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 71

QY 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 120
Db 72 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG 131

QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 162
Db 132 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGG 173

RESULT 14
US-09-043-816E-12
; Sequence 12, Application US/09043816E
; Patent No. 6414128
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Willson, Tracy
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Gainsford, Timothy
; APPLICANT: Alexander, Warren S.
; APPLICANT: Metcalf, Donald
; APPLICANT: Ng, Ashley
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; TITLE OF INVENTION: ENCODING SAME
; FILE REFERENCE: 11268
; CURRENT APPLICATION NUMBER: US/09/043,816E
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (27)..(68)
; OTHER INFORMATION: N is a o r g o r c o r t
; NAME/KEY: unsure
; LOCATION: (923)
; OTHER INFORMATION: R is g o r a
; NAME/KEY: unsure
; LOCATION: (2315)
; OTHER INFORMATION: S is g o r c
US-09-043-816E-12

Query Match      9.8%; Score 109.4; DB 3; Length 3909;
Best Local Similarity 91.9%; Pred. No. 4.6e-24;
Matches 113; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      49 CCGCGGCCCCAGTTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAG 108
Db      21 CCGCGGCCCCAGTTCGGGAGACATGGGGGCGTTAAAGCTCTCGTGNATTATCCTTCAG 80

QY      109 TGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATTATGGCGTTTA 168
Db      81 TGGGGTATTGGACTGACTTTTCTTATGCTGGGATGCGCTTAGAGGATTATGGATTGG 140

QY      169 CTG 171
Db      141 CAG 143

RESULT 15
US-08-780-562-6
; Sequence 6, Application US/08780562
; Patent No. 6541604
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/
; FILING DATE: 01/08/97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3102 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-780-562-6

Query Match      8.1%; Score 90.4; DB 4; Length 3102;
Best Local Similarity 98.9%; Pred. No. 5.4e-18;
Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      71 ATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 130
Db      15 ACGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTT 74

QY      131 CTTATGCTGGGATGTCCTTAGAGGATTATGG 162
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Job time : 236 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 22:52:44 ; Search time 4251 Seconds
(without alignments)
9974.970 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctggttggcaggctgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 917.2 | 82.3 | 1040 | 5 BX462364 | BX462364 BX462364 |
| 2 | 903.4 | 81.1 | 1050 | 1 AL550884 | AL550884 AL550884 |
| 3 | 881 | 79.1 | 1026 | 1 AL552981 | AL552981 AL552981 |
| 4 | 805.8 | 72.3 | 952 | 5 BX417049 | BX417049 BX417049 |
| 5 | 790.6 | 71.0 | 1004 | 5 BX417586 | BX417586 BX417586 |
| 6 | 784.4 | 70.4 | 786 | 1 AL571122 | AL571122 AL571122 |
| 7 | 776.8 | 69.7 | 805 | 1 AL709947 | AL709947 DKFZp686B |
| 8 | 775 | 69.6 | 811 | 5 BX378815 | BX378815 BX378815 |
| 9 | 771.6 | 69.3 | 996 | 5 BQ959135 | BQ959135 AGENCOURT |
| 10 | 767.2 | 68.9 | 914 | 5 BU189726 | BU189726 AGENCOURT |
| 11 | 766.4 | 68.8 | 899 | 5 BQ424209 | BQ424209 AGENCOURT |
| 12 | 763.4 | 68.5 | 835 | 7 CF594097 | CF594097 AGENCOURT |
| 13 | 747.2 | 67.1 | 786 | 6 CB956304 | CB956304 AGENCOURT |
| 14 | 731.8 | 65.7 | 765 | 6 CA311840 | CA311840 UI-CF-FN0 |
| 15 | 729.6 | 65.5 | 739 | 1 AL699934 | AL699934 DKFZp686G |
| 16 | 729.6 | 65.5 | 739 | 1 AL700785 | AL700785 DKFZp686G |
| 17 | 718.4 | 64.5 | 810 | 2 BE615001 | BE615001 601281218 |
| 18 | 710.6 | 63.8 | 811 | 4 BI667044 | BI667044 603291220 |
| 19 | 709.4 | 63.7 | 711 | 7 CN427830 | CN427830 170006000 |
| 20 | 707.8 | 63.5 | 822 | 7 CF593845 | CF593845 AGENCOURT |
| 21 | 707.2 | 63.5 | 728 | 5 BU634004 | BU634004 UI-H-FL1- |
| 22 | 706.8 | 63.4 | 746 | 5 BU620279 | BU620279 UI-H-FH1- |
| 23 | 702.2 | 63.0 | 828 | 5 BU932194 | BU932194 AGENCOURT |
| 24 | 701.6 | 63.0 | 853 | 4 BG503309 | BG503309 602550719 |

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| C | 25 | 697.4 | 62.6 | 738 | 1 | AI621226 | AI621226 | linear | EST 06-MAY-2004 |
| | 26 | 686.4 | 61.6 | 919 | 4 | BG170089 | BG170089 | | |
| | 27 | 684.2 | 61.4 | 803 | 4 | BG504619 | BG504619 | | |
| | 28 | 682.6 | 61.3 | 793 | 6 | CB990288 | CB990288 | | |
| C | 29 | 681.4 | 61.2 | 700 | 7 | CN480866 | CN480866 | UI-H-FT2- | |
| C | 30 | 681 | 61.1 | 698 | 6 | CD364970 | CD364970 | UI-H-FT2- | |
| | 31 | 680.6 | 61.1 | 773 | 2 | BE614786 | BE614786 | 601280203 | |
| | 32 | 667.2 | 59.9 | 699 | 4 | BI548174 | BI548174 | 603196619 | |
| C | 33 | 667 | 59.9 | 717 | 6 | CB529627 | CB529627 | UI-H-FT2- | |
| | 34 | 666.2 | 59.8 | 907 | 4 | BG166941 | BG166941 | 602339355 | |
| C | 35 | 656 | 58.9 | 696 | 6 | CB529317 | CB529317 | UI-H-FT2- | |
| | 36 | 652.4 | 58.6 | 983 | 4 | BM549405 | BM549405 | AGENCOURT | |
| | 37 | 651.8 | 58.5 | 880 | 6 | CB984985 | CB984985 | AGENCOURT | |
| | 38 | 645.6 | 58.0 | 720 | 6 | CA439961 | CA439961 | UI-H-DI0- | |
| | 39 | 644.6 | 57.9 | 676 | 6 | CD628274 | CD628274 | 56056437H | |
| | 40 | 642.4 | 57.7 | 706 | 4 | BG772424 | BG772424 | 602722361 | |
| | 41 | 640.6 | 57.5 | 690 | 1 | AV763446 | AV763446 | AV763446 | |
| | 42 | 639 | 57.4 | 653 | 5 | BU580876 | BU580876 | in33f12.Y | |
| | 43 | 632.8 | 56.8 | 752 | 4 | BI833417 | BI833417 | 603088066 | |
| | 44 | 632 | 56.7 | 990 | 4 | BI597500 | BI597500 | 603247025 | |
| | 45 | 626.8 | 56.3 | 731 | 4 | BG503050 | BG503050 | 602551030 | |

ALIGNMENTS

RESULT 1
BX462364
LOCUS BX462364 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA
DEFINITION clone CS0DG007YG08 5-PRIME, mRNA sequence.
ACCESSION BX462364
VERSION BX462364.2 GI:47065982
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1040)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31029418.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 384.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DG007BD04QP1&c=384.f.

FEATURES
source

Location/Qualifiers
1..1040
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG007YG08"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 82.3%; Score 917.2; DB 5; Length 1040;
Best Local Similarity 96.0%; Pred. No. 7.6e-242;

| | | | | | | | | | |
|--------------|------|---|------|------------|-----|--------|----|------|----|
| Matches 954; | | Conservative | 7; | Mismatches | 31; | Indels | 2; | Gaps | 2; |
| QY | 62 | TCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATATATCCTTCAGTGGGCTATTGGA | 121 | | | | | | |
| Db | 1 | TCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATATATCCTTCAGTGGGCTATTGGA | 60 | | | | | | |
| QY | 122 | CTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATATGGCGTTTACTGGCCCTTATTC | 181 | | | | | | |
| Db | 61 | CTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATATGGCGTTTACTGGCCCTTATTC | 120 | | | | | | |
| QY | 182 | GTCTCGATTTTCCACGCCATCTCCCCCATCCCCATTTCAATGGCCAAAGAGTCACCTAT | 241 | | | | | | |
| Db | 121 | GTCTCGATTTTCCACGCCATCTCCCCCATCCCCATTTCAATGGCCAAAGAGTCACCTAT | 180 | | | | | | |
| QY | 242 | GACTCAGATGCAACCCAGTAGTGCTGTGCGGAACTGGCATATTTCTTCACTACTGGAATT | 301 | | | | | | |
| Db | 181 | GACTCAGATGCAACCCAGTAGTGCTGTGCGGAACTGGCATATTTCTTCACTACTGGAATT | 240 | | | | | | |
| QY | 302 | GTGTGTTCTGCCTTTGGATTTCCTGTATTCTTGCTCGTGGCTGTGATCAATGGGGA | 361 | | | | | | |
| Db | 241 | GTGTGTTCTGCCTTTGGATTTCCTGTATTCTTGCTCGTGGCTGTGATCAATGGGGA | 300 | | | | | | |
| QY | 362 | GCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCAGGGTTTTTC | 421 | | | | | | |
| Db | 301 | GCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCAGGGTTTTTC | 360 | | | | | | |
| QY | 422 | CTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATCTGATT | 481 | | | | | | |
| Db | 361 | CTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTATCTGATT | 420 | | | | | | |
| QY | 482 | ACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 541 | | | | | | |
| Db | 421 | ACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 480 | | | | | | |
| QY | 542 | TACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACCTTTAAG | 601 | | | | | | |
| Db | 481 | TACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACCTTTAAG | 540 | | | | | | |
| QY | 602 | AAAGACTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAATAGACCTGTCAAATTTAGA | 661 | | | | | | |
| Db | 541 | AAAGACTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAATAGACCTGTCAAATTTAGA | 600 | | | | | | |
| QY | 662 | TTATGTACTCAAATTTATGTTACTTGTGCTGTTCATGTAGTCACGGTGCTCTCAGAA | 721 | | | | | | |
| Db | 601 | TTATGTACTCAAATTTATGTTACTTGTGCTGTTCATGTAGTCACGGTGCTCTCAGAA | 660 | | | | | | |
| QY | 722 | AATATATTAACGCAGTCTTTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTTG | 781 | | | | | | |
| Db | 661 | AATATATTAACGC - TCTTGTAGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTTG | 719 | | | | | | |
| QY | 782 | CTTGGGGATGTGCTTGGAGAGGAGATAAACGCTGAAGCAGGCCTCTCATGACCCAGGAAG | 841 | | | | | | |
| Db | 720 | CTTGGGGATGTGCTTGGAGAGGAGATAAACGCTGAAGCAGGCCTCTCATGACCCAGGAAG | 779 | | | | | | |
| QY | 842 | GCCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAAGTGTGGCCCCACAGACC | 901 | | | | | | |
| Db | 780 | GCCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAAGTGTGGCCCCACAGACC | 839 | | | | | | |
| QY | 902 | AAGAGCCTCAACATTTCTAGAGCCTTATTAGAAAATGCAGAACTCTGAAGCCCCACTTGG | 961 | | | | | | |
| Db | 840 | AAGAGCCTCAACATTTCTAGAGCCTTATTAGAAAATGCAGAACTCTGAAGCCCCACTTGG | 899 | | | | | | |
| QY | 962 | ACCCAGGACATTTTGTATGAGATCCAAAGAGTGTATGCACATGAAAGTTTGAGAAAGAT | 1021 | | | | | | |
| Db | 900 | ACCCAGGACATTTTGTATGAGATCC - AAGGAGGTGTATGMCATGAAAGTTTGRAGSATCAY | 958 | | | | | | |
| QY | 1022 | CATCATAGAGAAGTAACATCCACCCCACTTCC | 1055 | | | | | | |
| Db | 959 | MTAGRGAGTAACATCCMCCMACTTCTCCTAHCITCM | 992 | | | | | | |
| RESULT 2 | | | | | | | | | |
| AL550884 | | | | | | | | | |

| | | | | | |
|-----------------------|---|---|----------------|--------------|-----------------|
| LOCUS | AL550884 | 1050 bp | mrna | linear | EST 25-MAR-2004 |
| DEFINITION | AL550884 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI065YP15 5-PRIME, mRNA sequence. | | | | |
| ACCESSION | AL550884 | | | | |
| VERSION | AL550884.3 | GI:45751247 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| AUTHORS | Li, W.B., Gruber, C., Jessee, J. and Polayes, D. | | | | |
| TITLE | Full-length cDNA libraries and normalization | | | | |
| JOURNAL | Unpublished (2001) | | | | |
| COMMENT | On Feb 15, 2001 this sequence version replaced gi:31272701. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 384.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DI065CH08QP1&c=384.f. | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| ORIGIN | | | | | |
| Query Match | 81.1%; | Score 903.4; | DB 1; | Length 1050; | |
| Best Local Similarity | 95.8%; | Pred. No. 5e-238; | | | |
| Matches | 963; | Conservative 6; | Mismatches 32; | Indels 4; | Gaps 4; |
| QY | 50 | CGCGGCCCCAGTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCCTTCAGT | 109 | | |
| Db | 1 | CGCGGCCCCAGTTCGGGAGACATGGCGGGCGTTAAAGCTCTTGTGGCATTATCCCTTCAGT | 60 | | |
| QY | 110 | GGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGGCGTTTAC | 169 | | |
| Db | 61 | GGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGGCGTTTAC | 120 | | |
| QY | 170 | TGGCCCTTATTCGTCTGATTTTCCACGCCCATCTCCCCCATTTTCATTGCCCAA | 229 | | |
| Db | 121 | TGGCCCTTATTCGTCTGATTTTCCACGCCCATCTCCCCCATTTTCATTGCCCAA | 180 | | |
| QY | 230 | AGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTGCGGAACCTGGCATATTTCTTC | 289 | | |
| Db | 181 | AGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTGCGGAACCTGGCATATTTCTTC | 240 | | |
| QY | 290 | ACTACTGGAATTGTTTCTGCCCTTTGGATTTCTGTATTCTTGCTCGTGTGGCTGTG | 349 | | |
| Db | 241 | ACTACTGGAATTGTTTCTGCCCTTTGGATTTCTGTATTCTTGCTCGTGTGGCTGTG | 300 | | |
| QY | 350 | ATCAAAATGGGAGCCTCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATT | 409 | | |
| Db | 301 | ATCAAAATGGGAGCCTCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATT | 360 | | |
| QY | 410 | CAAGGGTTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCAC | 469 | | |
| Db | 361 | CAAGGGTTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCAC | 420 | | |

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QY 470 TTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCA 529
Db 421 TTATTCTGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCA 480
QY 530 CATCGGCGCATTTTACTATGAATTTAATATGCTGGGTTTTTAATACCTTTATATATCAT 589
Db 481 CATCGGCGCATTTTACTATGAATTTAATATGCTGGGTTTTTAATACCTTTATATATCAT 540
QY 590 GTTCACTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAAATAGACCT 649
Db 541 GTTCACTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAAATAGACCT 600
QY 650 GTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGGTGGTGTTCATGAGTCACG 709
Db 601 GTCAAATTTAGATTATGTTACTCAAATTATGTTACTTGGTGGTGTTCATGAGTCACG 660
QY 710 GTGCTCTCAGAAAATATATTAAACGAGTCTTGTAGGAGCTGCCACCTTATGCAGTGCAT 769
Db 661 GTGCTCTCAGAAAATATATTAAACGCA-TCTTGTAGGCAGCTG-CACCTTATGCAGTGCAT 718
QY 770 CGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCA 829
Db 719 CGAAACCTTTTGCTTGGGGATGTGCTTGGAGAGGCAGATAACGCTAAAGCAGGCTCTCA 778
QY 830 TGACCCAGGAAGCGGGTGGATCCCTCTTTGTGTGTAGTCCATGCTATTAAAAAGTGT 889
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QY 890 GGCCCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAAATCTGAA 949
Db 839 GGCCCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAAATCTGAA 898
QY 950 GCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAG 1009
Db 899 G-CCCACTCTGGACCCAGGACATTTTGATGAGAT-CMAAGGAGTTGTATGMCATGAAAKT 956
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RESULT 3
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LOCUS AL552981 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI072YL04 5-PRIME, mRNA sequence.
ACCESSION AL552981
VERSION AL552981.3 GI:45857751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1026)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31274795.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
384.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI072DF02QP1&c=384.f.
Location/Qualifiers
1. .1026
/organism="Homo sapiens"
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/mol_type="mRNA"
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/clone="CS0DI072YL04"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 79.1%; Score 881; DB 1; Length 1026;
Best Local Similarity 96.7%; Pred. No. 7.6e-232;
Matches 939; Conservative 11; Mismatches 16; Indels 5; Gaps 5;

QY 49 CCGCGCCCCAGTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTTCTTCAG 108
Db 10 CCGGATCCAGCTCGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTTCTTCAG 69
QY 109 TGGGGCTATTGGACTGACTTTTCTTATGCTGGATGTGCCCTTAGAGGATTATGGCGTTA 168
Db 70 TGGGGCTATTGGACTGACTTTTCTTATGCTGGATGTGCCCTTAGAGGATTATGGCGTTA 129
QY 169 CTGGCCCTTATTCTGCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAA 228
Db 130 CTGGCCCTTATTCTGCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAA 189
QY 229 AAGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTGCGGAACCTGGCATATTTCTT 288
Db 190 AAGAGTCACCTATGACTCAGATGCAACCAGTAGTGCCTGTGCGGAACCTGGCATATTTCTT 249
QY 289 CACTACTGGAATTGTGTTTCTGCCCTTTGGATTTCCTGTTATTCTTGCTCGTGGCTGT 348
Db 250 CACTACTGGAATTGTGTTTCTGCCCTTTGGATTTCCTGTTATTCTTGCTCGTGGCTGT 309
QY 349 GATCAAAATGGGAGCCTGCGGCCTTGTGTTGGAGGAGATGATTTTAGCTGGAGCAGTGCAGCAAT 408
Db 310 GATCAAAATGGGAGCCTGCGGCCTTGTGTTGGAGGAGCAATGCAGTCATTTTCCTTACAAT 369
QY 409 TCAAGGGTTTTTCCCTTATATTGGAAGAGGAGATGATTTTAGCTGGAGCAGTGCAGCA 468
Db 370 TCAAGGGTTTTTCCCTTATATTGGAAGAGGAGATGATTTTAGCTGGAGCAGTGCAGCA 429
QY 469 CTTTATTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACTATCTGTATACATGTGC 528
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QY 529 ACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCA 588
Db 490 ACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCA 549
QY 589 TGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAAATAGACC 648
Db 550 TGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAAATAGACC 609
QY 649 TGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTCAC 708
Db 610 TGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTCAC 669
QY 709 GGTGCTCTCAGAAAATATATTAAACGAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCA 768
Db 670 GGTGCTCTCAGAAAATATATTAAACGATCTTGTAGGCAGCTGCCACCTTATGCAGTGCA 729
QY 769 TCGAAACCTTTTGTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTC 828
Db 730 TCGAAACCTTTTGTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTC 789
QY 829 ATGACCCAGGAAGCC-GGGGTGGATCCCTCTTT-GTGTGTAGTCCATGCTATTAAAAAG 886
Db 790 ATGACCCAGGAAGCCGGGGTGGATCCCTCTTTTGGTGTGKAGTCCATGCTATTAAAAAG 849
QY 887 TGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAAATCT 946
Db 887 TGTGGCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAAATCT 946
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| | | | |
|-----------------------|------------|--|-------------------------------------|
| Db | 850 | TGTGGCCACAGAACAGAGCCTCCACATTTCTAGAGSCTTATTWGAATGCAKATCT | 909 |
| Qy | 947 | GAAGCCCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGATGCACATGA | 1006 |
| Db | 910 | GARG-CCCACCTCTGGA-CMGGACATTTTGATGAGATCCAAAGGAG-TGTATGCAMAGAA | 966 |
| Qy | 1007 | AAGTTTGAGAA | 1017 |
| Db | 967 | AGTTKRGARSA | 977 |
| RESULT 4 | | | |
| BX417049 | | | |
| LOCUS | BX417049 | Homo sapiens PLACENTA | 952 bp mRNA linear EST 01-MAY-2004 |
| DEFINITION | BX417049 | 5-PRIME, mRNA sequence. | |
| ACCESSION | BX417049 | | |
| VERSION | BX417049.2 | GI:46933188 | |
| KEYWORDS | | | |
| SOURCE | | Homo sapiens (human) | |
| ORGANISM | | Homo sapiens | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| AUTHORS | | Li,W.B., Gruber,C., Jessee,J. and Polayes,D. | |
| TITLE | | Full-length cDNA libraries and normalization | |
| JOURNAL | | Unpublished (2001) | |
| COMMENT | | On May 13, 2003 this sequence version replaced gi:30654341. | |
| FEATURES | | Location/Qualifiers | |
| source | | 1..952 | |
| | | /organism="Homo sapiens" | |
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| | | /clone="CS0DE003YJ23" | |
| | | /tissue_type="PLACENTA" | |
| | | /clone_lib="Homo sapiens PLACENTA" | |
| | | /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." | |
| | | Library was not normalized." | |
| | | This sequence belongs to sequence cluster 384.f | |
| | | For more information about this cluster, see | |
| | | http://www.genoscope.cns.fr/cdna?s=CS0DE003CE12QP1&c=384.f. | |
| Query Match | | 72.3%; | Score 805.8; DB 5; Length 952; |
| Best Local Similarity | | 98.4%; | Pred. No. 4.4e-211; |
| Matches | 835; | Conservative | 0; Mismatches 12; Indels 2; Gaps 2; |
| Qy | 49 | CCGGCCCCCAGTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCAATTATCCTTCAG | 108 |
| Db | 10 | CCGGATCCCAGCTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCAATTATCCTTCAG | 69 |
| Qy | 109 | TGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCTCTAGAGGATTATGGCGTTTA | 168 |
| Db | 70 | TGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTGCTCTAGAGGATTATGGCGTTTA | 129 |
| Qy | 169 | CTGGCCCTTATTCGTCCTGATTTTCCAGCCCATCTCCCCCATCCCCCATTTTCATTGCGCAA | 228 |
| Db | 130 | CTGGCCCTTATTCGTCCTGATTTTCCAGCCCATCTCCCCCATCCCCCATTTTCATTGCGCAA | 189 |
| Qy | 229 | AAGAGTCACTATGACTCAGATGCAACCAGTAGTGCCTGTGCGGAAGTGGCATAATTTCTT | 288 |

| | | | |
|------------|------------|---|-------------------------------------|
| Db | 190 | AAGAGTCACCTATGACTCAGATGCAACACAGTAGTGCCCTGTCGGGAACCTGGCATAATTTCTT | 249 |
| Qy | 289 | CACACTGGAAATTGTTGTTTTCGCCCTTTGGATTTCCCTGTTATTCTTGCTCGTGGCTGT | 348 |
| Db | 250 | CACACTGGAAATTGTTGTTTTCGCCCTTTGGATTTCCCTGTTATTCTTGCTCGTGGCTGT | 309 |
| Qy | 349 | GATCAAAATGGGGAGCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCTTACAAT | 408 |
| Db | 310 | GATCAAAATGGGGAGCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCTTACAAT | 369 |
| Qy | 409 | TCAAGGGTTTTTCTTATATTTTGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCA | 468 |
| Db | 370 | TCAAGGGTTTTTCTTATATTTTGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCA | 429 |
| Qy | 469 | CTTTATTCTGATTACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGC | 528 |
| Db | 430 | CTTTATTCTGATTACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGC | 489 |
| Qy | 529 | ACATGCGGCATTTTACTATGAAATTTAAATATGCTGGGTTTTTTTAATACCTTTATATATCA | 588 |
| Db | 490 | ACATGCGGCATTTTACTATGAAATTTAAATATGCTGGGTTTTTTTAATACCTTTATATATCA | 549 |
| Qy | 589 | TGTTCACTTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATTCAGCAAAATAGACC | 648 |
| Db | 550 | TGTTCACTTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATTCAGCAAAATAGACC | 609 |
| Qy | 649 | TGTCAAATTTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTCAC | 708 |
| Db | 610 | TGTCAAATTTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTCAC | 669 |
| Qy | 709 | GGTGCTCTCAGAAATATATTAAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTGCA | 768 |
| Db | 670 | GGTGCTCTCAGAAATATATTAAACGCA-TCTTGTAGGCAGCTGCCACCTTATGCAGTGCA | 728 |
| Qy | 769 | TCGAAACCTTTTGTGTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTC | 828 |
| Db | 729 | TCGAAACCTTTTGTGTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTC | 788 |
| Qy | 829 | ATGACCCAGGAAGCCGGGTGGATCCCTCTTTGTGTTAGTCCATGCTATTAAAGTG | 888 |
| Db | 789 | ATGACCCAGGAAGCCGGGTGGAT-CCTCTTTGTGTTAGTCCATGCTATTAAAGTG | 847 |
| Qy | 889 | TGGCCACACA | 897 |
| Db | 848 | GGCCACAGA | 856 |
| RESULT 5 | | | |
| BX417586 | | | |
| LOCUS | BX417586 | Homo sapiens PLACENTA | 1004 bp mRNA linear EST 01-MAY-2004 |
| DEFINITION | BX417586 | 5-PRIME, mRNA sequence. | |
| ACCESSION | BX417586 | | |
| VERSION | BX417586.2 | GI:46927707 | |
| KEYWORDS | | EST. | |
| SOURCE | | Homo sapiens (human) | |
| ORGANISM | | Homo sapiens | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| | | 1 (bases 1 to 1004) | |
| | | Li,W.B., Gruber,C., Jessee,J. and Polayes,D. | |
| | | Full-length cDNA libraries and normalization | |
| | | Unpublished (2001) | |
| | | On May 13, 2003 this sequence version replaced gi:30642089. | |
| | | Contact: Genoscope | |
| | | Genoscope - Centre National de Sequencage | |
| | | 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE | |
| | | Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr | |
| | | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |

This sequence belongs to sequence cluster 384.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE010CF02QP1&c=384.f.
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/clone_lib="Homo sapiens PLACENTA"
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ORIGIN

Query Match 71.0%; Score 790.6; DB 5; Length 1004;
Best Local Similarity 97.1%; Pred. No. 7.1e-207;
Matches 848; Conservative 0; Mismatches 19; Indels 6; Gaps 4;
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Db 1 AGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTTCTTATGCTGGGATG 60
QY 145 TGCCTTAGAGGATTATGGGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTC 204
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Db 121 CCCCATCCCCCATTTCAFTGCCAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGC 180
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QY 385 CAATGCAGTCATTTTCCTTACAATTCAAGGGTTTTTCCTTATATTGGAAGAGGAGATGA 444
Db 301 CAATGCAGTCATTTTCCTTACAATTCAAGGGTTTTTCCTTATATTGGAAGAGGAGATGA 360
QY 445 TTTTAGCTGGGAGCAGTGGTAGCACTTTATTTCTGATTACAGTGCAATTGAAATTTCTTAGAA 504
Db 361 TTTTAGCTGGGAGCAGTGGTAGCACTTTATTTCTGATTACAGTGCAATTGAAATTTCTTAGAA 420
QY 505 CTCATACTATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGG 564
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Db 481 GTTTTAAATACCTTTATATATCATGTTCACTTTAAGAAAGACTTTCATAAGTAGGAGATG 540
QY 625 AGTTTATTTCTCAGCAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTAC 684
Db 541 AGTTTATTTCTCAGCAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTAC 600
QY 685 TTGTTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGAAAATATATTAAACGCAGTCTGTAG 744
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Db 720 AGATAACGCTGAAGCAGGCTCTCATGACCCAGGAAGCCGGGTGGAT-CCCTCTTTGTG 778

QY 865 TTGTAGTCCATGCTATTAAAGTGTGGCCCAAGAGAGCCTCAACATTTCTTAGAG 924
Db 779 TTGTAGTCCATGCTATTAAAGTGTGG-CCACAGACCAAGAGCTCAACATTTCTTAGAG-- 835
QY 925 CCTTATTAGAAATGCAGAATCTGAAGCCCCACT 957
Db 836 -CTTATTAGAAATGCAGATCTGAAGCCCCACTCT 867
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AL571122
LOCUS
DEFINITION
AL571122 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI027YK17 5-PRIME, mRNA sequence.
AL571122
ACCESSION
VERSION
AL571122.3 GI:46237227
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 786)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31292526.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 384.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI027AF09QP1&c=384.f.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 70.4%; Score 784.4; DB 1; Length 786;
Best Local Similarity 99.9%; Pred. No. 3.5e-205;
Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 GAAGCCGGAAGCAGCGCGGCCAGTCGGGAGACATGGCGGCGTTAAAGCTCTCGTG 60
QY 95 GCATTATCCTTCAGTGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAGAG 154
Db 61 GCATTATCCTTCAGTGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAGAG 120
QY 155 GATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCCCC 214
Db 121 GATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCCCC 180
QY 215 CATTTCATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCCTGTGCGGAA 274
Db 181 CATTTCATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCCTGTGCGGAA 240

QY 275 CTGGCATATTTCTTCACTACTGGAATTGTTGTTTCTGCCCTTTGGATTTCCTGTTATTCCT 334
Db 241 CTGGCATATTTCTTCACTACTGGAATTGTTGTTTCTGCCCTTTGGATTTCCTGTTATTCCT 300
QY 335 GCTCGTGTGGCTGTGATCAAAATGGGGAGCCCTCGGCCCTTGTTGGCAGGCAATGCAGTC 394
Db 301 GCTCGTGTGGCTGTGATCAAAATGGGGAGCCCTCGGCCCTTGTTGGCAGGCAATGCAGTC 360
QY 395 ATTTTCTCTTACAATTCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTAGCTGG 454
Db 361 ATTTTCTCTTACAATTCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTAGCTGG 420
QY 455 GAGCAGTGGTAGCACCTTTATTTCTGATTACAGTGCAATTCGAATTTCTTAGAACTCATACTAT 514
Db 421 GAGCAGTGGTAGCACCTTTATTTCTGATTACAGTGCAATTCGAATTTCTTAGAACTCATACTAT 480
QY 515 CTGTATACATGTGCACATCGGGCATTTTACTATGAAATTTAAATATGCTGGGTTTTTAAAT 574
Db 481 CTGTATACATGTGCACATCGGGCATTTTACTATGAAATTTAAATATGCTGGGTTTTTAAAT 540
QY 575 ACCTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTC 634
Db 541 ACCTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTATTC 600
QY 635 TCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTACTTGTTTGGCT 694
Db 601 TCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTACTTGTTTGGCT 660
QY 695 GTTCATGTAGTCACGGTGCTCTCAGAAATAATATTAACCGAGTCTTGAGGCAGCTGCCA 754
Db 661 GTTCATGTAGTCACGGTGCTCTCAGAAATAATATTAACCGAGTCTTGAGGCAGCTGCCA 720
QY 755 CCTTATGCAGTGCATCGAAACCTTTTGCTGGGGATGTGCTTGGAGAGGCAGATAACGCT 814
Db 721 CCTTATGCAGTGCATCGAAACCTTTTGCTGGGGATGTGCTTGGAGAGGCAGATAACGCT 780
QY 815 GAAGCA 820
Db 781 GAAGCA 786

RESULT 7
AL709947
LOCUS
DEFINITION
AL709947 805 bp mRNA linear EST 04-SEP-2003
DKFZp686B1965_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686B1965_5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
AL709947
AL709947.1 GI:19693302
EST.
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 805)
Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and
Wiemann,S.

AUTHORS
TITLE
EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and
Wiemann,S.)
Unpublished (2001)
Contact: MIPS
MIPS

JOURNAL
COMMENT

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686B1965) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Location/Qualifiers
1..805

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686B1965"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 69.7%; Score 776.8; DB 1; Length 805;
Best Local Similarity 99.5%; Pred. No. 4.4e-203;
Matches 800; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 43 AAGCAGCCGCGGCCCCAGTTTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATC 102
Db 1 AAGCAGCCGCGGCCCCAGCTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATC 60
QY 103 CTTCAGTGGGCTATTGGACTGACTGACTTTTCTTATGCTGGGATGTCCCTAGAGGATTATGG 162
Db 61 CTTCAGTGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCCTAGAGGATTATGG 120
QY 163 CGTTTACTGGCCCTTATTCGTCCTGATTTTCACGCCCATCTCCCCATCCCCCATTTTCA 222
Db 121 CGTTTACTGGCCCTTATTCGTCCTGATTTTCACGCCCATCTCCCCATCCCCCATTTTCA 180
QY 223 TGCCAAAAGAGTCACCTATGACTCAGATGCAACCCAGTAGTGCTGCGGAACTGGCATA 282
Db 181 TGCCAAAAGAGTCACCTATGACTCAGATGCAACCCAGTAGTGCTGCGGATCTGGCATA 240
QY 283 TTTCTTCACTACTGGAAATGTTGTTTCTGCCCTTGGATTTCCTGTTATTTCTGCTCGTGT 342
Db 241 TTTCTTCACTACTGGAAATGTTGTTTCTGCCCTTGGATTTCCTGTTATTTCTTGTCTCGT 300
QY 343 GGCTGTGATCAAATGGGGAGCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCT 402
Db 301 GGCTGTGATCAAATGGGGAGCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCT 360
QY 403 TACAATTCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTG 462
Db 361 TACAATTCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTG 420
QY 463 GTAGCACTTTATTTCTGATTACAGTGCAATGAAATTTCTTAGAACTCATACTATCTGTATAC 522
Db 421 GTAGCACTTTATTTCTGATTACAGTGCAATGAAATTTCTTAGAACTCATACTATCTGTATAC 480
QY 523 ATGTGCACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTAAATACCTTTAT 582
Db 481 ATGTGCACATGCGGCATTTTACTATGAAATTTAATAATGCTGGGTTTTTAAATACCTTTAT 540
QY 583 ATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTTATTTCTCAGCAAA 642
Db 541 ATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTTTATTTCTCAGCAAA 600
QY 643 TAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTGTTGGCTGTTTCATGT 702
Db 601 TAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTGTTGGCTGTTTCATGT 660
QY 703 AGTCACGGTGTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTATGC 762
Db 661 AGTCACGGTGTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTATGC 720
QY 763 AGTGCATCGAAACCTTTTGTCTT-GGGGATGTGCTT-GGAGAGGCAGATAACGCTGAAGCA 820
Db 721 AGTGCATCGAAACCTTTTGTCTTGGGGGATGTGCTTGGGAGAGGCAGATAACGCTGAAGCA 780
QY 821 GGCCTCTCATGACCCAGGAAGGCC 844
Db 781 GGCCTCTCATGACCCAGGAAGGCC 804

RESULT 8

| | | | | | | | | | | |
|-----------------------|-----------------------------------|---------------------------|---|------------|---------------|-------------|------|------|----|--|
| ORIGIN | Note: this is a NIH_MGC Library." | | | | | | | | | |
| Query Match | 69.3%; | Score | 771.6; | DB | 5; | Length | 996; | | | |
| Best Local Similarity | 98.4%; | Pred. | No. 1.3e-201; | | | | | | | |
| Matches | 811; | Conservative | 0; | Mismatches | 9; | Indels | 4; | Gaps | 3; | |
| QY | 74 | GCGGGCGTTAAAGCTCTCGTGGCAT | TATCCTTCAGTGGGCTATTGGACTGACTTTTCTT | 133 | | | | | | |
| Db | 1 | GCGGGCGTTAAAGCTCTCGTGGCAT | TATCCTTCAGTGGGCTATTGGACTGACTTTTCTT | 60 | | | | | | |
| QY | 134 | ATGCTGGGATGTGCCCTTAGAGGAT | TATGGCGTTTACTGGCCCTTATTTCGTCCTGATTTTC | 193 | | | | | | |
| Db | 61 | ATGCTGGGATGTGCCCTTAGAGGAT | TATGGCGTTTACTGGCCCTTATTTCGTCCTGATTTTC | 120 | | | | | | |
| QY | 194 | CAGCCCATCTCCCCCATCCCCCAT | TTTCATTTGCCAAAAGAGTCACCTATGACTCAGATGCA | 253 | | | | | | |
| Db | 121 | CAGCCCATCTCCCCCATCCCCCAT | TTTCATTTGCCAAAAGAGTCACCTATGACTCAGATGCA | 180 | | | | | | |
| QY | 254 | ACCAGTAGTGCCTGTGCGGAACT | GGGCATATTTCTTCACTACTGGAATTGTTGTTCTGCC | 313 | | | | | | |
| Db | 181 | ACCAGTAGTGCCTGTGCGGAACT | GGGCATATTTCTTCACTACTGGAATTGTTGTTCTGCC | 240 | | | | | | |
| QY | 314 | TTTGGATTTCCTGTTATTCTTGCT | CGTGTGGCTGTGATCAAAATGGGAGCCTCGCGCCTT | 373 | | | | | | |
| Db | 241 | TTTGGATTTCCTGTTATTCTTGCT | CGTGTGGCTGTGATCAAAATGGGAGCCTCGCGCCTT | 300 | | | | | | |
| QY | 374 | GTGTTGGCAGGCAATGCAGTCA | TATTTCTTACAATCAAGGGTTTTTTCCTTATATTGGA | 433 | | | | | | |
| Db | 301 | GTGTTGGCAGGCAATGCAGTCA | TATTTCTTACAATCAAGGGTTTTTTCCTTATATTGGA | 360 | | | | | | |
| QY | 434 | AGAGGAGATGATTTTAGCTGGG | AGAGTGGTAGCACTTTTATCTGATTACAGTGCATTGA | 493 | | | | | | |
| Db | 361 | AGAGGAGATGATTTTAGCTGGG | AGAGTGGTAGCACTTTTATCTGATTACAGTGCATTGA | 420 | | | | | | |
| QY | 494 | ATTTCCTTAGAACTCATACTAT | CTGTATACATGTGCACATGCGGCATTTTACTATGAAATT | 553 | | | | | | |
| Db | 421 | ATTTCCTTAGAACTCATACTAT | CTGTATACATGTGCACATGCGGCATTTTACTATGAAATT | 480 | | | | | | |
| QY | 554 | TAATATGCTGGGTTTTTTTAA | TACCTTTATATATCATGTTTCACTTTAAGAAAGACTTCATA | 613 | | | | | | |
| Db | 481 | TAATATGCTGGGTTTTTTTAA | TACCTTTATATATCATGTTTCACTTTAAGAAAGACTTCATA | 540 | | | | | | |
| QY | 614 | AGTAGGAGATGAGTTTTTAT | TCTCAGCAAATAGACCTGTCAAATTTAGATTATGTTACTCA | 673 | | | | | | |
| Db | 541 | AGTAGGAGATGAGTTTTTAT | TCTCAGCAAATAGACCTGTCAAATTTAGATTATGTTACTCA | 600 | | | | | | |
| QY | 674 | AATTATGTTACTTGTGTTG | GCTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAAACG | 733 | | | | | | |
| Db | 601 | AATTATGTTACTTGTGTTG | GCTTCATGTAGTCACGGTGCTCTCAGAAAAATATATTAAACG | 660 | | | | | | |
| QY | 734 | CAGTCTTTGTAGGCAGCTG | CCACCTTATGCAGTGCATCGAAACCTTTTGTCTTGGGGATGTG | 793 | | | | | | |
| Db | 661 | CAGTCTTTGTAGGCAGCTG | CCACCTTATGCAGTGCATCGAAACCTTTTGTCTTGGGGATGTG | 720 | | | | | | |
| QY | 794 | CTTGAGAGGCAGATAACG | CTGAAGCAGGCCCTCTCATGACCCAGGAAGG--CCGGGGTGG | 851 | | | | | | |
| Db | 721 | CTTGAGAGAGG-AGATA | ACGCTGAAGCAGGCCCTCTCATGACCCAGGAAGGCGGGGGGA | 779 | | | | | | |
| QY | 852 | ATCCCTCTTTGTGTTGT | AGTCCATG-CTATTAAAAGTGTGGCCC | 894 | | | | | | |
| Db | 780 | TCCCTCTTTGTGTTGT | AGACCATGCCTATTAAAAGTGTGGGCC | 823 | | | | | | |
| RESULT 10 | | | | | | | | | | |
| BU189726 | | | | | | | | | | |
| LOCUS | BU189726 | 914 bp | mRNA | linear | EST | 04-SEP-2002 | | | | |
| DEFINITION | AGENCOURT_7858388 | NIH_MGC_72 | Homo sapiens | cDNA clone | IMAGE:6168548 | | | | | |
| ACCESSION | 5', mRNA sequence. | | | | | | | | | |
| VERSION | BU189726 | | | | | | | | | |
| KEYWORDS | BU189726.1 | GI:22703710 | | | | | | | | |
| SOURCE | EST. | | | | | | | | | |
| | Homo sapiens (human) | | | | | | | | | |

QY 587 CATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAAAATAGA 646
|||||
Db 541 CATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAAAATAGA 600
|||||
QY 647 CCTGTCAAATTTAGATTATGTTACTCAAAATTATGTTACTTGTGGCTGTTTCATGTAGTC 706
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Db 601 CCTGTCAAATTTAGATTATGTTACTCAAAATTATGTTACTTGTGGCTGTTTCATGTAGTC 660
|||||
QY 707 ACGGTGCTCTCAGAAATATATTAAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTG 766
|||||
Db 661 ACGGTGCTCTCAG-AAATATATTAAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCAGTG 719
|||||
QY 767 CATCGAAACCTTTTGTCTGGGATGTGC-TTGGAGAGCAGATAACGCTGAAGCAGGCCT 825
|||||
Db 720 CATCGAAACCTTTGGCCTTGGGATGTGCTTTGGAGAGCAGATAACGCTGAAGCAGGCCT 779
|||||
QY 826 CTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTCTGTGTGTAGT 871
|||||
Db 780 CTCATGACCCAGAANGSGNCAGNGTGATNCCCCTNCTTTTGGGGGT 825
|||||

RESULT 11
BQ424209 899 bp mRNA linear EST 23-MAY-2002
LOCUS
DEFINITION BQ424209 AGENCOURT_7894867 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158131
5', mRNA sequence.
ACCESSION BQ424209
VERSION BQ424209.1 GI:21119524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 899)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13505 row: b column: 20
High quality sequence stop: 638.
FEATURES Location/Qualifiers
source 1..899
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6158131"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

FEATURES
source
1..899
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6158131"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 68.8%; Score 766.4; DB 5; Length 899;
Best Local Similarity 98.6%; Pred. No. 3.4e-200;
Matches 783; Conservative 0; Mismatches 8; Indels 3; Gaps 1;
QY 86 GCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTTCTTATGCTGGGATGT 145
|||||
Db 11 GCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACTGACTTTTCTTATGCTGGGATGT 70
|||||
QY 146 GCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCC 205
|||||

Db 71 GCCTTAGAGGATTATGGCGTTTACTGGCCCTTATTTCGTCCTGATTTTCCACGCCATCTCC 130
QY 206 CCCATCCCCCATTTCAATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCC 265
|||||
Db 131 CCCATCCCCCATTTCAATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCC 190
|||||
QY 266 TGTGGGAACCTGGCATATTTCTTCACTACTGGAATTGTTGTTTCTGCCCTTTGGATTTCCT 325
|||||
Db 191 TGTGGGAACCTGGCATATTTCTTCACTACTGGAATTGTTGTTTCTGCCCTTTGGATTTCCT 250
|||||
QY 326 GTTATTCTTGTCTGTGTGGCTGTGATCAAATGGGGAGCCCTGCGGCCTTGTGTGGCAGGC 385
|||||
Db 251 GTTATTCTTGTCTGTGTGGCTGTGATCAAATGGGGAGCCCTGCGGCCTTGTGTGGCAGGC 310
|||||
QY 386 AATGCAGTCATTTTCTTCAATTAAGGGTTTTCTTATATTGGAAGAGGAGATGAT 445
|||||
Db 311 AATGCAGTCATTTTCTTCAATTAAGGGTTTTCTTATATTGGAAGAGGAGATGAT 370
|||||
QY 446 TTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGATTACAGTGCATTTGAATTTCTTAGAAC 505
|||||
Db 371 TTTAGCTGGGAGCAGTGGTAGCACTTTATTCTGATTACAGTGCATTTGAATTTCTTAGAAC 430
|||||
QY 506 TCATACTATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGG 565
|||||
Db 431 TCATACTATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGG 490
|||||
QY 566 TTTTAAATACCTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGA 625
|||||
Db 491 TTTTAAATACCTTTATATATCATGTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGA 550
|||||
QY 626 GTTTATTCTCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACT 685
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Db 551 GTTTATTCTCAGCAAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACT 610
|||||
QY 686 TGTTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGAAAATATATTAAACGCAGTCTTGTAGG 745
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Db 611 TGTTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGANAATATATTAAACGCAGTCTTGTAGG 670
|||||
QY 746 CAGCTGCCACCTTATGCAAGTGCATCGAAACCTTTTGTCTTGGGATGTGCTTGGAGAGGCA 805
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Db 671 CAGCTGCCACCTTATGCAAGTGCATCGAAACCTTTTGTCTTGGGATGTGCTTGGAGAGGCA 730
|||||
QY 806 GATAACGCTGAAGCAGGCCTCTCATGACCCAGGAAGCCGGGTGGATCCCTC---TTTG 862
|||||
Db 731 GATAACGCTANAGCAGGCCTCTCATGACCCAGGAAGCCGGGTGGATCCCTCNCNTTTG 790
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QY 863 TGTGTAGTCCATG 876
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Db 791 TGTGGAGTCCATG 804
|||||

RESULT 12
CF594097
LOCUS
DEFINITION CF594097 AGENCOURT_15624279 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30528070 5', mRNA sequence.
ACCESSION CF594097
VERSION CF594097.1 GI:36348247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM613 row: g column: 23
 High quality sequence stop: 589.
 Location/Qualifiers
 1. 835
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30528070"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 147"
 /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
 ali-XhoI; Site_2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: This is
 a NIH MGC library."

| | | | | | |
|--------|-----------------------|---|---------------------|---------------|-------------|
| ORIGIN | Query Match | 68.5%; | Score 763.4; | DB 7; | Length 835; |
| | Best Local Similarity | 98.9%; | Pred. No. 2.2e-199; | | |
| | Matches 790; | Conservative | 0; | Mismatches 6; | Indels 3; |
| | | | | | Gaps 2; |
| QY | 1 | GTCTGGCTTGGGCAGGCTGCCCGGGCCGTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAG | 60 | | |
| Db | 37 | | | | |
| QY | 61 | TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG | 120 | | |
| Db | 97 | TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGGCTATTGG | 156 | | |
| QY | 121 | ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT | 180 | | |
| Db | 157 | ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT | 216 | | |
| QY | 181 | CGTCCTGATTTTCCACGCGCATCTCCCCCATCCCCCATTTTCATTCGCCAAAAGAGTCACCTA | 240 | | |
| Db | 217 | CGTCCTGATTTTCCACGCGCATCTCCCCCATCCCCCATTTTCATTCGCCAAAAGAGTCGCCTA | 276 | | |
| QY | 241 | TGACTCAGATGCAACCAAGTAGTGCCCTGTTCGGGAACTCGGCATAATTTCTTCACTACTGGAAT | 300 | | |
| Db | 277 | TGACTCAGATGCAACCAAGTAGTGCCCTGTTCGGGAACTCGGCATAATTTCTTCACTACTGGAAT | 336 | | |
| QY | 301 | TGTTGTTTCTGCCCTTTGGATTTCCTGTTATTCTTGCTCGTGIGGCTGTGATCAAATGGGG | 360 | | |
| Db | 337 | TGTTGTTTCTGCCCTTTGGATTTCCTGTTATTCTTGCTCGTGIGGCTGTGATCAAATGGGG | 396 | | |
| QY | 361 | AGCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATCAAGGGTTTTT | 420 | | |
| Db | 397 | AGCCTGCGGCCCTTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATCAAGGGTTTTT | 456 | | |
| QY | 421 | CCTTATATTGGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTTATTCTTGAT | 480 | | |
| Db | 457 | CCTTATATTGGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTTATTCTTGAT | 516 | | |
| QY | 481 | TACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 540 | | |
| Db | 517 | TACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT | 576 | | |
| QY | 541 | TTACTATGAAATTTAATATGCTGGGTTTTTTTAAATACCTTTATATATCATGTTCACTTTAA | 600 | | |
| Db | 577 | TTACTATGAAATTTAATATGCTGGGTTTTTTTAAATACCTTTATATATCATGTTCACTTTAA | 636 | | |

| | | | |
|------------|-----|---|-----|
| QY | 601 | GAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACCTGTCAAATTAG | 660 |
| Db | 637 | GAAGACTTCATAAGTAGGAGATGAGTTTATTTCTCAGCAAAATAGACCTGTCAAATTAG | 696 |
| QY | 661 | ATTATGTTACTCAAATTATGTTACTTTGTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGA | 720 |
| Db | 697 | ATTATGTTACTCAAATTATGTTACTTTGTTGGCTGTTTCATGTAGTCACGGTGCTCTCAGA | 756 |
| QY | 721 | AAATATATTAACGCAG-TCTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAA--CCT | 777 |
| Db | 757 | AAATATATTAACGCAGTTCTTGTAGGCAGCTGCCACCTTAGCAGGGCATCGAAAACCTT | 816 |
| QY | 778 | TTTGCTTGGGGATGTGCTT | 796 |
| Db | 817 | TTTGCTTGGGGATGTGCTT | 835 |
| RESULT 13 | | | |
| CB956304 | | | |
| LOCUS | | | |
| DEFINITION | | | |
| ACCESSION | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |
| FEATURES | | | |
| source | | | |

ORIGIN

| | | | | |
|---------------------------|--------|---------------------|-------|-------------|
| Query Match | 67.1%; | Score 747.2; | DB 6; | Length 786; |
| Best Local Similarity | 98.7%; | Pred. No. 6.6e-195; | | |
| Matches 774. Conservative | | 0; Mismatches | 8; | Indels |
| | | | | 2; |
| | | | | Gaps |

Qy

Db 4 GGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGGACT 63

QY 124 GACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGGTTTACTGGCCCTTATTCGT 183

Db 64 GACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGGTTTACTGGCCCTTATTCGT 123

QY 184 CCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTATGA 243

Db 124 CCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCAAAAGAGTCACCTATGA 183

QY 244 CTCAGATGCAACCACTAGTGCCTGTGCGGAACCTGGCAATTTCTTCACTACTGGAATTGT 303

Db 184 CTCAGATGCAACCACTAGTGCCTGTGCGGAACCTGGCAATTTCTTCACTACTGGAATTGT 243

QY 304 TGTTCCTGCCTTTGGATTTCCTGTTATTCTTGTCTCGTGGCTGTGATCAAAATGGGGAGC 363

Db 244 TGTTCCTGCCTTTGGATTTCCTGTTATTCTTGTCTCGTGGCTGTGATCAAAATGGGGAGC 303

QY 364 CTGCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCAAAGGTTTTTCCT 423

Db 304 CTGCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCAAAGGTTTTTCCT 363

QY 424 TATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTTATTCTGATTAC 483

Db 364 TATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTTTATTCTGATTAC 423

QY 484 AGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATTTTA 543

Db 424 AGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATTTTA 483

QY 544 CTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACTTTAAGAA 603

Db 484 CTATGAAATTTAATATGCTGGGTTTTTTAATACCTTTATATATCATGTTCACTTTAAGAA 543

QY 604 AGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAATAGACCTGTCAAATTTAGATT 663

Db 544 AGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAATAGACCTGTCAAATTTAGATT 603

QY 664 ATGTTACTCAAATTATGTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTTCAGAAA 723

Db 604 ATGTTACTCAAATTATGTTACTTGTGTTGGCTGTTTCATGTAGTCACGGTCTTCAG-AAA 662

QY 724 TATATTAACGCAGTCTTGAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTTGCT 783

Db 663 TATATTAACACAGTCTTGAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTTGCT 722

QY 784 TGGGGATGTGCTTGG-AGAGGCAGATAACGCTGAAGCAGCGCTCTCATGACCCAGGAAG 842

Db 723 TGGGGATGTGCTTGGNAGAAGCAGATAACGCTGAGCAAGCCTCTCATGACCCAGGAAG 782

QY 843 CCGG 846

Db 783 CCGG 786

RESULT 14

CA311840/c

LOCUS

DEFINITION

UI-CF-FN0-afe-o-10-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone

UI-CF-FN0-afe-o-10-0-UI 3', mRNA sequence.

ACCESSION

CA311840

VERSION

CA311840.1 GI:24529938

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 765)

AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

9704477

8889548

PUBMED

COMMENT

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

The following repetitive elements were found in this cDNA sequence: 1-21, >AT rich#Low complexity (matched complement) 166-249, >MERSA#DNA/MER1_type (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..765

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-FN0-afe-o-10-0-UI"

/tissue_type="Human Lung Epithelial cells"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-CF-FN0"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu

TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS

6hr_to LPS 24h

TAG_LIB=UI-CF-FN0

TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 65.7%; Score 731.8; DB 6; Length 765;

Best Local Similarity 99.3%; Pred. No. 1.2e-190;

Matches 744; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 366 GCGGCCTTGTGTTGGCAGCAATGCAGTCATTTTCCTTACAATTCAAAGGTTTTTCCTTA 425

Db 765 GCGGCCTTGTGTTGGCAGCAATGCAGTCATTTTCCTTANCAATTCAAAGGTTTTTCCTTA 706

QY 426 TATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACCTTTATTCTGTATTACAG 485

Db 705 TATNTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACCTTTATTCTGTATTACAG 646

QY 486 TGCATTGAAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATTTTACT 545

Db 645 TGCATTGAAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATTTTACT 586

QY 546 ATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACTTTAAGAAAG 605

Db 585 ATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACTTTAAGAAAG 526

QY 606 ACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAAAATAGACCTGTCAAATTTAGATTAT 665

Db 525 ACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAAAATAGACCTGTCAAATTTAGATTAT 466

QY 666 GTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTCACGGTGCTCTCAGAAAATA 725

Db 465 GTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTCACGGTGCTCTCAGAAAATA 406

QY 726 TATTAACGCAGTCTTGTAGGCAGCTGCCACCTTATGCTAGTCATCGAAACCTTTTGCTTG 785

Db 405 TATTAACGCAGTCTTGTGTGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTTGCTTG 346

Qy 786 GGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAAGGCCG 845

Db 345 GGGATGTGCTTGGAGAGGCAGATAAC-CTGAAGCAGGCCTCTCATGACCCAGGAAGGCCG 287

Qy 846 GGGTGGATCCCTCTTTGTGTTGTAGTCCCATGCTATTAAAGTGTGGCCACAGACCAAGA 905

Db 286 GGGTGGATCCCTCTTTGTGTTGTAGTCCCATGCTATTAAAGTGTGGCCACAGACCAAGA 227

Qy 906 GCCTCAACATTTCTAGAGCCCTTATTAGAAATGCAGAAATCTGAAGCCCCCACTCTGGACCC 965

Db 226 GCCTCAACATTTCTAGAGCCCTTATTAGAAATGCAGAAATCTGAAGCCCCCACTCTGGACCC 167

Qy 966 AGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCATCATC 1025

Db 166 AGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCATCATC 107

Qy 1026 ATAGAGAACTAAACATCACACCCCACTTCTTATCTTTCCAGTGGCTAAACCACTTAAC 1085

Db 106 ATAGAGAACTAAACATCACACCCCACTTCTTATCTTTCCAGTGGCTAAACCACTTAAC 47

Qy 1086 TCTCTGGGTGTACCTGCTCATTTGTTTA 1114

Db 46 TCTCTGGGTGTACCTGCTCATTTGTTTA 18

RESULT 15

AL699934

LOCUS

DEFINITION

AL699934

DEFINITION

DKFZp686G13116 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

ACCESSION

AL699934

VERSION

AL699934.1 GI:19620474

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE

EST (Duesterhoeft, et al.)

JOURNAL

Unpublished (1999)

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.

This clone (DKFZp686G13116) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..739

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686G13116"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: hlcc3)"

/note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB; cDNA-collection"

ORIGIN

Query Match 65.5%; Score 729.6; DB 1; Length 739;

Best Local Similarity 99.2%; Pred. No. 4.7e-190;

Matches 732; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 28 GTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAGTTCGGGAGACATGGCGGCGTTAAAGC 87

Db 2 GTGGCAGGAAGCCGGAAGCAGCCGCGGCCCCAGTTCGGGAGACATGGCGGCGTTAAAGC 61

Qy 88 TCTCGTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTC 147

Db 62 TCTCGTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTC 121

Qy 148 CTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCCATCTCCCC 207

Db 122 CTTAGAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCCATCTCCCC 181

Qy 208 CATCCCCCATTTCAATTCGCAAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCCTG 267

Db 182 CATCCCCCATTTCAATTCGCAAAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCCTG 241

Qy 268 TCGGAACTGGCATATTTCTTCACCTACTGGAATTGTGTTTCTGCCCTTGGATTTCCTGT 327

Db 242 TCGGAACTGGCATATTTCTTCACCTACTGGAATTGTGTTTCTGCCCTTGGATTTCCTGT 301

Qy 328 TATTCTTGCTCGTGGCTGTGATCAAATGGGGAGCCCTGCGGCCCTTGTGTTGGCAGGCAA 387

Db 302 TATTCTTGCTCGTGGCTGTGATCAAATGGGGAGCCCTGCGGCCCTTGTGTTGGCAGGCAA 361

Qy 388 TGCAGTCATTTTCCCTTACAATTCAAGGGTTTTTCCCTTATATTGGAAGAGGAGATGATT 447

Db 362 TGCAGTCATTTTCCCTTACAATTCAAGGGTTTTTCCCTTATATTGGAAGAGGAGATGATT 421

Qy 448 TAGCTGGGAGCAGTGGTAGCACTTTTATCTGATTACAGTGCATTGAATTTCTTAGAACTC 507

Db 422 TAGCTGGGAGCAGTGGTAGCACTTTTATCTGATTACAGTGCATTGAATTTCTTAGAACTC 481

Qy 508 ATACTATCTGTATACATGTGCACATGCGGCATTTTACTATGAAAATTTAATAATATGCTGGGTT 567

Db 482 ATACTATCTGTATACATGTGCACATGCGGCATTTTACTATGAAAATTTAATAATATGCTGGGTT 541

Qy 568 TTTTAAATACCTTTATATATCATGTTCACTTTTAAAGAAAGACTTCATAAGTAGGAGATGAGT 627

Db 542 TTTTAAATACCTTTATATATCATGTTCACTTTTAAAGAAAGACTTCATAAGTAGGAGATGAGT 601

Qy 628 TTTTATCTCAGCAAAATAGACCTGTCAAAATTTAGATTATGTTACTCAAATTTATGTTACTTG 687

Db 602 TTTTATCTCAGCAAAATAGACCTGTCAATTTAGATTATGTTACTCANATTATGTTACTTG 661

Qy 688 TTTGGCTGTTTCATGTAGTCACGGTGTCTCAGAAAAATATATTAAACGCAGTCTTGTAGGCA 747

Db 662 TTTGGCTGTTTCATGTAGTCACGGTGTCTCAGAAAAATATATTNACGCAGTCTTGTAGGCA 721

Qy 748 GCTGCCACCTTATGCAGT 765

Db 722 GCTGCCACCTTATGCAGT 739

Search completed: August 18, 2005, 02:51:55

Job time : 4261 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 15:40:42 ; Search time 700 Seconds
(without alignments)
9420.845 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctggcttgccaggctgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1114 | 100.0 | 1114 | 13 | ADR27672 Leptin re |
| 2 | 1114 | 100.0 | 1114 | 13 | ADT71341 Human OB- |
| 3 | 1111.6 | 99.8 | 2732 | 3 | AAF18159 |
| 4 | 1069 | 96.0 | 1080 | 4 | AAK94760 Human ful |
| 5 | 1069 | 96.0 | 1080 | 12 | ADL31809 Full leng |
| 6 | 1067 | 95.8 | 2388 | 10 | ADF81560 Leukaemia |
| 7 | 909.2 | 81.6 | 1134 | 5 | AAS81135 DNA encod |
| 8 | 869.6 | 78.1 | 874 | 2 | AAV17683 |
| 9 | 648 | 58.2 | 648 | 13 | ADR27652 Leptin re |
| 10 | 588.4 | 52.8 | 629 | 4 | AAK93306 Human cdn |
| 11 | 588.4 | 52.8 | 629 | 4 | AAK91898 Human cdn |
| 12 | 588.4 | 52.8 | 629 | 12 | ADL29733 5' end of |
| 13 | 588.4 | 52.8 | 629 | 12 | ADL28325 5' end of |
| 14 | 577.4 | 51.8 | 647 | 10 | ADE85249 Farnesyl |
| 15 | 498.4 | 44.7 | 546 | 4 | AAK92657 Human cdn |
| 16 | 498.4 | 44.7 | 546 | 12 | ADL29084 3' end of |
| 17 | 396 | 35.5 | 396 | 6 | ABS51017 Human cdn |
| 18 | 396 | 35.5 | 396 | 13 | ADR27654 Human lep |
| 19 | 393 | 35.3 | 1128 | 13 | ADR27658 OB-RGRP Y |
| 20 | 393 | 35.3 | 1359 | 13 | ADR27656 OB-RGRP L |

| | | | | | | |
|----|-------|------|------|----|----------|--------------------|
| 21 | 357.4 | 32.1 | 447 | 10 | ADB52971 | Adb52971 Primary r |
| 22 | 246 | 22.1 | 246 | 8 | ACA56898 | Aca56898 Human CDN |
| 23 | 187.6 | 16.8 | 930 | 5 | AAS81134 | Aas81134 DNA encod |
| 24 | 174.6 | 15.7 | 674 | 3 | AAZ56536 | Aaz56536 Human lep |
| 25 | 174.6 | 15.7 | 697 | 3 | AAA15907 | Aaa15907 Human pro |
| 26 | 174.6 | 15.7 | 770 | 2 | AAX00682 | Aax00682 Human sec |
| 27 | 174.6 | 15.7 | 770 | 6 | ABL89990 | Ab189990 Human pol |
| 28 | 174.6 | 15.7 | 2652 | 5 | AAF93764 | Aaf93764 Human CDN |
| 29 | 174.6 | 15.7 | 2694 | 3 | AAZ65052 | Aaz65052 Membrane- |
| 30 | 174.6 | 15.7 | 2694 | 4 | AAS46028 | Aas46028 Human DNA |
| 31 | 174.6 | 15.7 | 2694 | 5 | AAF44198 | Aaf44198 Human PRO |
| 32 | 174.6 | 15.7 | 2694 | 6 | ABL88149 | Ab188149 Human PRO |
| 33 | 174.6 | 15.7 | 2694 | 6 | ABL95638 | Ab195638 Human ang |
| 34 | 174.6 | 15.7 | 2694 | 8 | ACA89478 | Aca89478 cDNA enco |
| 35 | 174.6 | 15.7 | 2694 | 8 | ACA73488 | Aca73488 Human sec |
| 36 | 174.6 | 15.7 | 2694 | 8 | ACA05803 | Aca05803 Human sec |
| 37 | 174.6 | 15.7 | 2694 | 8 | ACA66637 | Aca66637 cDNA enco |
| 38 | 174.6 | 15.7 | 2694 | 8 | ACA64344 | Aca64344 Novel hum |
| 39 | 174.6 | 15.7 | 2694 | 8 | ACF20212 | Acf20212 Human sec |
| 40 | 174.6 | 15.7 | 2694 | 8 | ACF19598 | Acf19598 Human sec |
| 41 | 174.6 | 15.7 | 2694 | 8 | ACD21886 | Acd21886 Human sec |
| 42 | 174.6 | 15.7 | 2694 | 8 | ACF13051 | Acf13051 Human sec |
| 43 | 174.6 | 15.7 | 2694 | 8 | ACD25154 | Acd25154 Human sec |
| 44 | 174.6 | 15.7 | 2694 | 8 | ACF00203 | Acf00203 Human sec |
| 45 | 174.6 | 15.7 | 2694 | 8 | ACA72260 | Aca72260 Novel hum |

ALIGNMENTS

RESULT 1
ADR27672
ID ADR27672 standard; DNA; 1114 BP.
XX
AC ADR27672;
XX
DT 04-NOV-2004 (first entry)
XX
DE Leptin receptor related protein, OB-RGRP, nucleotide sequence, SEQ ID 21.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
DR
XX
PT New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis; obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Claim 12; SEQ ID NO 21; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-

CC active against loss or gain of weight or diabetes in humans or animals.
CC The method comprises measuring the effect of a test compound on the
CC expression of at least one of the genes LEPOTL1 (leptin receptor
CC overlapping transcript-like 1) or OB-RGRP (leptin receptor gene related
CC protein). Alternatively the method comprises measuring the effect of the
CC compound on intracellular transport as far as the cell membrane (CM), the
CC presence at CM, and internalisation from the membrane of proteins (X)
CC encoded by the specified genes, or parts of them. Compounds of the
CC invention are used to treat or prevent obesity, weight loss and diabetes.
CC The current sequence represents the human OB-RGRP gene sequence.
XX

SQ Sequence 1114 BP; 266 A; 242 C; 259 G; 347 T; 0 U; 0 Other;

Query Match 100.0%; Score 1114; DB 13; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGGCTGCCCGGCGGTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
Db |||||
1 GTCTGGCTTGGCAGGCTGCCCGGCGGTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 60
QY 61 TTCGGGAGACATGGCGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120
Db |||||
QY 121 ACTGACTTTTCTTATGTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180
Db |||||
QY 121 ACTGACTTTTCTTATGTGGGATGTGCCCTTAGAGGATTATGGCGTTTACTGGCCCTTATT 180
Db |||||
QY 181 CGTCCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCCCAAAGAGTCACCTA 240
Db |||||
QY 181 CGTCCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTGCCCCAAAGAGTCACCTA 240
QY 241 TGACTCAGATGCAACCACTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACTACTGGAAT 300
Db |||||
QY 241 TGACTCAGATGCAACCACTAGTGCCTGTGCGGAACTGGGCATATTTCTTCACTACTGGAAT 300
QY 301 TGTGTTTCTGCGCTTTGGATTTCTGTTATTTCTGCTGCTGCTGCTGATCAAAATGGGG 360
Db |||||
QY 361 AGCCTGCGGCTTGTGTGGCAGGCAATGCAGTCAATTTCTTACAAATTCAGGGTTT 420
Db |||||
QY 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTCTGAT 480
Db |||||
QY 481 TACAGTGCAATTGAAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 540
Db |||||
QY 541 TTACTATGAAATTTAATATGCTGGGTTTTTAAATACCTTTATATATCATGTTCACTTTAA 600
Db |||||
QY 601 GAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAATTTAG 660
Db |||||
QY 661 ATTATGTTACTCAAATTTATGTTACTTGTGTTGCTGTTTATGATGTCACGGTCTCTCAGA 720
Db |||||
QY 721 AAATATATTAAACGAGTCTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780
Db |||||
QY 781 GCTTGGGATGTGCTTGGAGAGGCAGATAACCGTGAAGCAGGCCTCTCATGACCCAGGAA 840
Db |||||

QY 841 GGCCGGGTGGATCCCTCTTTTGTGTGTAGTCCATGCTATTAAGTGTGCCCCACAGAC 900
Db |||||
QY 901 CAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAACTCTGAAGCCCCACTCTG 960
Db |||||
QY 961 GACCCAGGACATTTTGATGAGATCCAAAGGAGTGTATGCACATGAAAGTTTGAGAAAGCA 1020
Db |||||
QY 1021 TCATCATAGAGAAAGTAAACATCACACCCCACTTCTTATCTTCCAGTGGCTAAACCACT 1080
Db |||||
QY 1081 TAACCTCTCTGGTGTACCTGCTCATTTGTTTA 1114
Db |||||

RESULT 3

AAF18159

ID AAF18159 standard; DNA; 2732 BP.

AC AAF18159;

DT 14-MAR-2001 (first entry)

XX Lung cancer associated polynucleotide sequence SEQ ID 178.

DE Human; lung cancer associated protein; neuroprotective; cytostatic;
XX cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease; ds.

OS Homo sapiens.

XX WO200055180-A2.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005918.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (ROSE/) ROSEN C A.

XX Ruben SM;

XX WPI; 2000-587514/55.

XX P-PSDB; AAB58283.

PT Lung cancer associated gene sequences, referred to as lung cancer

PT antigens, useful for treatment, prevention, and diagnosis of disorders

PT such as lung cancer.

XX Claim 1; Page 642; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the protein
CC or polynucleotide sequences. The lung cancer associated polynucleotide
CC sequences may be used for detection of lung cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The proteins may be used to treat disorders such as
CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,

CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterisation of the polynucleotide and protein sequences
XX
SQ Sequence 2732 BP; 777 A; 516 C; 546 G; 887 T; 0 U; 6 Other;
Query Match 99.8%; Score 1111.6; DB 3; Length 2732;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1111; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCTGGCTTGGCAGGCTGCCCGGCCGTGAGGAGTAAAGCTCTCGTGGCATATCCTTCAGTGGGCTATTGG 120
Db 18 GTCTGGCTTGGCAGGCTGCMCGGCCCGTAAAGCTCTCGTGGCATATCCTTCAGTGGGCTATTGG 137
QY 61 TTCGGGAGACATGGCGGCCGTAAAGCTCTCGTGGCATATCCTTCAGTGGGCTATTGG 120
Db 78 CTCGGGAGACATGGCGGCCGTAAAGCTCTCGTGGCATATCCTTCAGTGGGCTATTGG 137
QY 121 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTAATGGCGTTTACTGGCCCTTATT 180
Db 138 ACTGACTTTTCTTATGCTGGGATGTGCCTTAGAGGATTAATGGCGTTTACTGGCCCTTATT 197
QY 181 CGTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTCAATGCCAAAAGAGTCACCTA 240
Db 198 CGTCTGATTTTCCACGCCCATCTCCCCCATCCCCCATTTCAATGCCAAAAGAGTCACCTA 257
QY 241 TGACTCAGATGCAACACAGTAGTGCCCTGCGGAACTGGCATATTTCTTCACTACTGGAAT 300
Db 258 TGACTCAGATGCAACACAGTAGTGCCCTGCGGAACTGGCATATTTCTTCACTACTGGAAT 317
QY 301 TGTGTGTTTCTGCCCTTTGGATTTCCTGTTATTTCTGTGCTCGTGGTGTGATCAAAATGGGG 360
Db 318 TGTGTGTTTCTGCCCTTTGGATTTCCTGTTATTTCTGTGCTCGTGGTGTGATCAAAATGGGG 377
QY 361 AGCCTGCGGCCCTTGTGTGGCAGGCAATGCAGTCATTTTCCCTTACAATCAAGGGTTTTT 420
Db 378 AGCCTGCGGCCCTTGTGTGGCAGGCAATGCAGTCATTTTCCCTTACAATCAAGGGTTTTT 437
QY 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTATTCTGAT 480
Db 438 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTTATTCTGAT 497
QY 481 TACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 540
Db 498 TACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 557
QY 541 TTACTATGAATTTAAATATGCTGGGTTTTTTAATACCTTTATATATATCATGTTCACTTAA 600
Db 558 TTACTATGAATTTAAATATGCTGGGTTTTTTAATACCTTTATATATATCATGTTCACTTAA 617
QY 601 GAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAAAATAGACCTGTCAAAATTAG 660
Db 618 GAAAGACTTCATAAGTAGGAGATGAGTTTATTCTCAGCAAAATAGACCTGTCAAAATTAG 677
QY 661 ATTATGTTACTCAAATATATGTTACTTGTGGCTGTTCAATGATGACGGTGTCTCAGA 720
Db 678 ATTATGTTACTCAAATATATGTTACTTGTGGCTGTTCAATGATGACGGTGTCTCAGA 737
QY 721 AAATATATTACGCAGTCTTGTAGGCAGTGCCACCTTATGCAATGCAATCGAAACCTTTT 780
Db 738 AAATATATTACGCAGTCTTGTAGGCAGTGCCACCTTATGCAATGCAATCGAAACCTTTT 797
QY 781 GCTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCCCTTCATGACCCAGGAA 840
Db 798 GCTTGGGATGTGCTTGGAGAGGCAGATAACGCTRAAGCAGGCCCTTCATGACCCAGGAA 857
QY 841 GGCCGGGTGGATCCCTCTTGTGTGTAGTCCATGCTATTAAAGTGTGCCCCACAGAC 900
Db 858 GGCCGGGTGGATCCCTCTTGTGTGTAGTCCATGCTATTAAAGTGTGCCCCACAGAC 917
QY 901 CAAGAGCCTCAACATTTTCTTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCCACTCTG 960

Db 918 CAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGAAATCTGAAGCCCCACTCTG 977
QY 961 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1020
Db 978 GACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGAAGCA 1037
QY 1021 TCATCATAGAGAAAGTAAACATCACACCCAACTTCCTTATCTTCCAGTGGCTAAACCACT 1080
Db 1038 TCATCATAGAGAAAGTAAACATCACACCCAACTTCCTTATCTTCCAGTGGCTAAACCACT 1097
QY 1081 TAACTCTCTCTGGGTGTTTACCTGCTCATTTGTTTA 1114
Db 1098 TAACTCTCTCTGGGTGTTTACCTGCTCATTTGTTTA 1131
RESULT 4
AAK94760
ID AAK94760 standard; cDNA; 1080 BP.
XX
AC AAK94760;
XX
DT 06-NOV-2001 (first entry)
XX Human full-length cDNA, SEQ ID NO: 3842.
DE Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Homo sapiens.
OS
XX EP1130094-A2.
PN
XX 05-SEP-2001.
PD
XX 07-JUL-2000; 2000EP-00114089.
PF
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
PA
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
DR P-PSDB; AAM93804.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 3842; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a full length human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in CD-ROM format directly
CC from EPO
XX
SQ Sequence 1080 BP; 263 A; 232 C; 244 G; 341 T; 0 U; 0 Other;
Query Match 96.0%; Score 1069; DB 4; Length 1080;
Best Local Similarity 99.9%; Pred. No. 7.1e-312;
Matches 1080; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 33 AGGAAGCCGGAAGCAGCGCGGCCCCAGTTCCGGAGACATGGCGGCGTTAAAGCTCTCG 92

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Db      ||||||| 1 AGGAAGCCGGAAGCAGCCGCGGCCCCAGTTCGGGAGACATGGCGGCGTTAAAGCTCTCG 60
Qy      93 TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAG 152
Db      61 TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAG 120
Qy      153 AGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCC 212
Db      121 AGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCC 180
Qy      213 CCCATTTTCATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTTCGGG 272
Db      181 CCCATTTTCATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTTCGGG 240
Qy      273 AACTGGCATATTTCTTCACTACTGGAATTGTTGTTCTGCTTGGATTTCCTGTTATTC 332
Db      241 AACTGGCATATTTCTTCACTACTGGAATTGTTGTTCTGCTTGGATTTCCTGTTATTC 300
Qy      333 TTGCTCGTGTGGCTGTGATCAAATGGGGAGCCCTGGCGCCTTGTGTTGGCAGCAATGCAG 392
Db      301 TTGCTCGTGTGGCTGTGATCAAATGGGGAGCCCTGGCGCCTTGTGTTGGCAGCAATGCAG 360
Qy      393 TCATTTTTCCTTACAATCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCT 452
Db      361 TCATTTTTCCTTACAATCAAGGGTTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCT 420
Qy      453 GGGAGCAGTGTAGCACTTTATTTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACT 512
Db      421 GGGAGCAGTGTAGCACTTTATTTCTGATTACAGTGCATTTGAATTTCTTAGAACTCATACT 480
Qy      513 ATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA 572
Db      481 ATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTA 540
Qy      573 ATACCTTTATATATCATGTTCACTTTTAAGAAAGACTTCATAAGTAGGAGATGATTTTAT 632
Db      541 ATACCTTTATATATCATGTTCACTTTTAAGAAAGACTTCATAAGTAGGAGATGATTTTAT 600
Qy      633 TCTCAGCAAATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTACTGTTTG 692
Db      601 TCTCAGC-AATAGACCTGTCAAATTTAGATTATGTTACTCAAATTTAGTTACTGTTTG 659
Qy      693 CTGTTTCATGTAGTCACGGTGCTCTCAGAAATATATTAACGCAGTCTTGTAGGCAGCTGC 752
Db      660 CTGTTTCATGTAGTCACGGTGCTCTCAGAAATATATTAACGCAGTCTTGTAGGCAGCTGC 719
Qy      753 CACCTTATGCAGTGCATCGAAACCTTTTGTGTTGGGATGTCTTGGAGAGGAGCAGATAACG 812
Db      720 CACCTTATGCAGTGCATCGAAACCTTTTGTGTTGGGATGTCTTGGAGAGGAGCAGATAACG 779
Qy      813 CTGAAGCAGGCCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTTGTAGTC 872
Db      780 CTGAAGCAGGCCTCTCATGACCCAGGAAGCGGGGTGGATCCCTCTTTTGTGTTGTAGTC 839
Qy      873 CATGCTATTAAAGTGTGGCCCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTA 932
Db      840 CATGCTATTAAAGTGTGGCCCCACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTA 899
Qy      933 GAAATGCAGAAATCTGAAGCCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAG 992
Db      900 GAAATGCAGAAATCTGAAGCCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAG 959
Qy      993 TTGTATGCACATGAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCCACT 1052
Db      960 TTGTATGCACATGAAGTTTGAGAAGCATCATATAGAGAAGTAAACATCACACCCCACT 1019
Qy      1053 TCCTTATCTTTCCAGTGGCTAAACCACTTAACTCTCTGGGTGTTACCTGCTCATTTGTT 1112
Db      1020 TCCTTATCTTTCCAGTGGCTAAACCACTTAACTCTCTGGGTGTTACCTGCTCATTTGTT 1079
Qy      1113 T 1113
|
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Db      1080 T 1080

RESULT 5
ADL31809
ID      ADL31809 standard; cDNA; 1080 BP.
XX
AC      ADL31809;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Full length human cDNA clone SeqID 3842.
XX
KW      human; medicine; signal transduction; glycoprotein; transcription;
KW      oligo-capping method; ss; gene.
XX
OS      Homo sapiens.
XX
PN      EPI396543-A2.
XX
PD      10-MAR-2004.
XX
PF      07-JUL-2000; 2003EP-00025638.
XX
PR      08-JUL-1999; 99JP-00194486.
PR      11-JAN-2000; 2000JP-00118774.
PR      02-MAY-2000; 2000JP-00183865.
PR      07-JUL-2000; 2000EP-00114089.
XX
PA      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR      WPI; 2004-204755/20.
DR      P-PSDB; ADL31810.
XX
PT      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT      length human cDNAs.
XX
PS      Example 1; SEQ ID NO 3842; 1340pp; English.
XX
CC      This invention relates to a novel primers useful for synthesising full
CC      length cDNA molecules that encode human proteins. Specifically, it refers
CC      to secretory or membrane proteins that are potential therapeutic agents/
CC      target molecules in the field of medicine, and in particular genes
CC      encoding proteins that are associated with signal transduction,
CC      glycoproteins and transcription. The present invention describes a method
CC      for efficiently cloning a full length human cDNA from both the 5' and 3',
CC      ends using the oligo-capping method. This polynucleotide sequence is a
CC      full length human cDNA clone of the invention.
XX
SQ      Sequence 1080 BP; 263 A; 232 C; 244 G; 341 T; 0 U; 0 Other;

Query Match          96.0%; Score 1069; DB 12; Length 1080;
Best Local Similarity 99.9%; Pred. No. 7.1e-312;
Matches 1080; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      33 AGGAAGCCGGAAGCAGCCGCGGCCCCAGTTCGGGAGACATGGCGGCGTTAAAGCTCTCG 92
Db      1 AGGAAGCCGGAAGCAGCCGCGGCCCCAGTTCGGGAGACATGGCGGCGTTAAAGCTCTCG 60
Qy      93 TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAG 152
Db      61 TGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTAG 120
Qy      153 AGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCC 212
Db      121 AGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATCC 180
Qy      213 CCCATTTTCATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTTCGGG 272
Db      181 CCCATTTTCATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTTCGGG 240
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Db 421 TTTTCTTATATTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCAGCTTTATTC 480

Qy 477 TGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGG 536

Db 481 TGATTACAGTGCATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGG 540

Qy 537 CATTTTACTATGAATTTTAATATGCTGGGTTTTTAAATACCTTTATATATATCATGTTCACT 596

Db 541 CATTTTACTATGAATTTTAATATGCTGGGTTTTTAAATACCTTTATATATATCATGTTCACT 600

Qy 597 TTAAGAAAGACITTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAATAGACCTGTCAAAT 656

Db 601 TTAAGAAAGACITTCATAAGTAGGAGATGAGTTTTATTCTCAGCAAATAGACCTGTCAAAT 660

Qy 657 TTAGATTATGTTACTCAAATTATGTTTACTTTGTTGGCTGTTTCATGTAGTACAGGTGCTCT 716

Db 661 TTAGATTATGTTACTCAAATTATGTTTACTTTGTTGGCTGTTTCATGTAGTACAGGTGCTCT 720

Qy 717 CAGAAATATATTAAAGCAGTCTTGTAGGCAGCTGCGCACCTTATGTCAGTGCATCGAAACC 776

Db 721 CAGAAATATATTAAAGCAGTCTTGTAGGCAGCTGCCACCTTATGTCAGTGCATCGAAACC 780

Qy 777 TTTTGTCTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCATGACCCA 836

Db 781 TTTTGTCTGGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCATGACCCA 840

Qy 837 GGAAGGCCGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCAC 896

Db 841 GGAAGGCCGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAGTGTGGCCAC 900

Qy 897 AGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAAATCGAAGCCCCAC 956

Db 901 AGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCAGAAATCGAAGCCCCAC 960

Qy 957 TCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGA 1016

Db 961 TCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACATGAAAGTTTGAGA 1020

Qy 1017 AGCATCATCATAGAGAAGTAACATCACACCCCACTTCTTATCTTTCCAGTGGCTAAAC 1076

Db 1021 AGCATCATCATAGAGAAGTAACATCACACCCCACTTCTTATCTTTCCAGTGGCTAAAC 1080

Qy 1077 CACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 1114

Db 1081 CACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 1118

RESULT 7

AAS81135

ID AAS81135 standard; cDNA; 1134 BP.

XX

AC AAS81135;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #16939.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG16948.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX

PS Claim 1; SEQ ID NO 16939; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1134 BP; 274 A; 247 C; 266 G; 346 T; 0 U; 1 Other;

Query Match 81.6%; Score 909.2; DB 5; Length 1134;

Best Local Similarity 95.8%; Pred. No. 1.4e-263;

Matches 1086; Conservative 0; Mismatches 28; Indels 20; Gaps 14;

Qy 1 GTCTGGCTTGGCAGGCTGCCCGGCCGTGGCAGGAAGCCGCGGCCCCAG 60

Db 1 GTCTGGCTTGGCAGGCTGCCCGGCCGTGGCAGGAAGCCGCGGCCCCAG 60

Qy 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120

Db 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCATTATCCTTCAGTGGGCTATTGG 120

Qy 121 ACTGACTTTTCT--TATGCTGGGATGTGCTTAGAGGATTATGGCGTTTACTGGCCCTTA 178

Db 121 ACTGACTTTTCTNATATGCTGGGATGTGCTTAGAGGATTATGGCGTTTACTGGCCCTTA 180

Qy 179 TTCGTCTCTGA-TTTTCCACGCCATCTCCCCCATCCCCCATTTTCATTCGCAAAAGAGTCAC 237

Db 181 TTCGTCTCTGATTTTCCACGCCATTTCCTCCATCCCCCATTTTCATTCGCAAAAGAGTCAC 240

Qy 238 CTATGACTCAGATGCAACC-AGTAGTGCCTGTCCGGAAGTGGCATAATTTCTTCACTACTG 296

Db 241 CTATGACTCAGATGCAACCAGTAGTGCCTGTCCGGAAGTGGCATAATTTCTTCACTACTG 300

Qy 297 GAATTGTTGTTT-CTGCCTTTGGATTTTCCT--GTTATTCTGCTCGTGTGGCTGTGATC- 352

Db 301 GAATTGTTGTTTCTGCCTTTGGATTTCCCCCGGTAATTCCTTCCCGGTGGCTTGTATCA 360

Qy 353 AAATGGGGAGCCTGCGGCCCTT--GTGTTGGCAAGCAATGCAGTCATTTT-CCTTACAATT 409

Db 361 AAATGGGGAGCCTGCGGCCCTTGTGTGGCAAGCAATGCAGTCATTTTCCCTTACAATT 420

Qy 410 CAAGGG--TTTTTCTTATATTTGGAAGAGGAGATGATTTTAGCT-GGGAGCAGTGGTAG 466

Db 421 CAAGGGGTTTTCCTTATATTGGGAAGAGGAGATGATTTTAGCTGGGGAGCAGTGGTAG 480

Qy 467 CACTTTATTCTGATTACAGTGCAATTGAAATTTCTTTA-GAACTCATACTATCTGTATACATG 525

Db 481 ||||| CACTTTATCTGATTACAGTGCATTGAATTTCTTAGGAACCTACATACTATCTGTATACATG 540

QY 526 TGCACATGC-GGCATTTTACTATGAAATTTAATATGC---TGGTTTTTTTAATACCTTTA 581

Db 541 TGCACATCGGGCATTTTTACTATGAAATTTTAATAATGCTGGGGTTTTTAATACCTTTA 600

QY 582 TATATCATGTTTCACTTTAAG-AAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCA 640

Db 601 TATATCATGTTTCACTTTAAGAAAAGACTTCATAAGTAGGAGATGAGTTTTATTCTCAGCA 660

QY 641 AATAGACCTGTCAAATTTAGATTATGTTACTCAAAATATGTTACTTGTGGCTGTTTCAT 700

Db 661 AATAGACCTGTCAAATTTAGATTATGTTACTCAAAATATGTTACTTGTGGCTGTTTCAT 720

QY 701 GTAGTCACGGTGTCTCTCAGAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTAT 760

Db 721 GTAGTCACGGTGTCTCTCAGAAATATATTAACGCAGTCTTGTAGGCAGCTGCCACCTTAT 780

QY 761 GCAGTGCAATCGAAACCTTTTGTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCA 820

Db 781 GCAGTGCAATCGAAACCTTTTGTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCA 840

QY 821 GGCCTCTCATGACCCAGGAAGGCCGGGTGGATCCCTCTTGTGTGTAGTCCATGCTAT 880

Db 841 GGCCTCTCATGACCCAGGAAGGCCGGGTGGATCCCTCTTGTGTGTAGTCCATGCTAT 900

QY 881 TAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCA 940

Db 901 TAAAGTGTGGCCACAGACCAAGAGCCTCAACATTTCTAGAGCCTTATTAGAAATGCA 960

QY 941 GAATCTGAAGCCCTCTTGACCCAGGACATTTTGTATGATGAGATCCTCAAGGAGTTGTATGC 1000

Db 961 GAATCTGAAGCCCTCTTGACCCAGGACATTTTGTATGATGAGATCCTCAAGGAGTTGTATGC 1020

QY 1001 ACATGAAAGTTTGAGAGCATCATATAGAGAAGTAAACATCACACCACTTCCTTATC 1060

Db 1021 ACATGAAAGTTTGAGAGCATCATATAGAGAAGTAAACATCACACCACTTCCTTATC 1080

QY 1061 TTTCCAGTGGCTAAACCACCTTAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1114

Db 1081 TTTCCAGTGGCTAAACCACCTTAACCTCTCTGGGTGTACCTGCTCATTTGTTTA 1134

RESULT 8

AAV17683

ID AAV17683 standard; cDNA; 874 BP.

XX

AC AAV17683;

XX

DT 10-JUL-1998 (first entry)

XX

DE cDNA encoding a novel human leptin receptor gene-related protein.

XX

KW Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703; treatment; cancer; connective tissue disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT misc_feature 62..63

FT /*tag= c

FT /note= "intron contained in genomic sequence between these bases"

FT

FT

FT

FT CDS 71..466

FT /*tag= a

FT

FT intron 86..87

FT /*tag= b

FT /note= "intron contained in genomic sequence between these bases"

FT

FT misc_feature 349..350

FT /*tag= d

FT /note= "intron contained in genomic sequence between these bases"

FT

XX

PN WO9805792-A2.

XX

PD 12-FEB-1998.

XX

PF 25-JUL-1997; 97WO-US014191.

XX

PR 01-AUG-1996; 96US-00691071.

PR 15-APR-1997; 97US-00843370.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Akerbloom IE;

XX

DR WPI; 1998-145624/13.

DR P-PSDB; AAW48322.

XX

PT DNA encoding human leptin receptor gene-related protein - useful for, e.g. screening for drugs used in treatment of metabolic, reproductive, developmental and connective tissue disorders or cancer.

PT

XX

PS Claim 5; Fig 1A-C; 60pp; English.

XX

CC The present sequence encodes a human leptin receptor gene-related protein (LRGRP). The cDNA sequence was first isolated in Incyte clone 492703 from the hNT2 cell line cDNA library through a computer generated search for amino acid sequence alignments. The LRGRP protein has some homology to the membrane associated proteins of *Caenorhabditis elegans* ORF C30B.2 and *Saccharomyces cerevisiae* ORF YJR044C. The agonists of LRGRP can be used to treat metabolic, reproductive and developmental disorders, whilst antagonists of LRGRP can be used for treatment of cancer or connective tissue disorders e.g. rheumatoid arthritis and Sjogren's syndrome.

CC

CC Polynucleotides which hybridise to the LRGRP nucleotide sequence can be used for detection

XX

SQ Sequence 874 BP; 192 A; 182 C; 214 G; 283 T; 0 U; 3 Other;

Query Match 78.1%; Score 869.6; DB 2; Length 874;

Best Local Similarity 99.4%; Pred. No. 1.1e-251;

Matches 869; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCTGGCTTGGCAGGCTGCCGGGCCGTGGCAGGAGCCGCGGCCAG 60

Db 1 GTCTGGCTTGGCAGGCTGCCGGGCCGTGGCAGGAGCCGCGGCCAG 60

QY 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCAATTATCCTTCAGTGGGCTATTGG 120

Db 61 TTCGGGAGACATGGCGGGCGTTAAAGCTCTCGTGGCAATTATCCTTCAGTGGGCTATTGG 120

QY 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGCTTACTGGCCCTTATT 180

Db 121 ACTGACTTTTCTTATGCTGGGATGTCCTTAGAGGATTATGCGCTTACTGGCCCTTATT 180

QY 181 CGTCCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTCAATGCCCCAAAGAGTCACCTA 240

Db 181 CGTCCTGATTTTCCACGCCATCTCCCCCATCCCCCATTTCAATGCCCCAAAGAGTCACCTA 240

QY 241 TGACTCAGATGCAACCACTAGTGCCTGTCGGGAACTGGCATATTTCTTCACTACTGGAAT 300

Db 241 TGACTCAGATGCAACCACTAGTGCCTGTCGGGAACTGGCATATTTCTTCACTACTGGAAT 300

QY 301 TGTGTTTCTGCTTTGGATTTCTGTTATTTCTGCTCGTGGTGTGATCAAAATGGGG 360

Db 301 TGTGTTTCTGCTTTGGATTTCTGTTATTTCTGCTCGTGGTGTGATCAAAATGGGG 360

QY 361 AGCCTCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATCAAGGGTTTTT 420

Db 361 AGCCTCGGCCCTTGTGTTGGCAGGCAATGCAGTCATTTTCTTACAATCAAGGGTTTTT 420

QY 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTCTGAT 480

Db 421 CCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCATTATTCTGAT 480

QY 481 TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 540
DB 481 TACAGTGCAATTGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACATGCGGCATT 540
QY 541 TTACTATGAAATTTAATATGCTGGGTTTTTTTAAACCTTTATATATCATGTTCACCTTTAA 600
DB 541 TTACTATGAAATTTAATATGCTGGGTTTTTTTAAACCTTTATATATCATGTTCACCTTTAA 600
QY 601 GAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAATTTAG 660
DB 601 GAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGACCTGTCAAATTTAG 660
QY 661 ATTATGTTACTCAAATTTATGTTACTTGTGCTGCTTCATGTAGTCACGGTGCTCTCAGA 720
DB 661 ATTATGTTACTCAAATTTATGTTACTTGTGCTGCTTCATGTAGTCACGGTGCTCTCAGA 720
QY 721 AAATATATTAAACGCAGTCTTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780
DB 721 AAATATATTAAACGCAGTCTTTGTAGGCAGCTGCCACCTTATGCAGTGCATCGAAACCTTTT 780
QY 781 GCTTGGGGATGTGCTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAA 840
DB 781 GCTTGGGGATGTGCTGGAGAGGCAGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAA 840
QY 841 GGCCGGGGTGATCCCTCTTTGTGTTGTAGTCCA 874
DB 841 GGCCGGGGTGATCCCTCTTTKTTTTGTAGTCCA 874

RESULT 9
ADR27652
ID ADR27652 standard; DNA; 648 BP.
AC ADR27652;
XX
DT 04-NOV-2004 (first entry)
XX
DE Leptin receptor related protein, OB-RGRP, nucleotide sequence, SEQ ID 1.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW human; ds.
OS Homo sapiens.
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
DR WPI; 2004-595751/58.
XX
PT New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, haematopoiesis, and
PT angiogenesis.
XX
PS Claim 1; SEQ ID NO 1; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-

CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer.
XX
SQ Sequence 648 BP; 181 A; 133 C; 129 G; 205 T; 0 U; 0 Other;

Query Match 58.2%; Score 648; DB 13; Length 648;
Best Local Similarity 100.0%; Pred. No. 8.8e-185;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 467 CACTTTATTCTGATTACAGTGCATTGAAATTTCTTAGAACTCATACTATCTGTATACATGT 526
DB 1 CACTTTATTCTGATTACAGTGCATTGAAATTTCTTAGAACTCATACTATCTGTATACATGT 60
QY 527 GCACATGCGGCATTTTACTATGAAATTTAATATATGCTGGGTTTTTTTAATACCTTTATATAT 586
DB 61 GCACATGCGGCATTTTACTATGAAATTTAATATATGCTGGGTTTTTTTAATACCTTTATATAT 120
QY 587 CATGTTCACTTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGA 646
DB 121 CATGTTCACTTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTATCTCAGCAAAATAGA 180
QY 647 CCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTC 706
DB 181 CCTGTCAAATTTAGATTATGTTACTCAAATTTATGTTACTTGTGCTGTTTCATGTAGTC 240
QY 707 ACGGTGCTCTCAGAAAATATATTAACGCAGCTTGTAGGCAGCTGCCACCTTTATGCAGTG 766
DB 241 ACGGTGCTCTCAGAAAATATATTAACGCAGCTTGTAGGCAGCTGCCACCTTTATGCAGTG 300
QY 767 CATCGAAACCTTTTGTGCTGGGATGTCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTC 826
DB 301 CATCGAAACCTTTTGTGCTGGGATGTCTTGGAGAGGCAGATAACGCTGAAGCAGGCCTC 360
QY 827 TCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAG 886
DB 361 TCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAG 420
QY 887 TGTGGCCACACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGATCT 946
DB 421 TGTGGCCACACAGACCAAGAGCCTCAACATTTCTTAGAGCCTTATTAGAAATGCAGATCT 480
QY 947 GAAGCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAGTTGTATGCACATGA 1006
DB 481 GAAGCCCCACTCTGGACCCAGGACATTTTGTATGAGATCCAAAGGAGTTGTATGCACATGA 540
QY 1007 AAGTTTGAGAAGCATCATATAGAGAAGTAACATCACACCCCACTTCCTTATCTTTTCCA 1066
DB 541 AAGTTTGAGAAGCATCATATAGAGAAGTAACATCACACCCCACTTCCTTATCTTTTCCA 600
QY 1067 GTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 1114
DB 601 GTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCTCATTTGTTTA 648

RESULT 10
AAK93306
ID AAK93306 standard; cDNA; 629 BP.

XX AC AAK93306;
XX DT 06-NOV-2001 (first entry)
XX DE Human cDNA clone representative sequence, SEQ ID NO: 1766.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX XX Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX XX
DR WPI; 2001-524255/58.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX Example 11; SEQ ID NO 1766; 1380pp + Sequence Listing; English.
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence was used as the representative sequence
CC from a human clone which was used in homology searches to identify the
CC clone. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in CD-ROM format directly from
CC EPO
XX Sequence 629 BP; 144 A; 129 C; 140 G; 211 T; 0 U; 5 Other;
SQ
Query Match 52.8%; Score 588.4; DB 4; Length 629;
Best Local Similarity 98.6%; Pred. No. 8.8e-167;
Matches 622; Conservative 0; Mismatches 6; Indels 3; Gaps 3;
33 AGGAAGCCGGAAGCAGCCGCGCCCCCAGTTC-GGGAGACATGGCGGGCGTTAAAGCTCTC 91
1 AGGAAGCCGGAAGCAGCCGCGCCCCCAGTTCGGGGAGACATGGCGGGCGTTAAAGCTCTC 60
92 GTGGCATTATCCTTCAGTGGGGCTATTTGGACTGACTTTTCTTATGCTGGGATGTCCTTA 151
61 GTGGCATTATCCTTCAGTGGGGCTATTTGGACTGACTTTTCTTATGCTGGGATGTCCTTA 120
152 GAGGATTATGGCGTTTACTGGCCCTTATTGCTCCTGATTTTCCAGCCATCTCCCCCATC 211
121 GAGGATTATGGCGTTTACTGGCCCTTATTGCTCCTGATTTTCCAGCCATCTCCCCCATC 180
212 CCCCATTTCATTGCCAAAGAGTACCTATGACTCAGATGCAACCAAGTAGTGCCTGCGG 271
181 CCCCATTTCATTGCCAAAGAGTACCTATGACTCAGATGCAACCAAGTAGTGCCTGCGG 240
272 GAACCTGGCATATTTCTTCACACTAGGAATTGTTGTTTCTGCCTTTGGATTTCCTGTTATT 331
241 GAACCTGGCATATTTCTTCACACTAGGAATTGTTGTTTCTGCCTTTGGATTTCCTGTTATT 300

QY 332 CTTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCTGGCGCCTTGTGTTGGCAGGCAATGCA 391
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 CTTGCTCGTGTGGCTGTGATCAAAATGGGGAGCCTGGCGCCTTGTGTTGGCAGGCAATGCA 360
QY 392 GTCATTTTCCCTTACAATTCAAGGGTTTTTCCCTTATATTTGGAAGAGGAGATGATTTTAGC 451
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 NTCATTTTCCCTTACAATTCAAGGGTTTTTCCCTTATATTTGGAANAAGAGATGATTTTAGC 420
QY 452 TGGGAGCAGTGGTAGCACCTTTTATCTGTGATTACAGTGCAATGGAATTTCTTAGAACTCATAC 511
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TGGGAGCAGTGGTAGCACCTTTTATCTGTGATTACAGTGCAATGGAATTTCTTAGAACTCATAC 480
QY 512 TATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTT 571
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 TATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGTTTTTT 540
QY 572 AATACCTTTTATATCATGTTCACCTTTAAGAAAGACTTTCATAAGTAGGAGATGAGTTTTTA 631
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 AATACCTTTTATATCATGTTCACCTTTAAGAAAGAC-TCATAAGTNGGANATGAGTTTTTA 599
QY 632 TTCTCAGCAAAATAGACCTGTCAAATTTTAGAT 662
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
600 TTCTCANC-AATAGACCTGTCAAATTTTAGAT 629
RESULT 11
AAK91898
ID AAK91898 standard; cDNA; 629 BP.
XX AC AAK91898;
XX AC AAK91898;
DT 06-NOV-2001 (first entry)
XX Human cDNA 5'-end sequence, SEQ ID NO: 358.
DE Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
KW Homo sapiens.
XX OS EP1130094-A2.
XX PN 05-SEP-2001.
XX PD 07-JUL-2000; 2000EP-00114089.
XX PF 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX XX
DR WPI; 2001-524255/58.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX Claim 2; SEQ ID NO 358; 1380pp + Sequence Listing; English.
XX The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is the nucleotide sequence of the 5'-end of
CC a cDNA provided in the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in CD-
CC ROM format directly from EPO


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XX
SQ      Sequence 629 BP; 144 A; 129 C; 140 G; 211 T; 0 U; 5 Other;

Query Match      52.8%; Score 588.4; DB 4; Length 629;
Best Local Similarity 98.6%; Pred. No. 8.8e-167;
Matches 622; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY      33 AGGAAGCCGGAAGCAGCGCGGCCCCAGTTC-GGGAGACATGGCGGGCGTTAAAGCTCTC 91
Db      |||||||
Db      1 AGGAAGCCGGAAGCAGCGCGGCCCCAGTTCGGGAGACATGGCGGGCGTTAAAGCTCTC 60

QY      92 GTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTA 151
Db      |||||||
Db      61 GTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTA 120

QY      152 GAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATC 211
Db      |||||||
Db      121 GAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATC 180

QY      212 CCCCATTTTCATGCGCAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCGG 271
Db      |||||||
Db      181 CCCCATTTTCATGCGCAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCGG 240

QY      272 GAACTGGCATAATTTCTTCACTACTGGGAATGTTGTTCTGCCCTTTGGATTTCCTGTTATT 331
Db      |||||||
Db      241 GAACTGGCATAATTTCTTCACTACTGGGAATGTTGTTCTGCCCTTTGGATTTCCTGTTATT 300

RESULT 12
ADL29733
ID      ADL29733 standard; cDNA; 629 BP.
XX
AC      ADL29733;
XX
DT      20-MAY-2004 (first entry)
XX
DE      5' end of a representative human cDNA cluster SeqID 1766.
XX
KW      human; medicine; signal transduction; glycoprotein; transcription;
KW      oligo-capping method; ss.
XX
OS      Homo sapiens.
XX
PN      EP1396543-A2.
XX
PD      10-MAR-2004.
XX
PF      07-JUL-2000; 2003EP-00025638.
XX

PR      08-JUL-1999; 99JP-00194486.
PR      11-JAN-2000; 2000JP-00118774.
PR      02-MAY-2000; 2000JP-00183865.
PR      07-JUL-2000; 2000EP-00114089.
XX
PA      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR      WPI; 2004-204755/20.
XX
New oligonucleotide primers (830 cDNAs) useful for synthesizing full
length human cDNAs.
XX
Example 18; SEQ ID NO 1766; 1340pp; English.
XX
This invention relates to a novel primers useful for synthesising full
length cDNA molecules that encode human proteins. Specifically, it refers
to secretory or membrane proteins that are potential therapeutic agents/
target molecules in the field of medicine, and in particular genes
encoding proteins that are associated with signal transduction,
glycoproteins and transcription. The present invention describes a method
for efficiently cloning a full length human cDNA from both the 5' and 3'
ends using the oligo-capping method. This polynucleotide sequence is the
5' end of a representative human DNA cluster of the invention.
XX
SQ      Sequence 629 BP; 144 A; 129 C; 140 G; 211 T; 0 U; 5 Other;

Query Match      52.8%; Score 588.4; DB 12; Length 629;
Best Local Similarity 98.6%; Pred. No. 8.8e-167;
Matches 622; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY      33 AGGAAGCCGGAAGCAGCGCGGCCCCAGTTC-GGGAGACATGGCGGGCGTTAAAGCTCTC 91
Db      |||||||
Db      1 AGGAAGCCGGAAGCAGCGCGGCCCCAGTTCGGGAGACATGGCGGGCGTTAAAGCTCTC 60

QY      92 GTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTA 151
Db      |||||||
Db      61 GTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTTCTTATGCTGGGATGTCCTTA 120

QY      152 GAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATC 211
Db      |||||||
Db      121 GAGGATTATGGCGTTTACTGGCCCTTATTCGTCCTGATTTTCCACGCCATCTCCCCCATC 180

QY      212 CCCCATTTTCATGCGCAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCGG 271
Db      |||||||
Db      181 CCCCATTTTCATGCGCAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCGG 240

QY      272 GAACTGGCATAATTTCTTCACTACTGGGAATGTTGTTCTGCCCTTTGGATTTCCTGTTATT 331
Db      |||||||
Db      241 GAACTGGCATAATTTCTTCACTACTGGGAATGTTGTTCTGCCCTTTGGATTTCCTGTTATT 300

QY      332 CTTCGTCGTGGCTGATCAAAATGGGAGCCTTGTGTTGSCAGGCAATGCA 391
Db      |||||||
Db      301 CTTCGTCGTGGCTGATCAAAATGGGAGCCTTGTGTTGSCAGGCAATGCA 360

QY      392 GTCATTTTCCCTTACAAATCAAGGGTTTTTCCCTTATATTGGGAAGGAGATGATTTTAGC 451
Db      |||||||
Db      361 NTCAATTTTCCCTTACAAATCAAGGGTTTTTCCCTTATATTGGGAAGGAGATGATTTTAGC 420

QY      452 TGGGAGCAGTGGTAGCAGCTTTTATTTCTGATTACAGTGCATTGAATTTCTTAGAACTCATAC 511
Db      |||||||
Db      421 TGGGAGCAGTGGTAGCAGCTTTTATTTCTGATTACAGTGCATTGAATTTCTTAGAACTCATAC 480

QY      512 TATCTGTATACATGTGCACATGGGGCAATTTTACTATGAAATTTAATATGCTGGGTTTTTT 571
Db      |||||||
Db      481 TATCTGTATACATGTGCACATGGGGCAATTTTACTATGAAATTTAATATGCTGGGTTTTTT 540

QY      572 AATACCTTTTATATATCATGTTTCACTTTAAGAAAGACTTCATAAGTAGGAGATGAGTTTAA 631
Db      |||||||
Db      541 AATACCTTTTATATATCATGTTTCACTTTAAGAAAGAC-TCATAAGTNGGANATGAGTTTAA 599

QY      632 TTCTCAGCAAAATAGACCTGTCAAATTTAGAT 662
Db      |||||||
Db      600 TTCTCANC-AATAGACCTGTCAAATTTAGAT 629

ADL29733
ID      ADL29733 standard; cDNA; 629 BP.
XX
AC      ADL29733;
XX
DT      20-MAY-2004 (first entry)
XX
DE      5' end of a representative human cDNA cluster SeqID 1766.
XX
KW      human; medicine; signal transduction; glycoprotein; transcription;
KW      oligo-capping method; ss.
XX
OS      Homo sapiens.
XX
PN      EP1396543-A2.
XX
PD      10-MAR-2004.
XX
PF      07-JUL-2000; 2003EP-00025638.
XX
```


QY 632 TTCTCAGCAAAATAGACCTGTCAAATTTAGAT 662
| | | | | | | | | | | | | | | | | | | | | |
Db 600 TTCTCANC-AATAGACCTGTCAAATTTAGAT 629
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13
ADL28325
ID ADL28325 standard; cDNA; 629 BP.
XX
AC ADL28325;
XX
DT 20-MAY-2004 (first entry)
XX
DE 5' end of a human cDNA molecule SeqID 358.
XX
KW human; medicine; signal transduction; glycoprotein; transcription;
KW oligo-capping method; ss.
XX
OS Homo sapiens.
XX
PN EP1396543-A2.
XX
PD 10-MAR-2004.
XX
PF 07-JUL-2000; 2003EP-00025638.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2004-204755/20.
XX
PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
XX
PS Disclosure; SEQ ID NO 358; 1340pp; English.
XX
CC This invention relates to a novel primers useful for synthesising full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polynucleotide sequence is the
CC 5' end of a full length human cDNA sequence of the invention.
XX
SQ Sequence 629 BP; 144 A; 129 C; 140 G; 211 T; 0 U; 5 Other;

Query Match 52.8%; Score 588.4; DB 12; Length 629;
Best Local Similarity 98.6%; Pred. No. 8.8e-167;
Matches 622; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY 33 AGGAAGCCGGAAGCAGCCGCGGCCAGTTC-GGGAGACATGGCGGCGTTAAAGCTCTC 91
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AGGAAGCCGGAAGCAGCCGCGGCCAGTTCGGGGAGACATGGCGGCGTTAAAGCTCTC 60
| | | | | | | | | | | | | | | | | | | | | |
QY 92 GTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTCTTATGCTGGGATGCGCTTA 151
| | | | | | | | | | | | | | | | | | | | | |
Db 61 GTGGCATTATCCTTCAGTGGGGCTATTGGACTGACTTTCTTATGCTGGGATGCGCTTA 120
| | | | | | | | | | | | | | | | | | | | | |
QY 152 GAGGATTATGGCGTTTACTGGCCCTTATTGTCCTGATTTTCCACGCCATCTCCCCCATC 211
| | | | | | | | | | | | | | | | | | | | | |
Db 121 GAGGATTATGGCGTTTACTGGCCCTTATTGTCCTGATTTTCCACGCCATCTCCCCCATC 180
| | | | | | | | | | | | | | | | | | | | | |
QY 212 CCCCATTTTCATGCCCCAAAGAGTCACCTATGACTCAGATGCAACCCAGTAGTCGTGCGG 271
| | | | | | | | | | | | | | | | | | | | | |

Db 181 CCCCATTTTCATGCCCCAAAGAGTCACCTATGACTCAGATGCAACCAGTAGTCCTGTCTCGG 240
| | | | | | | | | | | | | | | | | | | | | |
QY 272 GAAC TGGCATA TTTCTTCACTACTGGAATGTTGTTTCTGCC TTTGGATTTCC TGTATT 331
| | | | | | | | | | | | | | | | | | | | | |
Db 241 GAACTGGCATA TTTCTTCACTACTGGAATGTTGTTTCTGCC TTTGGATTTCC TGTATT 300
| | | | | | | | | | | | | | | | | | | | | |
QY 332 CTTGCTCGTGTGGCTGTGATCAAATGGGAGCCTGCGGCCTTGTGTTGCGAGGCAATGCA 391
| | | | | | | | | | | | | | | | | | | | | |
Db 301 CTTGCTCGTGTGGCTGTGATCAAATGGGAGCCTGCGGCCTTGTGTTGCGAGGCAATGCA 360
| | | | | | | | | | | | | | | | | | | | | |
QY 392 GTCATTTTCC TTTACAATTC AAGGGTTTTTTCCTTATATTTTGAAGAGAGATGATTTTAGC 451
| | | | | | | | | | | | | | | | | | | | | |
Db 361 NTCATTTTCC TTTACAATTC AAGGGTTTTTTCCTTATATTTTGAANAAGAGATGATTTTAGC 420
| | | | | | | | | | | | | | | | | | | | | |
QY 452 TGGGAGCAGTGGTAGCACTTTTATCTGATTACAGTGCATTGAAATTTCTTAGAACTCATAC 511
| | | | | | | | | | | | | | | | | | | | | |
Db 421 TGGGAGCAGTGGTAGCACTTTTATCTGATTACAGTGCATTGAAATTTCTTAGAACTCATAC 480
| | | | | | | | | | | | | | | | | | | | | |
QY 512 TATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGTTTTTT 571
| | | | | | | | | | | | | | | | | | | | | |
Db 481 TATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGTTTTTT 540
| | | | | | | | | | | | | | | | | | | | | |
QY 572 AATACCTTTATATATCATGTTTCACTTTAAGAAAGACCTTCATAAGTAGGAGATGAGTTT 631
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Db 541 AATACCTTTATATATCATGTTTCACTTTAAGAAAGAC-TCATAAGTNGGANATGAGTTT 599
| | | | | | | | | | | | | | | | | | | | | |
QY 632 TTCTCAGCAAAATAGACCTGTCAAATTTAGAT 662
| | | | | | | | | | | | | | | | | | | | | |
Db 600 TTCTCANC-AATAGACCTGTCAAATTTAGAT 629
| | | | | | | | | | | | | | | | | | | | | |

RESULT 14
ADE85249
ID ADE85249 standard; DNA; 647 BP.
XX
AC ADE85249;
XX
DT 29-JAN-2004 (first entry)
XX
DE Farnesyl transferase inhibitor modulated leukemia associated gene #468.
XX
KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW quinolinone; leukemia; cancer.
XX
OS Homo sapiens.
XX
PN WO2003038129-A2.
XX
PD 08-MAY-2003.
XX
PF 30-OCT-2002; 2002WO-US034784.
XX
PR 30-OCT-2001; 2001US-0338997P.
PR 30-OCT-2001; 2001US-0340081P.
PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Raponi M;
XX
DR WPI; 2003-513497/48.
XX
PT Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
XX
PS Disclosure; SEQ ID NO 468; 346pp; English.
XX
CC The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a

CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.

SQ Sequence 647 BP; 174 A; 122 C; 144 G; 205 T; 0 U; 2 Other;

Query Match 51.8%; Score 577.4; DB 10; Length 647;
Best Local Similarity 98.6%; Pred. No. 1.9e-163;
Matches 644; Conservative 0; Mismatches 3; Indels 6; Gaps 6;

QY 352 CAAATGGGAGCCCTGCGGCTTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCA 411
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Db 1 CAAATGGGAGCCTGC-GCCTGTGTTGGCAGGCAATGCAGTCATTTTCCTTACAATTCA 59

QY 412 AGGGTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTT 471
|||||
Db 60 AGGGTTTTCCTTATATTTGGAAGAGGAGATGATTTTAGCTGGGAGCAGTGGTAGCACTT 119

QY 472 TATTCGTGATTACAGTGCATGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACA 531
|||||
Db 120 TATTCGTGATTACAGTGCATGAATTTCTTAGAACTCATACTATCTGTATACATGTGCACA 179

QY 532 TCGGGCATTTTACTATGAAATTTAATATATGCTGGGTTTTTAAATACCTTTATATATCATGT 591
|||||
Db 180 TCGGGCATTTTACTATGAAATTTAATATATGCTGGGTTTTTAAATACCTTTATATATCATGT 239

QY 592 TCACITTAAGAAAGACITTCATAAGTAGGAGATGAGITTTTATTCTCAGCAAAATAGACCTGT 651
|||||
Db 240 TCACITTAAGAAAGACITTCATAAGTAGGAGATGAGITTTTATTCTCAGCAAAATAGACCTGT 299

QY 652 CAAATTTAGATTATGTTACTCAAATTTATGTTACTTTGGCTGTTTCATGTAGTCACGGT 711
|||||
Db 300 CAAATTTAGATTATGTTACTCAAATTTATGTTACTTTGGCTGTTTCATGTAGTCACGGT 359

QY 712 GCTCTCAGAAAATATATTAACGCAGTCTTGTAGGCAGTGCCACCTTATGCAGTGCATCG 771
|||||
Db 360 GCTCTCAGAAAATATATTAACACAGTCTTGTAGGCAGTGCCACCTTATGCAGTGCATCG 419

QY 772 AAACCTTTTGCTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCATG 831
|||||
Db 420 AAACCTTTTGCTTGGGATGTGCTTGGAGAGGCAGATAACGCTGAAGCAGGCTCTCATG 479

QY 832 ACCCAGGAAGCGCGGGTGGATCCCTCTTTGTGTTGTAGTCCATGCTATTAAAAGTGTGG 891
|||||
Db 480 ACCCAGGAAGCGCGGGTGGATCCCT-TTTGTGTTGTAGTCCATGC-ATTAAAAGTGTGG 537

QY 892 CCCACAGACCAAGAGCCCTCAACATTTTCCTAGAGCCCTTATTAGAAATGCAGAACTCTGAAGC 951
|||||
Db 538 CCCACAGACCAAGAGCCCTCAACATTTTCCTAGAGCCCTTATTAGAAATGCAGAACTCTGAAG- 596

QY 952 CCCACTCTGGACCCAGGACATTTTGATGAGATCCAAAGGAGTTGTATGCACAT 1004
|||||
Db 597 CCCACTCTGGACCCAGGACA-TTTGATGAGATCC-AANGAGTTGTATGCNCAT 647

RESULT 15
AAK92657/c
ID AAK92657 standard; cDNA; 546 BP.

XX AAK92657;

AC AAK92657;

XX 06-NOV-2001 (first entry)

DT Human cDNA 3'-end sequence, SEQ ID NO: 1117.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

DE Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

PT 830 Primers useful for synthesizing full length cDNA clones and their use

PT in genetic manipulation.

XX Claim 3; SEQ ID NO 1117; 1380pp + Sequence Listing; English.

XX The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 3'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO

XX Sequence 546 BP; 160 A; 114 C; 115 G; 150 T; 0 U; 7 Other;

Query Match 44.7%; Score 498.4; DB 4; Length 546;
Best Local Similarity 96.2%; Pred. No. 1.3e-139;
Matches 528; Conservative 0; Mismatches 18; Indels 3; Gaps 2;

QY 565 GTTTTTTAATACCTTTATATATCATGTTTCATCTTAAAGAAAGACTTCATAAGTAGGAGATG 624
|||||
Db 546 GGTTTTTAAANCCCTTAAAAATCAANGTCCCTTTAAGAANG-CTTCATAAGTAGGAGATG 488

QY 625 AGTTTTTATCTCAGCAAAATAGACCTGTCAAAATTAGATTATGTTACTCAAATTATGTTAC 684
|||||
Db 487 AGTTTTTATCTCAGCAA--TAGCCTGTCAAAATTAGATTATGTTACTCAAATTATGTTAC 430

QY 685 TTGTTTGGCTGTTTCATGTAGTCACGGTGTCTCAGAAAAATATATTAACGCAGTCTGTAG 744
|||||
Db 429 TTGTTTGGCTGTTTCATGTAGTCACGGTGTCTCAGAAAAATATATTAACGCAGTCTGTAG 370

QY 745 GCAGTGCCACCTTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTTGGAGAGGC 804
|||||
Db 369 GCAGTGCCACCTTATGCAGTGCATCGAAACCTTTTGCTTGGGGATGTGCTTTGGAGAGGC 310

QY 805 AGATAACGCTGAAGCAGGCCTCTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTG 864
|||||
Db 309 AGATAACGCTGAAGCAGGCCTNTCATGACCCAGGAAGCGCGGGTGGATCCCTCTTTGTG 250

QY 865 TTGTAGTCCATGCTATTAAAAGTGTGGCCCAAGAGAGCCCTCAACATTTCTCTAGAG 924
|||||
Db 249 TTGTAGTCCATGCTATTAAAAGTGTGGCCCAAGAGAGCCCTCAACATTTCTCTAGAG 190

QY 925 CCTTATTAGAAATGCAGAAATCTGAAGCCCCCACTCTGGACCCAGGACATTTTGTAGATG 984
|||||
Db 189 CCTTATTAGAAATGCAGAAATNTGAAGCCCCCACTNTGGACCCAGGACATTTTGTAGATG 130

QY 985 CAAAGGAGTTGTATGCACATGAAAGTTTGAGAAAGCATCATCATAGAGAAGTAAACATCAC 1044
|||||
Db 129 CAAAGGAGTTGTATGCACATGAAAGTTTGAGAAAGCATCATCATAGAGAAGTAAACATCAC 70

QY 1045 ACCCAACTTCCTTATCTTTCCAGTGGGCTAAACCACTTAACCTCTCTGGGTGTACCTGCT 1104

```

|||||
Db      69 ACCCAACTTCCTTATCTTCCAGTGGCTAAACCACTTAACCTCTCTGGGTGTTACCTGCT 10
      |||||||
QY      1105 CATTGTTT 1113
      |||||||
Db      9 CATTGTTT 1
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Search completed: August 18, 2005, 00:13:52
Job time : 709 secs

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:59:27 ; Search time 9 Seconds
(without alignments)
2.633 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctggcttgccaggctgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 511 seqs, 10634 residues

Total number of hits satisfying chosen parameters: 1022

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 511 summaries

Database : pubdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 25 | 2.2 | 25 | 1 US-10-956-157-58122 | Sequence 58122, A |
| 3 | 25 | 2.2 | 25 | 1 US-10-956-157-58123 | Sequence 58123, A |
| 4 | 25 | 2.2 | 25 | 1 US-10-956-157-58124 | Sequence 58124, A |
| 5 | 25 | 2.2 | 25 | 1 US-10-956-157-58125 | Sequence 58125, A |
| 6 | 25 | 2.2 | 25 | 1 US-10-956-157-58126 | Sequence 58126, A |
| 7 | 25 | 2.2 | 25 | 1 US-10-956-157-58127 | Sequence 58127, A |
| 8 | 25 | 2.2 | 25 | 1 US-10-956-157-58128 | Sequence 58128, A |
| 9 | 25 | 2.2 | 25 | 1 US-10-956-157-58129 | Sequence 58129, A |
| 10 | 25 | 2.2 | 25 | 1 US-10-956-157-58130 | Sequence 58130, A |
| 11 | 25 | 2.2 | 25 | 1 US-10-956-157-58131 | Sequence 58131, A |
| 12 | 25 | 2.2 | 25 | 1 US-10-956-157-58132 | Sequence 58132, A |
| 13 | 25 | 2.2 | 25 | 1 US-10-956-157-58133 | Sequence 58133, A |
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| 20 | 25 | 2.2 | 25 | 1 US-10-956-157-58140 | Sequence 58140, A |
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| 38 | 25 | 2.2 | 25 | 1 US-10-956-157-209653 | Sequence 209653, |
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| 40 | 25 | 2.2 | 25 | 1 US-10-956-157-215150 | Sequence 215150, |
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| 65 | 23.4 | 2.1 | 25 | 1 US-10-719-956-674672 | Sequence 674672, |
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| 75 | 20.2 | 1.8 | 25 | 1 US-10-098-263B-110791 | Sequence 110791, |
| 76 | 20.2 | 1.8 | 25 | 1 US-10-719-900-377731 | Sequence 377731, |
| 77 | 20.2 | 1.8 | 25 | 1 US-10-719-956-92897 | Sequence 92897, A |
| 78 | 20.2 | 1.8 | 25 | 1 US-10-719-956-133887 | Sequence 133887, |
| 79 | 20 | 1.8 | 20 | 1 US-10-774-721-2 | Sequence 2, Appl |
| 80 | 20 | 1.8 | 20 | 1 US-10-774-721-22 | Sequence 22, Appl |
| 81 | 20 | 1.8 | 20 | 1 US-10-774-721-23 | Sequence 23, Appl |
| 82 | 20 | 1.8 | 20 | 1 US-10-774-721-24 | Sequence 24, Appl |
| 83 | 20 | 1.8 | 20 | 1 US-10-774-721-25 | Sequence 25, Appl |
| 84 | 20 | 1.8 | 20 | 1 US-10-774-721-26 | Sequence 26, Appl |
| 85 | 20 | 1.8 | 20 | 1 US-10-774-721-27 | Sequence 27, Appl |
| 86 | 20 | 1.8 | 20 | 1 US-10-774-721-28 | Sequence 28, Appl |
| 87 | 20 | 1.8 | 20 | 1 US-10-774-721-29 | Sequence 29, Appl |
| 88 | 20 | 1.8 | 20 | 1 US-10-774-721-30 | Sequence 30, Appl |
| 89 | 20 | 1.8 | 20 | 1 US-10-774-721-31 | Sequence 31, Appl |
| 90 | 20 | 1.8 | 20 | 1 US-10-774-721-33 | Sequence 33, Appl |
| 91 | 20 | 1.8 | 20 | 1 US-10-774-721-34 | Sequence 34, Appl |
| 92 | 20 | 1.8 | 21 | 1 US-10-774-721-38 | Sequence 38, Appl |
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c 268 14.8 1.3 21 1 US-10-627-253A-300 Sequence 300, App
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c 270 14.8 1.3 21 1 US-10-627-253A-302 Sequence 302, App
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c 281 14.8 1.3 21 1 US-10-484-577-296 Sequence 296, App
282 14.8 1.3 21 1 US-10-847-918-4920 Sequence 4920, App
283 14.4 1.3 16 1 US-10-451-805-6 Sequence 6, Appli
c 284 14.4 1.3 17 1 US-09-866-108-2565 Sequence 2565, Ap
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c 287 14.4 1.3 17 1 US-09-930-423-478 Sequence 478, App
c 288 14.4 1.3 17 1 US-09-930-423-1012 Sequence 1012, Ap
c 289 14.4 1.3 17 1 US-09-745-237A-478 Sequence 478, App
c 290 14.4 1.3 17 1 US-09-745-237A-1012 Sequence 1012, Ap
291 14.4 1.3 17 1 US-10-342-902-948 Sequence 948, App
c 292 14.4 1.3 17 1 US-10-138-674-7395 Sequence 7395, Ap
c 293 14.4 1.3 17 1 US-10-287-949A-7395 Sequence 7395, Ap
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ALIGNMENTS

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; Sequence 58121, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58121

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Fri Aug 19 11:00:02 2005

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; LENGTH: 25
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US-10-956-157-58129

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; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
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US-10-956-157-58130

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
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US-10-956-157-58128

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
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; LENGTH: 25
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US-10-956-157-58129

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
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US-10-956-157-58130

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
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US-10-956-157-58131

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58132
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58132
Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1040 ATCACACCCAACTTCCTTATCTTTC 1064
      |||||||
Db      1 ATCACACCCAACTTCCTTATCTTTC 25

RESULT 13
US-10-956-157-58133
; Sequence 58133, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58133
Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1039 CATCACACCCAACTTCCTTATCTTT 1063
      |||||||
Db      1 CATCACACCCAACTTCCTTATCTTT 25

RESULT 14
US-10-956-157-58134
; Sequence 58134, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58134
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58134
Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1034 GTAAACATCACACCCAACTTCCTTA 1058
      |||||||
Db      1 GTAAACATCACACCCAACTTCCTTA 25

RESULT 15
US-10-956-157-58135
; Sequence 58135, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58135
Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      676 TTATGTTACTTGTGGCTGTTTCAT 700
      |||||||
Db      1 TTATGTTACTTGTGGCTGTTTCAT 25

RESULT 16
US-10-956-157-58136
; Sequence 58136, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58136
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58136
Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1036 AAACATCACACCCAACTTCCTTATC 1060
      |||||||
Db      1 AAACATCACACCCAACTTCCTTATC 25

RESULT 17
US-10-956-157-58137
```



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; Sequence 58137, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58137

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1051 CTCCTTATCTTCCAGTGGCTAAA 1075
      |||||||
Db      1 CTCCTTATCTTCCAGTGGCTAAA 25

RESULT 18
US-10-956-157-58138
; Sequence 58138, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58138

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1052 TTCCTTATCTTCCAGTGGCTAAAC 1076
      |||||||
Db      1 TTCCTTATCTTCCAGTGGCTAAAC 25

RESULT 19
US-10-956-157-58139
; Sequence 58139, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58139
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Probe Sequence
US-10-956-157-58139

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1008 AGTTTGAGAAGCATCATCATAGAGA 1032
      |||||||
Db      1 AGTTTGAGAAGCATCATCATAGAGA 25

RESULT 20
US-10-956-157-58140
; Sequence 58140, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58140

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1023 ATCATAGAGAAGTAAACATCACACC 1047
      |||||||
Db      1 ATCATAGAGAAGTAAACATCACACC 25

RESULT 21
US-10-956-157-58141
; Sequence 58141, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58141
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58141

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      725 ATATTAACGCAGCTTGTAGGCAGC 749
      |||||||
Db      1 ATATTAACGCAGCTTGTAGGCAGC 25

RESULT 22
US-10-956-157-58142
; Sequence 58142, Application US/10956157
```

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; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58142
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58142

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      674 AATTATGTTACTTGTGGCTGTTTC 698
      |||||||
Db      1 AATTATGTTACTTGTGGCTGTTTC 25

RESULT 23
US-10-956-157-58143
; Sequence 58143, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58143
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58143

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1038 ACATCACACCCCACTTCCTTATCTT 1062
      |||||||
Db      1 ACATCACACCCCACTTCCTTATCTT 25

RESULT 24
US-10-956-157-58144
; Sequence 58144, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-58144
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US-10-956-157-58144

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1037 AACATCACACCCCACTTCCTTATCT 1061
      |||||||
Db      1 AACATCACACCCCACTTCCTTATCT 25

RESULT 25
US-10-956-157-126134
; Sequence 126134, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-126134

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      723 ATATATTAAAGCAGTCTTGTAGGCA 747
      |||||||
Db      1 ATATATTAAAGCAGTCTTGTAGGCA 25

RESULT 26
US-10-956-157-133680
; Sequence 133680, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-133680

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      820 AGGCCTCTCATGACCCAGGAAGGCC 844
      |||||||
Db      1 AGGCCTCTCATGACCCAGGAAGGCC 25

RESULT 27
US-10-956-157-137776
; Sequence 137776, Application US/10956157
; Publication No. US20050118625A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-137776

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      869 AGTCCATGCTATTAAAAAGTGTGGCC 893
      ||||||||||||||||||||||||
Db      1 AGTCCATGCTATTAAAAAGTGTGGCC 25

RESULT 28
US-10-956-157-140388
; Sequence 140388, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140388
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-140388

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      644 AGACCTGTCAAATTAGATTATGTT 668
      ||||||||||||||||||||||||
Db      1 AGACCTGTCAAATTAGATTATGTT 25

RESULT 29
US-10-956-157-140715
; Sequence 140715, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140715
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-140715
```

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Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      897 AGACCAAGAGCCTCAACATTTCCTA 921
      ||||||||||||||||||||||||
Db      1 AGACCAAGAGCCTCAACATTTCCTA 25

RESULT 30
US-10-956-157-146569
; Sequence 146569, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-146569

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      575 ACCTTTATATATCATGTTCACTTTA 599
      ||||||||||||||||||||||||
Db      1 ACCTTTATATATCATGTTCACTTTA 25

RESULT 31
US-10-956-157-158472
; Sequence 158472, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158472
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-158472

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      882 AAAAGTGTGCCCAAGACCAAGAG 906
      ||||||||||||||||||||||||
Db      1 AAAAGTGTGCCCAAGACCAAGAG 25

RESULT 32
US-10-956-157-168122
; Sequence 168122, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-168122

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      674 AATTATGTTACTTGTGTTGGCTGTTTC 698
Db      1 AATTATGTTACTTGTGTTGGCTGTTTC 25

RESULT 33
US-10-956-157-182572
; Sequence 182572, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182572
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-182572

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      776 CTTTGTCTGGGGATGTGCTTGGAG 800
Db      1 CTTTGTCTGGGGATGTGCTTGGAG 25

RESULT 34
US-10-956-157-198286
; Sequence 198286, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-198286
```

```

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      823 CCTCTCATGACCCAGGAAGCCGGG 847
Db      1 CCTCTCATGACCCAGGAAGCCGGG 25

RESULT 35
US-10-956-157-198863
; Sequence 198863, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198863
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-198863

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      855 CCTCTTTGTGTGTAGTCCATGCTA.879
Db      1 CCTCTTTGTGTGTAGTCCATGCTA 25

RESULT 36
US-10-956-157-199300
; Sequence 199300, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199300
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-199300

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1054 CCTTATCTTTCCAGTGGCTAAACCA 1078
Db      1 CCTTATCTTTCCAGTGGCTAAACCA 25

RESULT 37
US-10-956-157-204733
; Sequence 204733, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```



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; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 204733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-204733

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      766 GCATCGAAACCTTTTGCTTGGGGAT 790
      |||||||
Db      1 GCATCGAAACCTTTTGCTTGGGGAT 25

RESULT 38
US-10-956-157-209653
; Sequence 209653, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209653
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-209653

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      748 GCTGCCACCTTATGCAGTGCATCGA 772
      |||||||
Db      1 GCTGCCACCTTATGCAGTGCATCGA 25

RESULT 39
US-10-956-157-214737
; Sequence 214737, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214737
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-214737

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATGCAGTGCAT 769
      |||||||
Db      1 GCAGCTGCCACCTTATGCAGTGCAT 25

RESULT 41
US-10-956-157-216427
; Sequence 216427, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 216427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-216427

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      527 GCACATGCGGCATTTTACTATGAAA 551
      |||||||
Db      1 GCACATGCGGCATTTTACTATGAAA 25

RESULT 42
US-10-956-157-225248
; Sequence 225248, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

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Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      761 GCAGTGCATCGAAACCTTTTGCTTG 785
      |||||||
Db      1 GCAGTGCATCGAAACCTTTTGCTTG 25

RESULT 40
US-10-956-157-215150
; Sequence 215150, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215150
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-215150

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATGCAGTGCAT 769
      |||||||
Db      1 GCAGCTGCCACCTTATGCAGTGCAT 25

RESULT 41
US-10-956-157-216427
; Sequence 216427, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 216427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-216427

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      527 GCACATGCGGCATTTTACTATGAAA 551
      |||||||
Db      1 GCACATGCGGCATTTTACTATGAAA 25

RESULT 42
US-10-956-157-225248
; Sequence 225248, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225248
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225248

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 771 GAAACCTTTTGGTGGGATGTGCT 795
Db 1 GAAACCTTTTGGTGGGATGTGCT 25

RESULT 43
US-10-956-157-225301
; Sequence 225301, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225301

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1005 GAAAGTTTGAGAGCATCATCATAG 1029
Db 1 GAAAGTTTGAGAGCATCATCATAG 25

RESULT 44
US-10-956-157-231080
; Sequence 231080, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-231080

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 GAGCCTCAACATTTCCTAGAGCCTT 928
Db 1 GAGCCTCAACATTTCCTAGAGCCTT 25

RESULT 45
US-10-956-157-239117
; Sequence 239117, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-239117

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGTTGTATGCACATG 1005
Db 1 GATCCAAAGGAGTTGTATGCACATG 25

RESULT 46
US-10-956-157-239416
; Sequence 239416, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239416
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-239416

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 806 GATAACGCTGAAGCAGGCCTCTCAT 830
Db 1 GATAACGCTGAAGCAGGCCTCTCAT 25

RESULT 47
US-10-956-157-244137
; Sequence 244137, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 244137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-244137

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      695 GTTCATGTAGTCACGGTGCTCTCAG 719
Db      1 GTTCATGTAGTCACGGTGCTCTCAG 25

RESULT 48
US-10-956-157-246391
; Sequence 246391, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 246391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-246391

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      687 GTTTGGCTGTTTCATGTAGTCACGGT 711
Db      1 GTTTGGCTGTTTCATGTAGTCACGGT 25

RESULT 49
US-10-956-157-247073
; Sequence 247073, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 247073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-247073

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      701 GTAGTCACGGTGCTCTCAGAAAATA 725
Db      1 GTAGTCACGGTGCTCTCAGAAAATA 25

RESULT 50
US-10-956-157-250507
; Sequence 250507, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250507
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-250507

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      704 GTCACGGTGCTCTCAGAAAATATAT 728
Db      1 GTCACGGTGCTCTCAGAAAATATAT 25

RESULT 51
US-10-956-157-254092
; Sequence 254092, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-254092

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      791 GTGCTTGGAGAGGCAGATAACGCTG 815
Db      1 GTGCTTGGAGAGGCAGATAACGCTG 25

RESULT 52
US-10-956-157-261903
; Sequence 261903, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

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; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 261903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-261903

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 GGGGATGCTTGGAGAGGCAGATA 809
|||||
Db 1 GGGGATGCTTGGAGAGGCAGATA 25

RESULT 53
US-10-956-157-265849
; Sequence 265849, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 265849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-265849

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 GGATCCCTCTTTGTGTTGTAGTCCA 874
|||||
Db 1 GGATCCCTCTTTGTGTTGTAGTCCA 25

RESULT 54
US-10-956-157-267654
; Sequence 267654, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 267654
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-267654

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAGATGAGTTTATTCTCAGCAA 642
|||||
Db 1 GGAGATGAGTTTATTCTCAGCAA 25

RESULT 55
US-10-956-157-269226
; Sequence 269226, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269226
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-269226

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 960 GGACCCAGGACATTTTGATGAGATC 984
|||||
Db 1 GGACCCAGGACATTTTGATGAGATC 25

RESULT 56
US-10-956-157-292875
; Sequence 292875, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-292875

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1088 TCTGGGTGTACCTGCTCATTGTT 1112
|||||
Db 1 TCTGGGTGTACCTGCTCATTGTT 25

RESULT 57
US-10-956-157-298706
; Sequence 298706, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
;

; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 298706
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-298706

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 TCAACATTTCCTAGAGCCCTTATTAG 933
Db 1 TCAACATTTCCTAGAGCCCTTATTAG 25

RESULT 58
US-10-956-157-301719
; Sequence 301719, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301719
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-301719

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 TACATGTGCACATGCGGGCATTTTAC 544
Db 1 TACATGTGCACATGCGGGCATTTTAC 25

RESULT 59
US-10-956-157-304297
; Sequence 304297, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 304297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-304297

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 TAGAGAAGTAAACATCACACCCCAAC 1051

Db 1 TAGAGAAGTAAACATCACACCCCAAC 25

RESULT 60
US-10-956-157-308375
; Sequence 308375, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 308375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-308375

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 630 TATTCTCAGCAAATAGACCTGTCAA 654
Db 1 TATTCTCAGCAAATAGACCTGTCAA 25

RESULT 61
US-10-956-157-309122
; Sequence 309122, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 309122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-309122

Query Match 2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 TTTGTGTTGTAGTCCATGCTATTAA 883
Db 1 TTTGTGTTGTAGTCCATGCTATTAA 25

RESULT 62
US-10-956-157-316779
; Sequence 316779, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157

```
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 316779
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-316779

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      916 TTCCTAGAGCCTTATTAGAAATGCA 940
      |||
Db      1 TTCCTAGAGCCTTATTAGAAATGCA 25

RESULT 63
US-10-956-157-317103
; Sequence 317103, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 317103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-317103

Query Match      2.2%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1052 TTCCTTATCTTTCCAGTGGCTAAAC 1076
      |||
Db      1 TTCCTTATCTTTCCAGTGGCTAAAC 25

RESULT 64
US-10-719-956-417007
; Sequence 417007, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417007
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-417007

Query Match      2.1%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 36;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      271 GGAAGTGGCATATTTCTTCACTACT 295
      |||
```

```
Db      1 GGAAGTGGCATATTTCTTCACTACT 25

RESULT 65
US-10-719-956-674672
; Sequence 674672, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674672
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-674672

Query Match      2.1%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 36;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      330 TTCTTGCTCGTGTGGCTGTGATCAA 354
      |||
Db      1 TTCTTGCTCGTGTGGCTGTGATCAA 25

RESULT 66
US-10-719-956-345761
; Sequence 345761, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 345761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-345761

Query Match      2.0%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      152 GAGGATTATGGCGTTTACTGGCCC 175
      |||
Db      1 GAGGACTATGGCGTTTACTGGCCC 24

RESULT 67
US-10-774-721-32/c
; Sequence 32, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
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; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS11
US-10-774-721-32

Query Match          2.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      264 CCTGTCGGGAAGTGGCATATTT 285
Db      22 CCTGTCGGGAAGTGGCATATTT 1

RESULT 68
US-10-719-900-377733
; Sequence 377733, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 377733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-377733

Query Match          2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1085 CTCTCTGGGTGTACCTGCTCATTT 1109
Db      1 CTCTCTGGGTGTGCAATGCTCATTT 25

RESULT 69
US-10-719-956-92898
; Sequence 92898, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 92898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-92898
```

```

Query Match          2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      254 ACCAGTAGTGCCTGTCGGGAACCTGG 278
Db      1 ACTAGCAGTGCCTGTCGGGAACCTGG 25

RESULT 70
US-10-719-956-417006
; Sequence 417006, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-417006

Query Match          2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      271 GGAAGTGGCATATTTCTTCACTACT 295
Db      1 GGAAGTGGCATAAATTTCTTCACTACT 25

RESULT 71
US-10-719-956-674671
; Sequence 674671, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-674671

Query Match          2.0%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 56;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      330 TTCTTGCTCGTGGCTGTGATCAA 354
Db      1 TTCTTGCTCGGAGGCTGTGATCAA 25

RESULT 72
US-10-719-956-345760
; Sequence 345760, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 345760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-345760
```

```

Query Match          1.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      152 GAGGATTATGGCGTTTACTGGCCC 175
          ||||| ||||| ||||| ||||| |||||
Db       1 GAGGACTATGGCCTTTACTGGCCC 24
```

```

RESULT 73
US-10-719-956-445812
; Sequence 445812, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ.ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 445812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-445812
```

```

Query Match          1.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      379 GGCAGGCAATGCAGTCAATTTTCCT 402
          ||| ||||| ||||| ||||| |||||
Db       1 GGCTGGCAATGCAGTTATTTTCCT 24
```

```

RESULT 74
US-10-719-956-456463
; Sequence 456463, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 456463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-456463
```

```

Query Match          1.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 74;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      76 GGGCGTTAAAGCTCTCGTGGCATT 99
          ||||| ||||| ||||| ||||| |||||
Db       1 GGGCGTTAAAGCTCTTGTGGCACT 24
```

```

RESULT 75
US-10-098-263B-110791
; Sequence 110791, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110791
```

```

Query Match          1.8%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      179 TTCGTCTCGATTTCCACGCCATCT 203
          ||| ||||| ||||| ||||| |||||
Db       1 TTCATCTCGAGTTTCCACGCCGTCT 25
```

```

RESULT 76
US-10-719-900-377731
; Sequence 377731, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 377731
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-377731
```

```

Query Match          1.8%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      1085 CTCTCTGGGTGTACCTGCTCATTT 1109
          ||||| ||||| ||||| ||||| |||||
Db       1 CTCTCTGGGTGTAGCATGCTCATTT 25
```

```

RESULT 77
US-10-719-956-92897
; Sequence 92897, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
```



```

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 92897
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-92897

Query Match          1.8%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 254 ACCAGTAGTCCTGTGCGGAACTGG 278
   |||||
Db 1 ACTAGCAGTCCCACTCGGGAACCTGG 25

RESULT 78
US-10-719-956-133887
; Sequence 133887, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 133887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-133887

Query Match          1.8%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 59 AGTTCGGGAGACATGGCGGCGTTA 83
   |||||
Db 1 AGCTCCAGAGACATGGCGGCGTTA 25

RESULT 79
US-10-774-721-2/c
; Sequence 2, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS14
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: antisens AS14
US-10-774-721-2

Query Match          1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 ACATGTGCACATGCGGCATT 540
   |||||
Db 20 ACATGTGCACATGCGGCATT 1

RESULT 80
US-10-774-721-22/c
; Sequence 22, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS01
US-10-774-721-22

Query Match          1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGGCCGTGGCAGGAAGC 39
   |||||
Db 20 CCCGGCCGTGGCAGGAAGC 1

RESULT 81
US-10-774-721-23/c
; Sequence 23, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which Inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```

; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS02
US-10-774-721-23

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CCCAGTTCGGGAGACATGGC 75
|||||
Db 20 CCCAGTTCGGGAGACATGGC 1

RESULT 82

US-10-774-721-24/c
; Sequence 24, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS03
US-10-774-721-24

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 CGGGAGACATGGCGGCGTT 82
|||||
Db 20 CGGGAGACATGGCGGCGTT 1

RESULT 83

US-10-774-721-25/c
; Sequence 25, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07

; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS04
US-10-774-721-25

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ATGGCGGGCGTTAAAGCTCT 90
|||||
Db 20 ATGGCGGGCGTTAAAGCTCT 1

RESULT 84

US-10-774-721-26/c
; Sequence 26, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS05
US-10-774-721-26

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AAGCTCTCGTGGCATTATCC 103
|||||
Db 20 AAGCTCTCGTGGCATTATCC 1

RESULT 85

US-10-774-721-27/c
; Sequence 27, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005

; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS10
US-10-774-721-31

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TGCCTGTCTGGGAAGTGGCAT 281
| | | | | | | | | | | | | | | |
Db 20 TGCCTGTCTGGGAAGTGGCAT 1

RESULT 90
US-10-774-721-33/c
; Sequence 33, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS12
US-10-774-721-33

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 269 CGGGAAGTGGCATATTTCTT 288
| | | | | | | | | | | | | | | |
Db 20 CGGGAAGTGGCATATTTCTT 1

RESULT 91
US-10-774-721-34/c
; Sequence 34, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP

; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AS13
US-10-774-721-34

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 CCTTGTGTTGGCAGCAATG 389
| | | | | | | | | | | | | | | |
Db 20 CCTTGTGTTGGCAGCAATG 1

RESULT 92
US-10-774-721-38/c
; Sequence 38, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-38

Query Match 1.8%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 AGTGCCTGTCGGGAAGTGGC 279
| | | | | | | | | | | | | | | |
Db 20 AGTGCCTGTCGGGAAGTGGC 1

RESULT 93
US-09-918-702-59/c
; Sequence 59, Application US/09918702
; Patent No. US20020146678A1
; GENERAL INFORMATION:
; APPLICANT: Benvenisty, Nissim
; TITLE OF INVENTION: Directed Differentiation of Embryonic Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 1822/113
; CURRENT APPLICATION NUMBER: US/09/918,702
; CURRENT FILING DATE: 2001-07-31


```
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: 3' primer of Parathyroid Hormone
US-09-918-702-59

Query Match          1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 794 CTTGGAGAGCGAGATAACGCTGA 816
Db 23 CTTGGAGAGCGAGACAAAGCTGA 1

RESULT 94
US-10-719-956-178975
; Sequence 178975, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 178975
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-178975

Query Match          1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 308 TCTGCCTTTGGATTTCCTGTAT 330
Db 2 TCAGCCTCTGGATTTCCTGTAT 24

RESULT 95
US-10-774-721-37
; Sequence 37, Application US/10774721
; Publication No. US2005009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Artificial
US-10-774-721-37

Query Match          1.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 76;
Matches 16; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 261 GTGCCTGTCGGGAACCTGGCAT 281
Db 1 GUGCCUGUGCGGAACUGGCTT 21

RESULT 96
US-10-719-956-48484
; Sequence 48484, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-48484

Query Match          1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 229 AAGAGTCACCTATGACTCAGATGC 252
Db 1 AAGGTCACCTATGACTCGGACGC 24
```

```
RESULT 97
US-10-719-956-445813
; Sequence 445813, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 445813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-445813

Query Match          1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 379 GGCAGGCAATGCAGTCATTTTCCT 402
Db 1 GGCTGGCAATGCTGTATTTCCT 24

RESULT 98
US-10-719-956-456462
; Sequence 456462, Application US/10719956
```

```
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 456462
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-456462
```

```
Query Match 1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 76 GGGCGTTAAAGCTCTCGTGCATT 99
Db 1 GGGCGTTAAAGCACTTGTGGCACT 24
```

RESULT 99

```
US-10-719-956-511569/c
; Sequence 511569, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 511569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-511569
```

```
Query Match 1.7%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 737 TCTTGTTAGGCAGCTGCCAC 755
Db 19 TCTTGTTAGGCAGCTGCCAC 1
```

RESULT 100

```
US-10-809-189-107033/c
; Sequence 107033, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107033
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-107033
```

```
Query Match 1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 626 GTTTTATTCTCAGCAATAGAC 647
Db 25 GTTTTATTCTCAGCCAAGAGAC 4
```

RESULT 101

```
US-10-956-157-97217/c
; Sequence 97217, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97217
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97217
```

```
Query Match 1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 926 CTTATTAGAAATGCAGAACTCTG 947
Db 22 CTTGTTAGAAATGCAGAGTCTG 1
```

RESULT 102

```
US-10-956-157-97220/c
; Sequence 97220, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97220
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97220
```

```
Query Match 1.7%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 926 CTTATTAGAAATGCAGAACTCTG 947
Db 23 CTTGTTAGAAATGCAGAGTCTG 2
```

Fri Aug 19 11:00:02 2005

```
; SEQ ID NO 262562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-262562

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 874 ATGCTATTAAAGTGTGGCCACAG 898
Db 1 ATGCTTTTCAAAGTGTGCTCCACAG 25

RESULT 106
US-10-719-900-464383
; Sequence 464383, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 464383
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-464383

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 318 GATTTCCTGTTATTCTTGCTCGTGT 342
Db 1 GACTTCATGTTATTCTTGCTAGTTT 25

RESULT 107
US-10-809-189-125800
; Sequence 125800, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-125800

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 103
US-10-719-956-553897
; Sequence 553897, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553897
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-553897

Query Match
Best Local Similarity 1.7%; Score 18.8; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 682 TACTTGTTGGCTGTTTCATGTA 703
Db 1 TACTGGTTTGGCTGCTCATGTA 22

RESULT 104
US-10-098-263B-110792
; Sequence 110792, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-110792

Query Match
Best Local Similarity 1.7%; Score 18.6; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 179 TTCGTCCTGATTTCACGCCATCT 203
Db 1 TTCATCCTGAGTATCCACGCCGTCT 25

RESULT 105
US-10-719-900-262562
; Sequence 262562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

QY 864 GTGTAGTCCATGCTATTAAAGTG 888
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCTGTACTTCATGCTGTTAAAGTG 25
| | | | | | | | | | | | | | | | | | | | | |
RESULT 108
US-10-956-157-97213/c
; Sequence 97213, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97213
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97213
Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 922 GAGCCTTATTAGAAATGCAGATCT 946
| | | | | | | | | | | | | | | | | | | | | |
Db 25 GAAACTTGTAGAAATGCAGATCT 1
| | | | | | | | | | | | | | | | | | | | | |
RESULT 109
US-10-956-157-314866
; Sequence 314866, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 314866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-314866
Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 284 TTCTTCACTACTGGAATGTTGTTT 308
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTCTTCACTACTGGAATGTTGTTT 25
| | | | | | | | | | | | | | | | | | | | | |
RESULT 110
US-10-719-956-16848/c
; Sequence 16848, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 231988
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-16848
Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 32 CAGGAAGCCGAGACCGCGGCC 56
| | | | | | | | | | | | | | | | | | | | | |

; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-16848
Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 374 GTGTTGGCAGGCAATGCAGTCATTT 398
| | | | | | | | | | | | | | | | | | | | | |
Db 25 GGGCTGTCAGGCACTGCAGTCATTT 1
| | | | | | | | | | | | | | | | | | | | | |
RESULT 111
US-10-719-956-133888
; Sequence 133888, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 133888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-133888
Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 59 AGTTCGGGAGACATGCGGGCGTTA 83
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AGCTCCAGAGACTTGGCGGGCGTTA 25
| | | | | | | | | | | | | | | | | | | | | |
RESULT 112
US-10-719-956-231988
; Sequence 231988, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 231988
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-231988
Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 32 CAGGAAGCCGAGACCGCGGCC 56
| | | | | | | | | | | | | | | | | | | | | |

Db 1 AAAGTTGTTCCTTGTTGGCTG 23

RESULT 118

US-10-956-157-250112/c

; Sequence 250112, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 250112

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-250112

Query Match 1.6%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 104 TTCAGTGGGGCTATTGGACTGAC 126

|||||

Db 23 TTCAGTGGGAGTATTGGTCTGAC 1

RESULT 119

US-10-843-527-4769/c

; Sequence 4769, Application US/10843527

; Publication No. US20050136395A1

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: Eric Schell

; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus

; FILE REFERENCE: 3602.1

; CURRENT APPLICATION NUMBER: US/10/843,527

; CURRENT FILING DATE: 2004-05-10

; PRIOR APPLICATION NUMBER: 60/469,545

; PRIOR FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 238196

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 4769

; LENGTH: 25

; TYPE: DNA

; ORGANISM: SARS Virus

US-10-843-527-4769

Query Match 1.6%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 892 CCCACAGACCAAGAGCCTCAACA 914

|||||

Db 24 CCCACAGACCAAGAGCATCGAGA 2

RESULT 120

US-10-843-527-233408

; Sequence 233408, Application US/10843527

; Publication No. US20050136395A1

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: Eric Schell

; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus

; FILE REFERENCE: 3602.1

; CURRENT APPLICATION NUMBER: US/10/843,527

; CURRENT FILING DATE: 2004-05-10

; PRIOR APPLICATION NUMBER: 60/469,545

; PRIOR FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 238196

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 233408

; LENGTH: 25

; TYPE: DNA

; ORGANISM: SARS Virus

US-10-843-527-233408

Query Match 1.6%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 892 CCCACAGACCAAGAGCCTCAACA 914

|||||

Db 2 CCCACAGACCAAGAGCATCGAGA 24

RESULT 121

US-10-719-956-178976

; Sequence 178976, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 178976

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-178976

Query Match 1.6%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 308 TCTGCCTTTGGATTTCCTGTAT 330

|||||

Db 2 TCAGCCTCTGGTTTCTCTGTAT 24

RESULT 122

US-08-779-457-30/c

; Sequence 30, Application US/08779457

; Publication No. US20020193571A1

; GENERAL INFORMATION:

; APPLICANT: Carter, Paul J.

; APPLICANT: Chiang, Nancy Y.

; APPLICANT: Kyung, Jin Kim

; APPLICANT: Matthews, William

; APPLICANT: Rodrigues, Maria L.

; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:


```
QY      136 GCTGGGATGTCCTTAGA 153
Db      18 GCTGGGATGTCCTTAGA 1

RESULT 125
US-10-214-802-31
; Sequence 31, Application US/10214802
; Publication No. US20030004109A1
; GENERAL INFORMATION:
;   APPLICANT: Matthews, William
;             Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/214,802
;   FILING DATE: 06-Aug-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/780,562
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: 08/585005
;   FILING DATE: 08-Jan-97
;   APPLICATION NUMBER: 60/
;   FILING DATE: 08-Jan-97
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lee, Wendy M.
;   REGISTRATION NUMBER: 40,378
;   REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-1994
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 31:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 18 base pairs
;     TYPE: Nucleic Acid
;     STRANDEDNESS: Single
;     TOPOLOGY: Linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-214-802-31

Query Match      1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      136 GCTGGGATGTCCTTAGA 153
Db      1 GCTGGGATGTCCTTAGA 18

RESULT 126
US-10-921-710-30/c
; Sequence 30, Application US/10921710
; Publication No. US20050019325A1
; GENERAL INFORMATION:
;   APPLICANT: Carter, Paul J.
;   APPLICANT: Chiang, Nancy Y.
;   APPLICANT: Kim, Kyung Jin
;   APPLICANT: Matthews, William
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT
```

```
; TITLE OF INVENTION: DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN
; TITLE OF INVENTION: OBESE ANIMAL
; FILE REFERENCE: GENENT.53CP2C1
; CURRENT APPLICATION NUMBER: US/10/921,710
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 08/779457
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 60/064855
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/585005
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/667197
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide sequence
US-10-921-710-30

Query Match      1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      136 GCTGGGATGTCCTTAGA 153
Db      18 GCTGGGATGTCCTTAGA 1

RESULT 127
US-10-921-710-31
; Sequence 31, Application US/10921710
; Publication No. US20050019325A1
; GENERAL INFORMATION:
;   APPLICANT: Carter, Paul J.
;   APPLICANT: Chiang, Nancy Y.
;   APPLICANT: Kim, Kyung Jin
;   APPLICANT: Matthews, William
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT
; TITLE OF INVENTION: DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN
; TITLE OF INVENTION: OBESE ANIMAL
; FILE REFERENCE: GENENT.53CP2C1
; CURRENT APPLICATION NUMBER: US/10/921,710
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 08/779457
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 60/064855
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/585005
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/667197
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide sequence
US-10-921-710-31

Query Match      1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      136 GCTGGGATGTCCTTAGA 153
Db      1 GCTGGGATGTCCTTAGA 18
```


Fri Aug 19 11:00:02 2005

```
RESULT 128
US-10-719-900-300059
; Sequence 300059, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 300059
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-300059

Query Match          1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      773 AACCTTTTGCTTGGGATGTG 793
      ||||| ||||| ||||| ||||| |||||
Db      5 AACCTTTTGCTTGAGCAGTG 25

RESULT 129
US-10-719-900-708562
; Sequence 708562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 708562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-708562

Query Match          1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      888 GTGGCCCAACAGACCAAGAGCC 908
      ||||| ||||| ||||| ||||| |||||
Db      1 GTGGAGCACAGACCAAGAGCC 21

RESULT 130
US-10-719-900-793561
; Sequence 793561, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 793561
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-793561

Query Match          1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      470 TTTATTCTGATTACAGTGCAT 490
      ||||| ||||| ||||| ||||| |||||
Db      4 TCTATTCTGATTACAGTGCCT 24

RESULT 131
US-10-719-900-979209
; Sequence 979209, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979209
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-979209

Query Match          1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      299 ATTGTTGTTTCTGCCTTTGGA 319
      ||||| ||||| ||||| ||||| |||||
Db      2 ATTGCGTTACTGCCTTTGGA 22

RESULT 132
US-10-719-956-152720
; Sequence 152720, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152720
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-152720

Query Match          1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      123 TGACITTTTCTTATGCTGGAT 143
      ||||| ||||| ||||| ||||| |||||
Db      4 TGACTTTTCTAATGCTGGTT 24

RESULT 133
US-10-719-956-152720
; Sequence 152720, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152720
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-152720

Query Match          1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      123 TGACITTTTCTTATGCTGGAT 143
      ||||| ||||| ||||| ||||| |||||
Db      4 TGACTTTTCTAATGCTGGTT 24
```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-571667

Query Match      1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      299 ATTGTTGTTCTGCCTTTGGA 319
      ||||| ||| ||||| |||||
Db      2 ATTGTCGTTACTGCCTTTGGA 22

RESULT 136
US-09-841-366A-60/c
; Sequence 60, Application US/09841366A
; Patent No. US20020058265A1
; GENERAL INFORMATION:
; APPLICANT: Bacher, Jeffery W.
; APPLICANT: Flanagan, Laura
; APPLICANT: Nassif, Nadine
; TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN
; TITLE OF INVENTION: DIAGNOSIS OF TUMORS
; FILE REFERENCE: 16026-9267
; CURRENT APPLICATION NUMBER: US/09/841,366A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/663,020
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BAT-25 primer
US-09-841-366A-60

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921 AGAGCCTTATTAGAAATGCAGAAT 944
      ||||| ||| ||||| |||||
Db      24 AGAGCCATAGTTAAATGCAGAAT 1

RESULT 137
US-09-992-665-263
; Sequence 263, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-263

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
;

```

Fri Aug 19 11:00:02 2005

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 834 CCAGGAAGCCGGGTGGATCCCT 857
||||| ||||| ||||| ||||| |||||

Db 1 CCAATATGGCCGGGATGGATACCT 24

RESULT 138

US-10-314-810-60/c

; Sequence 60, Application US/10314810

; Publication No. US20030180758A1

; GENERAL INFORMATION:

; APPLICANT: Bacher, Jeffery W.

; APPLICANT: Flanagan, Laura

; APPLICANT: Nassif, Nadine

; TITLE OF INVENTION: DETECTION OF MICROSATELLITE INSTABILITY AND ITS USE IN

; TITLE OF INVENTION: DIAGNOSIS OF TUMORS

; FILE REFERENCE: 16026-9267

; CURRENT APPLICATION NUMBER: US/10/314,810

; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: US/09/841,366

; PRIOR FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 09/663,020

; PRIOR FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 60

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: BAT-25 primer

US-10-314-810-60

Query Match 1.6%; Score 17.6; DB 1; Length 24;

Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 921 AGAGCCTTATTAGAAATGCAGAA 944
||||| ||| ||||| ||||| |||||

Db 24 AGAGCCATAGTTAAATGCAGAA 1

RESULT 139

US-10-098-263B-87092/c

; Sequence 87092, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 87092

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-87092

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 652 CAAATTTAGATTATGTTACTCAA 675
||||| ||| ||||| ||||| |||||

Db 24 CAAATTTAAACTATGTCACCTGAA 1

RESULT 140

US-10-719-900-143190

; Sequence 143190, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 143190

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-143190

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 297 GAATTGTTGTTTCTGCCCTTTGGAT 320
||||| ||||| ||||| ||||| |||||

Db 2 GAAGTGTGTTTCTGTCATGTGTAT 25

RESULT 141

US-10-719-900-217495

; Sequence 217495, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 217495

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-217495

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 885 AGTGTGGCCACAGACCAAGAGCC 908
||||| ||||| ||||| ||||| |||||

Db 1 AGTGGGTTCCACAGACCAATAGCC 24

RESULT 142

US-10-719-900-266991/c

; Sequence 266991, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 266991

; LENGTH: 25


```
; ORGANISM: Mus musculus
US-10-719-900-767443

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      121 ACTGACTTTTCTTATGCTGGGATG 144
      ||||| ||||| ||||| ||||| |||||
Db       2 ACTGACTTTCCTTGTACTGGGCTG 25

RESULT 148
US-10-719-900-878694
; Sequence 878694, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 878694
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-878694

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      295 TGGAAATGTTGTTTCTGCCTTTGG 318
      ||||| ||||| ||||| ||||| |||||
Db       1 TGGAAATGCTGTTTCTCCGTGIG 24

RESULT 149
US-10-719-900-884508
; Sequence 884508, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 884508
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-884508

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1068 TGGCTAAACCACTTAACCTCTCTG 1091
      ||||| ||||| ||||| ||||| |||||
Db       1 TGGCCAAATCACTTACCTCCCTG 24

RESULT 150
US-10-719-900-899808/c
; Sequence 899808, Application US/10719900
```

```
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 899808
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-899808

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      588 ATGTTCACTTTAAGAAAGACTTCA 611
      ||||| ||||| ||||| ||||| |||||
Db       24 ATGTGCACTCTAAGAAACACTACA 1

RESULT 151
US-10-809-189-20048/c
; Sequence 20048, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-20048

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      957 TCTGGACCCAGGACATTTTGATGA 980
      ||||| ||||| ||||| ||||| |||||
Db       25 TCTTGACCCCAAGACACTTTGGTGA 2

RESULT 152
US-10-956-157-97212/c
; Sequence 97212, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
```

```

; SOFTWARE: PatentIn version 3.2.2
; SEQ ID NO 97212
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-97212

```

```
Query Match      1.6%   Score 17.6;  DB 1;  Length 25;
Best Local Similarity 83.3%   Pred. No. 1.7e+02;
Matches 20;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;
```

Qy 922 GAGCCTTATTAGAAATGCAGAATC 945
 ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 GAAACTTGTTAGAAATGCAGATC 1

RESULT 153
US-10-956-157-97218/c
; Sequence 97218, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

```

Query Match      1.6%;   Score 17.6;   DB 1;   Length 25;
Best Local Similarity 83.3%;   Pred. No. 1.7e+02;
Matches 20;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

```

Qy 919 CTAGAGCCTTATTAGAAATGCAGA 942
||| ||| ||| ||| ||| ||| |||
Db 25 CTGGAAACTTGTTAGAAATGCAGA 2

RESULT 154
US-10-956-157-155162
; Sequence 155162, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy

620 AGATGAGT~~TTTATTCTCAGCAAA~~TTCAGCAAAT 643

| | | | | | | | | | | | | |

Dd

1 AAATCAGC~~TTTATTCTTAAGCAA~~AAT 24

RESULT 155
US-10-956-157-316449
; Sequence 316449, Application US/10956157
; Publication NO. US20050118625A1
; GENERAL INFORMATION:

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 591 TTCACCTTTTAAGAAAGACTTCATAA 614

Db 1 TTCTCTTTTCTGAATGACTTCATAA 24

RESULT 156
US-10-843-527-8674
; Sequence 8674, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:

```
Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20: Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 920 TAGAGCCTTATTAGAAATGCAGAA 943
||| ||| ||| ||| ||| ||| ||| |||
Dp 2 TAAAGACTTGTTAGTAATGCAGAA 25

RESULT 157
US-10-843-527-105776/c
; Sequence 105776, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:

```

; APPLICANT: ERIC SHELLE
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08

```

FILE REFERENCE: 2004-05-10
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08


```
US-10-681-773-103264/c
; Sequence 103264, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 103264
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-103264

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1000 CACATGAAAGTTTGAGAGCATCA 1023
      ||| ||| ||| ||| ||| ||| ||| |||
Db      24 CACTTAAAACTTTGAGAGCTTCA 1

RESULT 163
US-10-719-956-48483
; Sequence 48483, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48483
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-48483

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      229 AAGAGTCACCTATGACTCAGATGC 252
      ||| ||| ||| ||| ||| ||| |||
Db      1 AAGGGTCACCTAAGACTCGGACGC 24

RESULT 164
US-10-719-956-276484
; Sequence 276484, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
```

```
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 276484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-276484

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      137 CTGGGATGTCCTTAGAGGATTAT 160
      ||| ||| ||| ||| ||| ||| |||
Db      1 CTGTGATGTGCTTAGAGGGTTCT 24

RESULT 165
US-10-719-956-357405/c
; Sequence 357405, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 357405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-357405

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      975 TGATGAGATCCAAAGGAGTTGTAT 998
      ||| ||| ||| ||| ||| ||| |||
Db      25 TGATGAGGTCCAAACGAGTGTAT 2

RESULT 166
US-10-719-956-649616/c
; Sequence 649616, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 649616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-649616

Query Match      1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      446 TTTAGCTGGGAGCAGTGCTAGCAC 469
      ||| ||| ||| ||| ||| ||| |||
```


Fri Aug 19 11:00:02 2005

Db 25 TTTAGCTGACAGCAAAAGGTAGCAC 2

RESULT 167

US-10-719-956-685651/c

; Sequence 685651, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 685651

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-685651

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 874 ATGCTATTAAAGTGTGGCCACA 897

Db 25 ATGCTGATAACAGTGTGGTCCACA 2

RESULT 168

US-10-231-778-208/c

; Sequence 208, Application US/10231778

; Publication No. US20030126647A1

; GENERAL INFORMATION:

; APPLICANT: Bilodeau, Pierre

; APPLICANT: Chaudhury, Abdul M.

; APPLICANT: Dennis, Elizabeth S.

; APPLICANT: Koltunow, Anna M.G.

; APPLICANT: Luo, Ming

; APPLICANT: Peacock, William J.

; TITLE OF INVENTION: Method for inducing seed development by down-regulating

; TITLE OF INVENTION: expression of the FIS2 gene

; FILE REFERENCE: 72-98A

; CURRENT APPLICATION NUMBER: US/10/231,778

; CURRENT FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: 09/398,237

; PRIOR FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: 60/101,184

; PRIOR FILING DATE: 1998-09-21

; PRIOR APPLICATION NUMBER: AU PP6061

; PRIOR FILING DATE: 1998-09-22

; PRIOR APPLICATION NUMBER: AU PP6062

; PRIOR FILING DATE: 1998-09-22

; PRIOR APPLICATION NUMBER: AU PP6063

; PRIOR FILING DATE: 1998-09-22

; PRIOR APPLICATION NUMBER: AU PQ1345

; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: AU PQ1346

; PRIOR FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 208

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Oligonucleotide primer

US-10-231-778-208

Query Match 1.5%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 1.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 606 ACTTCATAAGTAGGAGATGA 625

Db 20 ACTTCATAAGGAAGAGATGA 1

RESULT 169

US-09-911-088-1

; Sequence 1, Application US/09911088

; Patent No. US20020123145A1

; GENERAL INFORMATION:

; APPLICANT: OW, DAVID

; TITLE OF INVENTION: METHODS FOR THE REPLACEMENT, TRANSLOCATION, AND

; TITLE OF INVENTION: STACKING OF DNA IN EUKARYOTIC GENOMES

; FILE REFERENCE: 16313-0052

; CURRENT APPLICATION NUMBER: US/09/911,088

; CURRENT FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: 60/220,062

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-911-088-1

Query Match 1.5%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTGTTCTGCC 313

Db 5 CTGAAATTGTTGCTTCTGCC 24

RESULT 170

US-10-913-085-1

; Sequence 1, Application US/10913085

; Publication No. US20050009182A1

; GENERAL INFORMATION:

; APPLICANT: OW, DAVID

; TITLE OF INVENTION: METHODS FOR THE REPLACEMENT, TRANSLOCATION, AND

; TITLE OF INVENTION: STACKING OF DNA IN EUKARYOTIC GENOMES

; FILE REFERENCE: 16313-0052

; CURRENT APPLICATION NUMBER: US/10/913,085

; CURRENT FILING DATE: 2004-08-06

; PRIOR APPLICATION NUMBER: US/09/911,088

; PRIOR FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: 60/220,062

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-913-085-1

Query Match 1.5%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTGTTCTGCC 313

Db 5 CTGAAATTGTTGCTTCTGCC 24

```

; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TGR342Right PCR
; OTHER INFORMATION: expression profiling primer
US-09-990-940-23

Query Match      1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      117 TTGGACTGACTTTTCTTATGC 137
      ||||| || ||||| ||||| ||
Db      22 TTGGAATGCCCTTTCTTATTC 2

RESULT 174
US-10-681-199-23
; Sequence 23, Application US/10681199
; Publication No. US20040138441A1
; GENERAL INFORMATION:
; APPLICANT: KERE, Juha
; TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLLEXIA
; FILE REFERENCE: 0933-0214P
; CURRENT APPLICATION NUMBER: US/10/681,199
; CURRENT FILING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER EKN1-1R
US-10-681-199-23

Query Match      1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1000 CACATGAAAGTTTGAGAAGCA 1020
      ||||| ||||| ||||| ||
Db      1 CACACCAAAGTTTGAGAACCA 21

RESULT 175
US-10-913-280-633/c
; Sequence 633, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
```

```

; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TGR342Right PCR
; OTHER INFORMATION: expression profiling primer
US-09-990-940-23

Query Match      1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      117 TTGGACTGACTTTTCTTATGC 137
      ||||| || ||||| ||||| ||
Db      22 TTGGAATGCCCTTTCTTATTC 2

RESULT 174
US-10-681-199-23
; Sequence 23, Application US/10681199
; Publication No. US20040138441A1
; GENERAL INFORMATION:
; APPLICANT: KERE, Juha
; TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLLEXIA
; FILE REFERENCE: 0933-0214P
; CURRENT APPLICATION NUMBER: US/10/681,199
; CURRENT FILING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER EKN1-1R
US-10-681-199-23

Query Match      1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1000 CACATGAAAGTTTGAGAAGCA 1020
      ||||| ||||| ||||| ||
Db      1 CACACCAAAGTTTGAGAACCA 21

RESULT 175
US-10-913-280-633/c
; Sequence 633, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
```

; APPLICANT: Ginns, Edward I.
; APPLICANT: Galdzicka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 07917-238001
; CURRENT APPLICATION NUMBER: US/10/913,280
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-913-280-633

Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 91 CGTGGCATTATCCTTCAGTGG 111
Db 21 CGTGGCCTTCTCCCTCAGTGG 1

RESULT 176
US-11-038-360-23/c
; Sequence 23, Application US/11038360
; Publication No. US20050170397A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Novel Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/11/038,360
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/09/990,940
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TGR342Right PCR
; OTHER INFORMATION: expression profiling primer
US-11-038-360-23

Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 117 TTGACTGACCTTTTCTTATGC 137
Db 22 TTGGAATGCCTTTTCTTATTC 2

RESULT 177
US-10-774-721-45/c
; Sequence 45, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRAV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-45

Query Match 1.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 CTTGCTCGTGTGGCTG 347
Db 16 CTTGCTCGTGTGGCTG 1

RESULT 178
US-10-339-793-47
; Sequence 47, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-47

Query Match 1.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 981 GATCCAAAGGAGTTGT 996
Db 1 GATCCAAAGGAGTTGT 16

RESULT 179

US-10-159-339-21
; Sequence 21, Application US/10159339
; Publication No. US20030166540A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
; TITLE OF INVENTION: HGPRTMY30
; FILE REFERENCE: D0169NP
; CURRENT APPLICATION NUMBER: US/10/159,339
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,411
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-339-21

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107
|||||
Db 5 GGTGTTACCTGCTCAT 20

RESULT 180
US-10-280-183A-284/c
; Sequence 284, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn ver. 3.1
; SEQ ID NO 284
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-183A-284

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107
|||||
Db 16 GGTGTTACCTGCTCAT 1

RESULT 181
US-10-280-183A-286/c
; Sequence 286, Application US/10280183A
; Publication No. US20040081964A1

; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn ver. 3.1
; SEQ ID NO 286
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-183A-286

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107
|||||
Db 16 GGTGTTACCTGCTCAT 1

RESULT 182
US-10-923-516-391
; Sequence 391, Application US/10923516
; Publication No. US20050176025A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of B-Cell CLL/Lymphoma-2
; TITLE OF INVENTION: (BCL2) Gene Expression Using Short Interfering Nucleic Acid (siN
; FILE REFERENCE: 400/173 (MBHB02-714-F)
; CURRENT APPLICATION NUMBER: US/10/923,516
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US 03/04908
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/396,905
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 882
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 391


```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-48

Query Match      1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      783 TTGGGGATGTGCTTGGAGA 801
Db      1 TTGTAGATGTGCTTGGAGA 19

RESULT 187
US-10-655-847-196/c
; Sequence 196, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/655,847
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US/10/160,807
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 196
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-655-847-196

Query Match      1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      783 TTGGGGATGTGCTTGGAGA 801
Db      20 TTGTAGATGTGCTTGGAGA 2

RESULT 188
US-09-816-814-7/c
; Sequence 7, Application US/09816814
; Publication No. US20030027136A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-816-814-7

Query Match      1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      38 GCCGGAAGCAGCCGCGGCC 56
Db      21 GCTGGAAGCAGCCGCGGCC 3
```

```

RESULT 189
US-10-786-720-15221/c
; Sequence 15221, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15221
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-786-720-15221

Query Match      1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      932 AGAATGCAGATCTGAAG 950
Db      20 AGACATGCAGATCTCAAG 2

RESULT 190
US-10-751-736-45418/c
; Sequence 45418, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45418
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-45418

Query Match      1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      283 TTTCTTCACTACTGGAATT 301
Db      20 TTTCTTCACTACTGGAATT 2

RESULT 191
US-10-032-585-4031/c
; Sequence 4031, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
```

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; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4031
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4031

Query Match      1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAA 355
Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 192
US-10-882-104-382/c
; Sequence 382, Application US/10882104
; Publication No. US20050079619A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Targets Discovery
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/10/882,104
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: US/09/792,024
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer
US-10-882-104-382

Query Match      1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAA 355
Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 193
US-10-035-978A-29
; Sequence 29, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
; TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; FILE REFERENCE: INNOG2.001C1
; CURRENT APPLICATION NUMBER: US/10/035,978A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/284,725
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: EP 97870133.2
```

```
; PRIOR FILING DATE: 1997-09-09
; PRIOR APPLICATION NUMBER: EP 96870131.8
; PRIOR FILING DATE: 1996-10-16
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P4S1 vacA-derived probe
US-10-035-978A-29

Query Match      1.4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 103 CTTCACTGGGGCTATTGG 120
Db 2 CTTTAGTRGGGYTATTGG 19

RESULT 194
US-10-263-594-29
; Sequence 29, Application US/10263594
; Publication No. US20030175746A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: Probes, methods and kits for detection and
; typing of Helicobacter pylori nucleic acids in biological
; samples.
; NUMBER OF SEQUENCES: 280
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/263,594
; FILING DATE: 02-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,725
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP96/870131.8
; FILING DATE: 16-OCT-1996
; APPLICATION NUMBER: PCT/EP97/05614
; FILING DATE: 10-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: INNOG2.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 760-0404
; TELEFAX: (949) 760-9395
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-263-594-29
```

```

Query Match      1.4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      103 CTTCAGTGGGGCTATTGG 120
Db      2 CTTTAGTRGGGYTATTGG 19

RESULT 195
US-10-795-667-93
; Sequence 93, Application US/10795667
; Publication No. US20040209298A1
; GENERAL INFORMATION:
; APPLICANT: KAMBEROV, EMMANUEL
; APPLICANT: SUN, TONG
; APPLICANT: BRUENING, ERIC EGON
; APPLICANT: PINTER, JONATHON H.
; APPLICANT: SLEPTSOVA, IRINA
; APPLICANT: KURIHARA, TAKAO
; APPLICANT: MAKAROV, VLADIMIR L.
; TITLE OF INVENTION: AMPLIFICATION AND ANALYSIS OF WHOLE GENOME AND WHOLE
; TITLE OF INVENTION: TRANSCRIPTOME LIBRARIES GENERATED BY A DNA
; TITLE OF INVENTION: POLYMERIZATION PROCESS
; FILE REFERENCE: RUBC:022US
; CURRENT APPLICATION NUMBER: US/10/795,667
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/453,060
; PRIOR FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-795-667-93

Query Match      1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      297 GAATTGTTGTTCTGCCTTTGG 318
Db      1 GAATTGTTGTTCTGCTTTGG 22

RESULT 196
US-10-797-333A-95
; Sequence 95, Application US/10797333A
; Publication No. US20040209299A1
; GENERAL INFORMATION:
; APPLICANT: PINTER, JONATHON H.
; APPLICANT: KURIHARA, TAKAO
; APPLICANT: SLEPTSOVA, IRINA
; APPLICANT: BRUENING, ERIC EGON
; APPLICANT: ZIEHLER, WILLIAM
; APPLICANT: MAKAROV, VLADIMIR L.
; TITLE OF INVENTION: IN VITRO DNA IMMORTALIZATION AND WHOLE GENOME
; TITLE OF INVENTION: AMPLIFICATION USING LIBRARIES GENERATED FROM RANDOMLY
; TITLE OF INVENTION: FRAGMENTED DNA
; FILE REFERENCE: RUBC:021US
; CURRENT APPLICATION NUMBER: US/10/797,333A
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/453,071
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 22
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-797-333A-95

Query Match      1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      297 GAATTGTTGTTCTGCCTTTGG 318
Db      1 GAATTGTTGTTCTGCTTTGG 22

RESULT 197
US-10-349-143-11660
; Sequence 11660, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11660
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-21246 for SEQ 3795, in complen
US-10-349-143-11660

Query Match      1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      104 TTCAGTGGGGCTATTGG 120
Db      2 TTCAATGGGGCTATTGG 18

RESULT 198
US-10-281-479A-9
; Sequence 9, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THEN
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
```


Fri Aug 19 11:00:02 2005

; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-9

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
| | | | | | | | | | | | | | | |
Db 3 GTTGTATGCACATGAGA 19

RESULT 199
US-10-275-180A-9
; Sequence 9, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
; FILE REFERENCE: 21085.0029U5
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-9

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
| | | | | | | | | | | | | | | |
Db 3 GTTGTATGCACATGAGA 19

RESULT 200
US-10-286-132A-9
; Sequence 9, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.

; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-9

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 GTTGTATGCACATGAAA 1008
| | | | | | | | | | | | | | | |
Db 3 GTTGTATGCACATGAGA 19

RESULT 201
US-10-688-706-2397
; Sequence 2397, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2397
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2397

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 553 TTAATATGCTGGGTTTT 569
| | | | | | | | | | | | | | | |
Db 4 TTAATAAGCTGGGTTTT 20

RESULT 202
US-10-688-706-2465
; Sequence 2465, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706

```
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2465
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2465

Query Match      1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      553 TTAATATGCTGGGTTT 569
Db      1 TTAATAAGCTGGGTTT 17

RESULT 205
US-09-817-913-33
; Sequence 33, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-33

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACCTTATGC 762
Db      1 AGCCAGCTGCCACTTGATGC 20

RESULT 206
US-09-817-538-33
; Sequence 33, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-33

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACCTTATGC 762
Db      1 AGCCAGCTGCCACTTGATGC 20

; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2465
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2465

Query Match      1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      553 TTAATATGCTGGGTTT 569
Db      2 TTAATAAGCTGGGTTT 18

RESULT 203
US-10-688-706-2492
; Sequence 2492, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2492
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2492

Query Match      1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      553 TTAATATGCTGGGTTT 569
Db      3 TTAATAAGCTGGGTTT 19

RESULT 204
US-10-688-706-2639
; Sequence 2639, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2639
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
```


Fri Aug 19 11:00:02 2005

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
;
US-10-210-429-95

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      801 AGGCAGATAACGCTGAAGCA 820
      ||||| ||||| ||||| |||||
Db      1 AGGCAGAAAACCCCTGAAGGA 20

RESULT 216
US-10-189-818B-30
; Sequence 30, Application US/10189818B
; Publication No. US20040072770A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
;
US-10-189-818B-30

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      743 AGGCAGCTGCCACCTTATGC 762
      || ||||| ||||| |||||
Db      1 AGCCAGCTGCCACTTGAUGC 20

RESULT 217
US-10-673-886A-9/c
; Sequence 9, Application US/10673886A
; Publication No. US20040132139A1
; GENERAL INFORMATION:
; APPLICANT: GENODYSSEE
; TITLE OF INVENTION: New Polynucleotides and Polypeptides of the IFNalpha-21 Gene
; FILE REFERENCE: BIF022965 PCT
; CURRENT APPLICATION NUMBER: US/10/673,886A
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: FR 0 104 404
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-673-886A-9

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
```

```

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      608 TTCATAAGTAGGAGATGAGT 627
      ||| ||||| ||||| |||||
Db      20 TTCCCAAGTAGCAGATGAGT 1

RESULT 218
US-10-870-587-33
; Sequence 33, Application US/10870587
; Publication No. US20040266718A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/10/870,587
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US/09/817,913
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
;
US-10-870-587-33

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      743 AGGCAGCTGCCACCTTATGC 762
      || ||||| ||||| |||||
Db      1 AGCCAGCTGCCACTTGATGC 20

RESULT 219
US-10-913-280-249/c
; Sequence 249, Application US/10913280
; Publication No. US2005008984A1
; GENERAL INFORMATION:
; APPLICANT: Ginns, Edward I.
; APPLICANT: Galdzicka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 07917-238001
; CURRENT APPLICATION NUMBER: US/10/913,280
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
;
US-10-913-280-249

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      92 GTGGCATTATCCTTCAGTGG 111
      ||||| ||||| ||||| |||||
Db      20 GTGGCCTTCTCCCTCAGTGG 1
```

```
RESULT 220
US-10-498-505A-18
; Sequence 18, Application US/10498505A
; Publication No. US20050090642A1
; GENERAL INFORMATION:
; APPLICANT: MIYAWAKI, Atsushi
; APPLICANT: KARASAWA, Satoshi
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: P25481
; CURRENT APPLICATION NUMBER: US/10/498,505A
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/JP02/13363
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-498-505A-18

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      497 TCTTAGAACTCATCTATCT 516
      ||||| ||||| ||||| |||||
Db      1 TCTTCGAACTCAAACTTTCT 20

RESULT 221
US-10-831-901A-14585
; Sequence 14585, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14585
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14586

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1004 TGAAGTTTGAGAGCATCA 1023
      ||| ||||| ||||| |||||
Db      1 TGACAGTTTGAAAAGCAACA 20

RESULT 222
US-10-831-901A-14586
; Sequence 14586, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14586
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14586

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1004 TGAAGTTTGAGAGCATCA 1023
      ||| ||||| ||||| |||||
Db      1 TGACAGTTTGAAAAGCAACA 20

RESULT 223
US-10-831-901A-15629
; Sequence 15629, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
```

Fri Aug 19 11:00:02 2005

```
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15629
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15629
```

```
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1016 AAGCATCATCATAGAGAAAGT 1035
||| ||||| ||||| |||||
Db 1 AAGAATCATCATGGAGAAAT 20
```

```
RESULT 224
US-10-831-901A-26184/c
; Sequence 26184, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
```

```
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26184
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26184
```

```
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 318 GATTCCTGTTATTCTTGCT 337
||||| ||||| ||||| |||||
Db 20 GCTTCGGTGTATTCTTGCT 1
```

```
RESULT 225
US-10-831-901A-26186/c
; Sequence 26186, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26186
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26186
```

```
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 320 TTTCCTGTTATTCTTGCTCG 339
||||| ||||| ||||| |||||
Db 20 TTTCGTGGTATTCTTGCTAG 1
```

```
RESULT 226
US-10-831-901A-26187/c
; Sequence 26187, Application US/10831901A
```

```
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26187

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.le+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      321 TTCCTGTTATTCTTGCTCGT 340
      ||| ||| ||| ||| ||| ||| |||
Db      20 TTCGTGGTATTCTTGCTAGT 1

RESULT 227
US-10-831-901A-26489/c
; Sequence 26489, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26187
```

```
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26489
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26489

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.le+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      658 TAGATTATGTTACTCAAATT 677
      ||| ||| ||| ||| ||| ||| |||
Db      20 TGGATTATGTTACTACAATT 1

RESULT 228
US-10-257-158A-4773/c
; Sequence 4773, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Zirvi, Monib
; APPLICANT: Gerry, Norman P.
; APPLICANT: Favis, Reyna
; APPLICANT: Kliman, Richard
; TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC AC
; TITLE OF INVENTION: SEQUENCE DIFFERENCES USING LIGASE DETECTION REACTION
; FILE REFERENCE: 19603/2834
; CURRENT APPLICATION NUMBER: US/10/257,158A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/US01/10958
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/197,271
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 9544
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4773
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
; US-10-257-158A-4773

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.le+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      767 CATCGAAACCTTTTGCTTGG 786
      ||| ||| ||| ||| ||| ||| |||
Db      20 CATCGACACCGTTTGCTTCG 1

RESULT 229
US-10-786-720-7299
; Sequence 7299, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
```


; Sequence 632, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Gimms, Edward I.
; APPLICANT: Galdzicka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 07917-238001
; CURRENT APPLICATION NUMBER: US/10/913,280
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 632
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-913-280-632

Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 92 GTGGCATTATCCTTCAGTGG 111
Db 20 GTGGCCTTCTCCCTCAGTGG 1

RESULT 235
US-10-847-918-8793
; Sequence 8793, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8793
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-8793

Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 462 GGTAGCACTTTATTCTGATT 481
Db 2 GGCUGCACUUUAUCCUGAUU 21

RESULT 236
US-10-210-838-82/c
; Sequence 82, Application US/10210838
; Publication No. US20040023905A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Sanjay Bhanot

; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF LAR EXPRESSION
; FILE REFERENCE: PTS-0013
; CURRENT APPLICATION NUMBER: US/10/210,838
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-838-82

Query Match 1.3%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1079 CTTAACCTCTCTGGG 1093
Db 20 CTTAACCTCTCTGGG 6

RESULT 237
US-10-751-736-26321
; Sequence 26321, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26321
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-26321

Query Match 1.3%; Score 15; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 342 TGGCTGTGATCAAT 356
Db 6 UGGCUGUGAUCAAU 20

RESULT 238
US-09-749-709-6
; Sequence 6, Application US/09749709
; Publication No. US20010032340A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHENGYU
; APPLICANT: COSTANTINI, FRANKLIN
; APPLICANT: WANG, JIN
; TITLE OF INVENTION: CONTROLLING OFFSPRING'S SEX RATIO BY TARGETING
; TITLE OF INVENTION: TRANSGENES ONTO THE SEX CHROMOSOMES
; FILE REFERENCE: 19412-1773
; CURRENT APPLICATION NUMBER: US/09/749,709
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,096
; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 8

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-749-709-6

Query Match          1.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 934 AAATGCAGAAATCTGAAGC 951
Db 1 AAATGCACAATCTAAAGC 18

RESULT 239
US-09-734-847A-16
; Sequence 16, Application US/09734847A
; Patent No. US20020049173A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Monia, Brett P.
; APPLICANT: Freir, Susan
; APPLICANT: McKay, Robert
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation of mRNA
; FILE REFERENCE: ISPH-0524
; CURRENT APPLICATION NUMBER: US/09/734,847A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-734-847A-16

Query Match          1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 240
US-09-800-629A-152
; Sequence 152, Application US/09800629A
; Patent No. US20020128216A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G.
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/09/800,629A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/07318
; PRIOR FILING DATE: 2000-03-17
```

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; PRIOR APPLICATION NUMBER: 09/280,799
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-800-629A-152

Query Match          1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 241
US-09-858-152A-9/c
; Sequence 9, Application US/09858152A
; Publication No. US20030044419A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: Marchetti, Antonio
; APPLICANT: Buttitta, Fiamma
; APPLICANT: Smith, Gilbert H.
; APPLICANT: Callahan, Robert
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6
; FILE REFERENCE: 4239-59122
; CURRENT APPLICATION NUMBER: US/09/858,152A
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-858-152A-9

Query Match          1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 CTTATTAGAAATGCAGAA 943
Db 20 CTAAATTAATAATGCAGAA 3

RESULT 242
US-10-002-974-52/c
; Sequence 52, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
```

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-002-974-52

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. NO. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      784 TGGGATGTGCTTGGAGA 801
      |||||
Db      18 TGGGATGTGGTTGAAGA 1

RESULT 243
US-10-012-984-68/c
; Sequence 68, Application US/10012984
; Publication No. US20030118561A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
; FILE REFERENCE: RTS-0334
; CURRENT APPLICATION NUMBER: US/10/012,984
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-012-984-68

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. NO. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      418 TTTCCTTATATTGGAAG 435
      |||||
Db      18 TTGCCTTATATTGGAAG 1

RESULT 244
US-10-444-206-314/c
; Sequence 314, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: Modulation of the Expression of B7 Protein
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 314
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

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US-10-317-478-40/c
; Sequence 40, Application US/10317478
; Publication No. US20040115636A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF INTERLEUKIN 18 EXPRESSION
; FILE REFERENCE: PTS-0025
; CURRENT APPLICATION NUMBER: US/10/317,478
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-478-40
Query Match      1.3%;   Score 14.8;   DB 1;   Length 20;
Best Local Similarity 88.9%;   Pred. No. 2.4e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      748 GCTGCCACCTTATGCAGT 765
Db      20 GCTGCCACCTGCTGCAGT 3

RESULT 248
US-10-317-478-96
; Sequence 96, Application US/10317478
; Publication No. US20040115636A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF INTERLEUKIN 18 EXPRESSION
; FILE REFERENCE: PTS-0025
; CURRENT APPLICATION NUMBER: US/10/317,478
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-317-478-96
Query Match      1.3%;   Score 14.8;   DB 1;   Length 20;
Best Local Similarity 88.9%;   Pred. No. 2.4e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      748 GCTGCCACCTTATGCAGT 765
Db      1 GCTGCCACCTGCTGCAGT 18

RESULT 249
US-10-679-532-152
; Sequence 152, Application US/10679532
; Publication No. US20040121376A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/10/679,532
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/800,629A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/07318
; 
```

```
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/280,799
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-679-532-152
Query Match      1.3%;   Score 14.8;   DB 1;   Length 20;
Best Local Similarity 88.9%;   Pred. No. 2.4e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      1050 ACTTCCTTATCTTTCCAG 1067
Db      2 ACTTCCTTACCTTTCCTG 19

RESULT 250
US-10-783-415-9/c
; Sequence 9, Application US/10783415
; Publication No. US20040141918A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Marchetti, Antonio
; APPLICANT: Buttitta, Fiamma
; APPLICANT: Smith, Gilbert H.
; APPLICANT: Callahan, Robert
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6
; FILE REFERENCE: 4239-59122
; CURRENT APPLICATION NUMBER: US/10/783,415
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 09/858,152
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-10-783-415-9
Query Match      1.3%;   Score 14.8;   DB 1;   Length 20;
Best Local Similarity 88.9%;   Pred. No. 2.4e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      926 CTTATTAGAAATGCAGAA 943
Db      20 CTAATTAAATGCAGAA 3

RESULT 251
US-10-619-739-1118
; Sequence 1118, Application US/10619739
; Publication No. US20040175719A1
; GENERAL INFORMATION:
; APPLICANT: Christians, Frederick C.
; TITLE OF INVENTION: Synthetic Tag Genes
; FILE REFERENCE: 3502.1
; CURRENT APPLICATION NUMBER: US/10/619,739
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,530
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 2068
; SOFTWARE: FastSEQ for Windows Version 4.0
; 
```

; SEQ ID NO 1118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-739-1118

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 697 TCATGTCAGTCACGGTGCT 714
Db 2 TCATGTCAGTCACAGTGCT 19

RESULT 252
US-10-659-473-47
; Sequence 47, Application US/10659473
; Publication No. US20040197906A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA REGULATORY SUBUNIT RII BETA EXPRESSION
; FILE REFERENCE: RTS-0218
; CURRENT APPLICATION NUMBER: US/10/659,473
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/915,485A
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-659-473-47

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 663 TATGTTACTCAAATTATG 680
Db 3 TATGTTACTGACATTATG 20

RESULT 253
US-10-641-962-314/c
; Sequence 314, Application US/10641962
; Publication No. US20040235164A1
; GENERAL INFORMATION:
; APPLICANT: Bennett et al.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: 30566/39578
; CURRENT APPLICATION NUMBER: US/10/641,962
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 314
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-641-962-314

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 AAATAGACCTGTCAATT 657
Db 20 AAATAGACCTCTCAATT 3

RESULT 254
US-10-773-678-222/c
; Sequence 222, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karrias, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 222
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-222

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 548 GAAATTTAATATGCTGGG 565
Db 18 GAAATTTAATATGCTGGG 1

RESULT 255
US-10-831-901A-15630
; Sequence 15630, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10

Fri Aug 19 11:00:02 2005

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; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15630
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15630

Query Match          1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1016 AAGCATCATCATAGAGAA 1033
Db      2 AAGAATCATCATGGAGAA 19

RESULT 256
US-10-831-901A-15631
; Sequence 15631, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15631
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15631

Query Match          1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1016 AAGCATCATCATAGAGAA 1033
Db      3 AAGAATCATCATGGAGAA 20

RESULT 257
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US-10-831-901A-25596
; Sequence 25596, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25596
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-25596

Query Match          1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      718 AGAAAAATATATTAAACGCA 735
Db      1 AGAAAAATATATCAAGGCA 18

RESULT 258
US-10-831-901A-25597
; Sequence 25597, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15631
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15631
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; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25597
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-25597

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 718 AGAAATATATTAAACGCA 735
Db 2 AGAAATATATCAAGGCA 19

RESULT 259
US-10-831-901A-25598
; Sequence 25598, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25598
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-25598

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 718 AGAAATATATTAAACGCA 735
Db 3 AGAAATATATCAAGGCA 20

RESULT 260
US-10-831-901A-26089/c
; Sequence 26089, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26089
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26089

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 993 TTGTATGCACATGAAAGT 1010
Db 18 TTGTAAGCACACAGAAAGT 1

RESULT 261
US-10-831-901A-26090/c
; Sequence 26090, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

Fri Aug 19 11:00:02 2005

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;
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26090
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26090

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 TTGTATGCACATGAAAGT 1010
Db 19 TTGTAAGCACACAAGAAAGT 2

RESULT 262
US-10-831-901A-26091/c
; Sequence 26091, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
;
```

```
;
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26091

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 TTGTATGCACATGAAAGT 1010
Db 20 TTGTAAGCACACAAGAAAGT 3

RESULT 263
US-10-831-901A-26185/c
; Sequence 26185, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
; US-10-831-901A-26185
```

```
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 320 TTTCTCTGTTATTCTTGCT 337
Db 19 TTTCGTGGTATTCTTGCT 2

RESULT 264
US-10-831-901A-26490/c
; Sequence 26490, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
```

```
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26490
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26490

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      660 GATTATGTTACTCAAATT 677
      |||||
Db      19 GATTATGTTACTACAATT 2

RESULT 265
US-10-831-901A-26491/c
; Sequence 26491, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
```

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; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26491
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26491

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      660 GATTATGTTACTCAAATT 677
      |||||
Db      20 GATTATGTTACTACAATT 3

RESULT 266
US-10-956-373-29
; Sequence 29, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ErbB-2 POLYPEPTIDES AND KITS AND
; TITLE OF INVENTION: METHODS USING SAME
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-956-373-29

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      359 GGAGCCTGGCGCCTTG 376
      |||||
Db      3 GGAGCTGGCGCCTTG 20

RESULT 267
US-10-627-253A-299
; Sequence 299, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS.
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
```

Fri Aug 19 11:00:02 2005

; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-299

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
||| ||| ||| ||| ||| ||| |||
Db 4 AATCACTCAACCTCTCTG 21

RESULT 268
US-10-627-253A-300/c
; Sequence 300, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 300
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-300

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
||| ||| ||| ||| ||| ||| |||
Db 18 AATCACTCAACCTCTCTG 1

RESULT 269
US-10-627-253A-301
; Sequence 301, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24

; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-301

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
||| ||| ||| ||| ||| ||| |||
Db 4 AATCACTMAACCTCTCTG 21

RESULT 270
US-10-627-253A-302/c
; Sequence 302, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 302
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-302

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
||| ||| ||| ||| ||| ||| |||
Db 18 AATCACTMAACCTCTCTG 1

RESULT 271
US-10-627-253A-303
; Sequence 303, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A

```

; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 303
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-303

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1074 AACCACTTAACCTCTCTG 1091
      || ||| ||| ||| ||| ||| ||| |||
Db      4 AATCACTAAACCTCTCTG 21

RESULT 272
US-10-627-253A-304/c
; Sequence 304, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
; APPLICANT: BRINKMANN, ULRICH
; APPLICANT: HOFFMEYER, SVEN
; APPLICANT: MORNHINWEG, ESTHER
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
; TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
; FILE REFERENCE: VOS-42 CON
; CURRENT APPLICATION NUMBER: US/10/627,253A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/EP02/00796
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP 01101651.6
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 304
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-10-627-253A-304

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1074 AACCACTTAACCTCTCTG 1091
      || ||| ||| ||| ||| ||| ||| |||
Db      18 AATCACTAAACCTCTCTG 1

RESULT 273
US-10-786-720-15220/c
; Sequence 15220, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
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; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15220
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-720-15220

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      933 GAAATGCAGAAATCTGAAG 950
      || ||| ||| ||| ||| ||| ||| |||
Db      21 GACATGCAGAAATCTCAAG 4

RESULT 274
US-10-786-720-15222
; Sequence 15222, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15222
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-786-720-15222

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 72.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      933 GAAATGCAGAAATCTGAAG 950
      || ||| ||| ||| ||| ||| ||| |||
Db      1 GACAUGCAGAAUCUCAAG 18

RESULT 275
US-10-751-736-29451
; Sequence 29451, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29451
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-29451

Query Match      1.3%; Score 14.8; DB 1; Length 21;
```



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Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 8; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 495 TTCTTAGAACTCATACT 512
Db 1 UUUCUUAGAUCUCUUACU 18

RESULT 276
US-10-751-736-31083/c
; Sequence 31083, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31083
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-31083

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 597 TTAAGAAAGACTTCATAA 614
Db 18 TCAAGAAAGACGTCATAA 1

RESULT 277
US-10-751-736-45419/c
; Sequence 45419, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45419
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-45419

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 283 TTCTTCACTACTGGAAT 300
Db 18 TTCTTCAACTGGAAT 1
```

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RESULT 278
US-10-484-577-293
; Sequence 293, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
; TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UG71A
; FILE REFERENCE: F2285PCT-1
; CURRENT APPLICATION NUMBER: US/10/484,577
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/08220
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: EP 01 11 7608.8
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: EP 02011710.7
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 683
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 293
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-484-577-293

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTAAACCTCTCTG 21

RESULT 279
US-10-484-577-294/c
; Sequence 294, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
; TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UG71.
; FILE REFERENCE: F2285PCT-1
; CURRENT APPLICATION NUMBER: US/10/484,577
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/08220
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: EP 01 11 7608.8
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: EP 02011710.7
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 683
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 294
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-484-577-294

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTAAACCTCTCTG 1

RESULT 280
US-10-484-577-295
; Sequence 295, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
```

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; TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGT1A
; FILE REFERENCE: F2285PCT-1
; CURRENT APPLICATION NUMBER: US/10/484,577
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/08220
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: EP 01 11 7608.8
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: EP 02011710.7
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 683
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 295
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: m=a or c
US-10-484-577-295

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1074 AACCACTTAACCTCTCTG 1091
Db      4 AATCACTMAACCTCTCTG 21

RESULT 281
US-10-484-577-296/c
; Sequence 296, Application US/10484577
; Publication No. US20050032724A1
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie Aktiengesellschaft
; TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGT1A
; FILE REFERENCE: F2285PCT-1
; CURRENT APPLICATION NUMBER: US/10/484,577
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/08220
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: EP 01 11 7608.8
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: EP 02011710.7
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 683
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 296
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: k=g or t
US-10-484-577-296

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1074 AACCACTTAACCTCTCTG 1091
Db      18 AATCACTMAACCTCTCTG 1

RESULT 282
US-10-847-918-4920
; Sequence 4920, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
```

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; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4920
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-4920

Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy      284 TTCTTCACTACTGGAATT 301
Db      4 UUCCUCACUACUGAAAUU 21

RESULT 283
US-10-451-805-6
; Sequence 6, Application US/10451805
; Publication No. US20040248099A1
; GENERAL INFORMATION:
; APPLICANT: Goppelt, Andreas
; APPLICANT: Alzheimer, Christian
; APPLICANT: Kogel, Heidi
; TITLE OF INVENTION: Use of Intermediate-Conductance
; TITLE OF INVENTION: Potassium Channels and Modulators For Diagnosing and
; TITLE OF INVENTION: Treating Diseases Having Disturbed Keratinocyte Activity
; FILE REFERENCE: 50125/080001
; CURRENT APPLICATION NUMBER: US/10/451,805
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/15317
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/277,453
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: DE 10065475.4
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-451-805-6

Query Match      1.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      265 CTGTCGGGAACCTGGCA 280
Db      1 CTGGCGGGAACCTGGCA 16

RESULT 284
US-09-866-108-2565/c
; Sequence 2565, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
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; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 948
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-948

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      569 TTTAATACCTTTATAT 584
Db      1 UUUAAUGCCUUUAU 16
      :::||: ||::|::|:

RESULT 287
US-09-930-423-478/c
; Sequence 478, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-478

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCAGCCGGCGCCCCAG 60
Db      17 GCAGCCGCAGCCCCAG 2
      ||||| |||||

RESULT 288
US-09-930-423-1012/c
; Sequence 1012, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1012

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCAGCCGGCGCCCCAG 60
Db      17 GCAGCCGCAGCCCCAG 2
      ||||| |||||

RESULT 289
US-09-745-237A-478/c
; Sequence 478, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-478

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCAGCCGGCGCCCCAG 60
Db      17 GCAGCCGCAGCCCCAG 2
      ||||| |||||

RESULT 290
US-09-745-237A-1012/c
; Sequence 1012, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1012

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCAGCCGGCGCCCCAG 60
Db      16 GCAGCCGCAGCCCCAG 1
      ||||| |||||

RESULT 291
US-10-342-902-948
; Sequence 948, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
```

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      ||||| |||||
Db      16 GCAGCCGCAGCCCCAG 1

RESULT 289
US-09-745-237A-478/c
; Sequence 478, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-478

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCAGCCGGCGCCCCAG 60
Db      17 GCAGCCGCAGCCCCAG 2
      ||||| |||||

RESULT 290
US-09-745-237A-1012/c
; Sequence 1012, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1012

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      45 GCAGCCGGCGCCCCAG 60
Db      16 GCAGCCGCAGCCCCAG 1
      ||||| |||||

RESULT 291
US-10-342-902-948
; Sequence 948, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
```


Fri Aug 19 11:00:02 2005

; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 948
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-948

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATAT 584
::||: ||::||:
Db 1 UUUAAUGCCUUUAU 16

RESULT 292

US-10-138-674-7395/c
; Sequence 7395, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7395
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7395

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCACAGAA 641
||||| |||||
Db 17 GTTTATGCTCAGAA 2

RESULT 293

US-10-287-949A-7395/c
; Sequence 7395, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7395
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7395

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCACAGAA 641
||||| |||||
Db 17 GTTTATGCTCAGAA 2

RESULT 294

US-10-669-841-948
; Sequence 948, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 948
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-948

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTAAATACCTTTATAT 584
::|||: ||::||:
Db 1 UUUUAUGCCUUUAU 16

RESULT 295
US-10-723-361-2565/c
; Sequence 2565, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2565
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2565

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
|||||||
Db 17 AGGCAGCTGCCGCCTT 2

RESULT 296
US-10-723-361-2566/c
; Sequence 2566, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2566
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2566

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
|||||||
Db 16 AGGCAGCTGCCGCCTT 1

RESULT 297
US-10-712-633-347/c
; Sequence 347, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674

```
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-347

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTTATTCTCAGCAA 641
Db      17 GTTTTATGCTCAGCAA 2

RESULT 298
US-09-969-373-2494
; Sequence 2494, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2494
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2494

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      314 TTTGGATTTCCTGTTA 329
Db      1 TTTGGCTTTCCTGTTA 16

RESULT 299
US-10-731-739-588
; Sequence 588, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/10/731,739
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-731-739-588

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TGGAATTGTTGTTTCT 310
Db      1 TGGAATTGTTGTGTCT 16

RESULT 300
US-10-477-238A-588
; Sequence 588, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
; APPLICANT: BabiJ, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-212
; CURRENT APPLICATION NUMBER: US/10/477,238A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-238A-588

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TGGAATTGTTGTTTCT 310
Db      1 TGGAATTGTTGTGTCT 16

RESULT 301
US-10-680-287A-588
; Sequence 588, Application US/10680287A
; Publication No. US20040244069A1
; GENERAL INFORMATION:
; APPLICANT: BabiJ, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
```

```
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-680-287A-588

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TGAATTGTTGTTTCT 310
Db      1 TGAATTGTTGTGCT 16

RESULT 302
US-10-477-173-588
; Sequence 588, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul
; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: US/10/477,173
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-173-588

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TGAATTGTTGTTTCT 310
Db      1 TGAATTGTTGTGCT 16

RESULT 303
US-10-834-377-588
; Sequence 588, Application US/10834377
; Publication No. US20050142617A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
```

```
; CURRENT APPLICATION NUMBER: US/10/834,377
; CURRENT FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US/09/543,771B
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-834-377-588

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      295 TGAATTGTTGTTTCT 310
Db      1 TGAATTGTTGTGCT 16

RESULT 304
US-09-854-883-297
; Sequence 297, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 297
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-297

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      343 GGCTGTGATCAAAATGG 358
Db      1 GGCTGTGATCAAAAGG 16

RESULT 305
US-09-917-963-91/c
; Sequence 91, Application US/09917963
; Publication No. US20030086912A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
; FILE REFERENCE: EXPRESSION
```



```
; FILE REFERENCE: ISPH-0591
; CURRENT APPLICATION NUMBER: US/09/917,963
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 137
; SEQ ID NO 91
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-917-963-91

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      130 TCTTATGCTGGGATGT 145
      |||||
Db      18 TCTTATGCTGGCATGT 3

RESULT 306
US-09-953-318-37
; Sequence 37, Application US/09953318
; Publication No. US20030105036A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-318-37

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTTATTCTCAGCAA 641
      |||||
Db      4 GTTTTATGCTCAGCAA 19

RESULT 307
US-10-085-906-317
; Sequence 317, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 317
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```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-317

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      721 AAATATATTAAACGCAG 736
      |||||
Db      5 AAATATATTAAACCCAG 20

RESULT 308
US-10-446-373-37
; Sequence 37, Application US/10446373
; Publication No. US20030204076A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/10/446,373
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-446-373-37

Query Match          1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTTATTCTCAGCAA 641
      |||||
Db      4 GTTTTATGCTCAGCAA 19

RESULT 309
US-10-360-510-297
; Sequence 297, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 297
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-297

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      343 GGCTGTGATCAAAATGG 358
Db      1 GGCTGTGATCAAAAGG 16

RESULT 310
US-10-349-143-6795
; Sequence 6795, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6795
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-19464 for SEQ 2861,
US-10-349-143-6795

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      218 TTCATTGCCAAAGAG 233
Db      5 TTCTTTGCCAAAGAG 20

RESULT 311
US-10-289-762-1803/c
; Sequence 1803, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1803
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1803

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      287 TTCACTACTGGAATG 302
Db      19 TTCACTACGGGATG 4

RESULT 312
US-10-455-229-23/c
; Sequence 23, Application US/10455229
; Publication No. US20040016030A1
; GENERAL INFORMATION:
; APPLICANT: LOWE, BRENDA A.
; APPLICANT: CHOMET, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES
; TITLE OF INVENTION: WITH INCREASED TRANSFORMABILITY
; FILE REFERENCE: DEKM:195US
; CURRENT APPLICATION NUMBER: US/10/455,229
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,522
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-455-229-23

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      775 CCTTTTGCTTGGGGAT 790
Db      19 CCTTTTGCTAGGGGAT 4

RESULT 313
US-10-293-864-44/c
; Sequence 44, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-44

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      812 GCTGAAGCAGGCCTCT 827
Db      16 GCTGCAGCAGGCCTCT 1

RESULT 314
US-10-293-864-45/c
; Sequence 45, Application US/10293864
; Publication No. US20040092465A1
```

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
FILE REFERENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
CURRENT FILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 45
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-45

Query Match
Best Local Similarity 1.3%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 813 CTGAAGCAGGCCTCTC 828
Db 20 CTGCAGCAGGCCTCTC 5

RESULT 315
US-10-293-864-120
Sequence 120, Application US/10293864
Publication No. US20040092465A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
FILE REFERENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
CURRENT FILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 120
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-293-864-120

Query Match
Best Local Similarity 1.3%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 GCTGAAGCAGGCCTCT 827
Db 5 GCTGCAGCAGGCCTCT 20

RESULT 316
US-10-293-864-121
Sequence 121, Application US/10293864
Publication No. US20040092465A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
FILE REFERENCE: RTS-0432
CURRENT APPLICATION NUMBER: US/10/293,864
CURRENT FILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 121
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-293-864-121

Query Match
Best Local Similarity 1.3%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 813 CTGAAGCAGGCCTCTC 828
Db 1 CTGCAGCAGGCCTCTC 16

RESULT 317
US-10-688-706-2537
Sequence 2537, Application US/10688706
Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2537
LENGTH: 20
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: human GFAT antisense
US-10-688-706-2537

Query Match
Best Local Similarity 1.3%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 553 TTAATATGCTGGGTTT 568
Db 5 TTAATAAGCTGGGTTT 20

RESULT 318
US-10-688-706-2670
Sequence 2670, Application US/10688706
Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2670
LENGTH: 20
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: human GFAT antisense
US-10-688-706-2670

Query Match
Best Local Similarity 1.3%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 554 TAATATGCTGGGTTT 569
Db 1 TAATAAGCTGGGTTT 16

RESULT 319
US-10-831-901A-4408
Sequence 4408, Application US/10831901A
Publication No. US20050100885A1

```
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4408
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4408
```

```
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 568 TTTTAATACCTTTATA 583
||||| |||||
Db 1 TTTTAATTCCTTTATA 16
```

```
RESULT 320
US-10-831-901A-4409
; Sequence 4409, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
```

```
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4409
```

```
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 568 TTTTAATACCTTTATA 583
||||| |||||
Db 2 TTTTAATTCCTTTATA 17
```

```
RESULT 321
US-10-831-901A-4410
; Sequence 4410, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4410
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-4410
```

```
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 568 TTTTAATACCTTTATA 583
||||| |||||
```


Fri Aug 19 11:00:02 2005

Db 3 TTTTAATTCCTTTATA 18

RESULT 322

US-10-831-901A-4411

; Sequence 4411, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.

; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)

; FILE REFERENCE: ISIS0083-100 (BIOL0008US)

; CURRENT APPLICATION NUMBER: US/10/831,901A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/466,426

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: 60/468,562

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/467,770

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: 60/468,627

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/477,637

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: 60/483,579

; PRIOR FILING DATE: 2003-06-27

; NUMBER OF SEQ ID NOS: 30063

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4411

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense compound

US-10-831-901A-4411

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 568 TTTTAATACCTTTATA 583

Db 4 TTTTAATTCCTTTATA 19

RESULT 323

US-10-831-901A-4412

; Sequence 4412, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.

; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)

; FILE REFERENCE: ISIS0083-100 (BIOL0008US)

; CURRENT APPLICATION NUMBER: US/10/831,901A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/466,426

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: 60/468,562

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/467,770

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: 60/468,627

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/477,637

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: 60/483,579

; PRIOR FILING DATE: 2003-06-27

; NUMBER OF SEQ ID NOS: 30063

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4412

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense compound

US-10-831-901A-4412

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 568 TTTTAATACCTTTATA 583

Db 5 TTTTAATTCCTTTATA 20

RESULT 324

US-11-008-747-297

; Sequence 297, Application US/11008747

; Publication No. US20050095710A1

; GENERAL INFORMATION:

; APPLICANT: Lex M. Cowser

; APPLICANT: Jacqueline Wyatt

; APPLICANT: Susan M. Freier

; APPLICANT: Brett P. Monia

; APPLICANT: Madeline M. Butler

; APPLICANT: Robert McKay

; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

; FILE REFERENCE: ISPH-0576

; CURRENT APPLICATION NUMBER: US/11/008,747

; CURRENT FILING DATE: 2004-09-04

; PRIOR APPLICATION NUMBER: US/09/854,883

; PRIOR FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 09/629,644

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 09/487,368

; PRIOR FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 389

; SEQ ID NO 297

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-11-008-747-297

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 GGCTGTGATCAATGG 358

Db 1 GGCTGTGATCAAAAGG 16

RESULT 325

US-10-388-578-48

```
; Sequence 48, Application US/10388578
; Publication No. US20030224411A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; APPLICANT: Shelton, Dawne
; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Human Embryonic Stem Cells
; FILE REFERENCE: 135/001
; CURRENT APPLICATION NUMBER: US/10/388,578
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Custom
; SEQ ID NO 48
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-578-48

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      827 TCATGACCCAGGAAGGCCG 845
Db      1 TCATAAGCCAGGAAGCCCG 19

RESULT 326
US-10-389-431-48
; Sequence 48, Application US/10389431
; Publication No. US20040180347A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Human Embryonic Stem Cells
; FILE REFERENCE: 135/002
; CURRENT APPLICATION NUMBER: US/10/389,431
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-389-431-48

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      827 TCATGACCCAGGAAGGCCG 845
Db      1 TCATAAGCCAGGAAGCCCG 19

RESULT 327
US-10-858-500-599
; Sequence 599, Application US/10858500
; Publication No. US20050014257A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
```

```
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: BIOL0014US
; CURRENT APPLICATION NUMBER: US/10/858,500
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 09/912,724
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/475,272
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/540,042
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 627
; SEQ ID NO 599
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-858-500-599

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      56 CCCAGTTCGGGAGACATGG 74
Db      1 CCCATTTCAGGAGACCTGG 19

RESULT 328
US-10-478-633A-147
; Sequence 147, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 147
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed oligonucleotide probe as Mycol170-probe to detect a DNA fragment amplifying a portion of ATPase operon from Mycoplasma pneumoniae.
US-10-478-633A-147

Query Match      1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1064 CCAGTGGCTAAACCACTTA 1082
Db      1 CCAGAGGCTGAACCACTTA 19

RESULT 329
US-10-783-128-527
; Sequence 527, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repeats Expanding Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
```

```
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 527
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-527

Query Match      1.3%;   Score 14.2;   DB 1;   Length 19;
Best Local Similarity 73.7%;   Pred. No. 2.5e+02;
Matches 14;   Conservative 2;   Mismatches 3;   Indels 0;   Gaps 0;

QY      804 CAGATAACGCTGAAGCAGG 822
Db      1 CAAAUAAGCUGAUGCAGG 19

RESULT 330
US-10-783-128-642
; Sequence 642, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repetitive Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 527
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-527

Query Match      1.3%;   Score 14.2;   DB 1;   Length 19;
Best Local Similarity 73.7%;   Pred. No. 2.5e+02;
Matches 14;   Conservative 2;   Mismatches 3;   Indels 0;   Gaps 0;

QY      804 CAGATAACGCTGAAGCAGG 822
Db      1 CAAAUAAGCUGAUGCAGG 19
```

```
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 642
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-642

Query Match      1.3%;   Score 14.2;   DB 1;   Length 19;
Best Local Similarity 73.7%;   Pred. No. 2.5e+02;
Matches 14;   Conservative 2;   Mismatches 3;   Indels 0;   Gaps 0;

QY      194 CAGCCCATCTCCCCCATCC 212
Db      1 CAGCCUGCUCCCUCAUCC 19

RESULT 331
US-10-783-128-1088
; Sequence 1088, Application US/10783128
; Publication No. US20050096284A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Polyglutamine (PolyQ) Repetitive Expansion Diseases Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 04-105 (400.146)
; CURRENT APPLICATION NUMBER: US/10/783,128
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/652,791
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: US 10/422,704
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3577
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-783-128-1088

Query Match      1.3%;   Score 14.2;   DB 1;   Length 19;
Best Local Similarity 63.2%;   Pred. No. 2.5e+02;
Matches 12;   Conservative 4;   Mismatches 3;   Indels 0;   Gaps 0;

QY      358 GGGAGCCTGCGGCTTG 376
Db      1 GGAAGUCUGCGCCUUGUG 19
```


Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 358 GGGAGCTGCGCCTTG 376
Db 19 GGAAGTCTGCGCCTTG 1

RESULT 335
US-09-771-357-79
; Sequence 79, Application US/09771357
; Publication No. US20030017454A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William
; APPLICANT: DAVIDSON, Nancy
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630
; CURRENT APPLICATION NUMBER: US/09/771,357
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-09-771-357-79

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGGCGTTT 167
Db 1 TTCGAAGTTTATGGCGTTT 19

RESULT 336
US-09-918-187-73
; Sequence 73, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-73

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 814 TGAAGCAGGCCTCTCATGA 832
Db 2 TCAAGCAGGCATCTCATGA 20

RESULT 337

US-10-054-225-12
; Sequence 12, Application US/10054225
; Publication No. US20020164623A1
; GENERAL INFORMATION:
; APPLICANT: Saint Jude Children's Research Hospital
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Atkinson, Robyn M
; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
; FILE REFERENCE: SJ-01-0022
; CURRENT APPLICATION NUMBER: US/10/054,225
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)..(20)
; OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VnCS SNP
US-10-054-225-12

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 ATTGAATTTCTTAGAACTC 507
Db 1 ATTGATTTTCTTCTAACTC 19

RESULT 338
US-10-024-450-12/c
; Sequence 12, Application US/10024450
; Publication No. US20030032606A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; APPLICANT: Chadwick, Robert B.
; TITLE OF INVENTION: Methods of Detecting and Treating
; TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
; FILE REFERENCE: P-LJ 5101
; CURRENT APPLICATION NUMBER: US/10/024,450
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,582
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic primer
US-10-024-450-12

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 966 AGGACATTTTGATGAGATC 984
Db 19 ACGACATTTTGCTGAGCTC 1

RESULT 339
US-10-006-883A-73/c
; Sequence 73, Application US/10006883A
; Publication No. US20030119767A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION
; FILE REFERENCE: RTS-0337

```
; CURRENT APPLICATION NUMBER: US/10/006,883A
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 73
; LENGTH: 20.
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-883A-73

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1096 TTACCTGCTCATTTGTTTA 1114
Db      19 TTGCCCGCTCATTTGTTAA 1

RESULT 340
US-10-059-579-79
; Sequence 79, Application US/10059579
; Publication No. US20030138783A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: PACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-10-059-579-79

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      149 TTAGAGGATTATGCGGTTT 167
Db      1 TTCGAAGTTTATGCGGTTT 19

RESULT 341
US-10-348-485-86/c
; Sequence 86, Application US/10348485
; Publication No. US20030148989A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Holmlund, Jon T.
; APPLICANT: Dorr, F. Andrew
; TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
; FILE REFERENCE: ISIS4954
; CURRENT APPLICATION NUMBER: US/10/348,485
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/10/025,139
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 08/829,637
; PRIOR FILING DATE: 1997-03-31
```

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; PRIOR APPLICATION NUMBER: US 08/478,178
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/089,996
; PRIOR FILING DATE: 1993-07-09
; PRIOR APPLICATION NUMBER: US 07/852,852
; PRIOR FILING DATE: 1992-03-16
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-86

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      434 AGAGGAGATGATTTTAGCT 452
Db      19 AGAGAAGAGGATTTTGCT 1

RESULT 342
US-10-428-617-12
; Sequence 12, Application US/10428617
; Publication No. US20030175796A1
; GENERAL INFORMATION:
; APPLICANT: Saint Jude Children's Research Hospital
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Atkinson, Robyn M
; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
; FILE REFERENCE: SJ-01-0022
; CURRENT APPLICATION NUMBER: US/10/428,617
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US/10/054,225
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(20)
; OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
US-10-428-617-12

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      489 ATTGAATTTCTTAGAATC 507
Db      1 ATTGATTTTCTTCTAATC 19

RESULT 343
US-10-240-046A-56/c
; Sequence 56, Application US/10240046A
; Publication No. US20030190639A1
; GENERAL INFORMATION:
; APPLICANT: HUGOT, JEAN-PIERRE
; APPLICANT: THOMAS, GILLES
; APPLICANT: ZOUALI, MOHAMED
; APPLICANT: LESAGE, SUZANNE
; APPLICANT: CHAMAILLARD, MATHIAS
; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 37991-0009
```



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; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement
US-10-349-143-9409

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      427 ATTGGAAGAGGAGATGAT 445
Db      19 AGTTGGAGGGGAGATGAT 1

RESULT 349
US-10-188-470-69
; Sequence 69, Application US/10188470
; Publication No. US20040005707A1
; GENERAL INFORMATION:
; APPLICANT: Scott Cooper
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 5 EXPRESSION
; FILE REFERENCE: PTS-0024
; CURRENT APPLICATION NUMBER: US/10/188,470
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-470-69

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1029 GAGAAGTAAACATCACACC 1047
Db      1 GAGAAGGAACATCATGTC 19

RESULT 350
US-10-190-366-111/c
; Sequence 111, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
```

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; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
; FILE REFERENCE: PTS-0023
; CURRENT APPLICATION NUMBER: US/10/190,366
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 111
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-190-366-111

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      95 GCATTATCCTTCAGTGGG 113
Db      19 GCATTATTCCTCAGAAGG 1

RESULT 351
US-10-190-366-308
; Sequence 308, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
; FILE REFERENCE: PTS-0023
; CURRENT APPLICATION NUMBER: US/10/190,366
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 308
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-190-366-308

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      95 GCATTATCCTTCAGTGGG 113
Db      2 GCATTATTCCTCAGAAGG 20

RESULT 352
US-10-289-762-2125
; Sequence 2125, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2125

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
```


Fri Aug 19 11:00:02 2005

```
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 AGAATCTGAAGCCCCCACTC 958
      ||||| ||| |||||
Db 1 AGAATCGGAACCCACGC 19

RESULT 353
US-10-289-762-4121
; Sequence 4121, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4121

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 771 GAAACCTTTTCTTGGGA 789
      ||||| ||| |||||
Db 1 GAGACCTTTTCTTGGGA 19

RESULT 354
US-10-289-762-5159
; Sequence 5159, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5159

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAATTGTTGTTTC 309
      ||||| ||| |||||
Db 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 355
US-10-289-762-5166
; Sequence 5166, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
```

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; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5166

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAATTGTTGTTTC 309
      ||||| ||| |||||
Db 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 356
US-10-289-762-6581
; Sequence 6581, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6581
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6581

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 460 GTGCTAGCACCTTTATTCTG 478
      ||||| ||| |||||
Db 2 GTGCTAGCACTATAACCTG 20

RESULT 357
US-10-317-500-76/c
; Sequence 76, Application US/10317500
; Publication No. US20040115637A1
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
; FILE REFERENCE: RFS-0380
; CURRENT APPLICATION NUMBER: US/10/317,500
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 276
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-500-76

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 266 TGTGGGAACTGGCATATT 284
      ||||| ||| |||||
Db 20 TGTAGGTAACCGGCATATT 2
```

```
RESULT 358
US-10-731-739-310/c
; Sequence 310, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/10/731,739
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-731-739-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCACAGAC 900
Db      19 AATATTGTGGCCACAC 1

RESULT 359
US-10-424-041-105/c
; Sequence 105, Application US/10424041
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL0005US
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-105

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      382 AGGCAATGCAGTCATTTC 400
Db      20 ATGCAATGCAAGCATTTC 2

RESULT 360
US-10-424-041-179
```

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; Sequence 179, Application US/10424041
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL0005US
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 179
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-424-041-179

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 57.9%; Pred. No. 2.7e+02;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      382 AGGCAATGCAGTCATTTC 400
Db      1 AUGCAAUGCAAGCAUUC 19

RESULT 361
US-10-477-238A-310/c
; Sequence 310, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
; APPLICANT: BabiJ, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-212
; CURRENT APPLICATION NUMBER: US/10/477,238A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-238A-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCACAGAC 900
Db      19 AATATTGTGGCCACAC 1

RESULT 362
US-10-680-287A-310/c
; Sequence 310, Application US/10680287A
; Publication No. US20040244069A1
; GENERAL INFORMATION:
; APPLICANT: BabiJ, Philip
; APPLICANT: Yaworsky, Paul
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Fri Aug 19 11:00:02 2005

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; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-680-287A-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCCCACAGAC 900
Db      19 AATATTGTGGCCCCACACAC 1

RESULT 363
US-10-476-960-4
; Sequence 4, Application US/10476960
; Publication No. US20040248828A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
; FILE REFERENCE: RTSP-0392
; CURRENT APPLICATION NUMBER: US/10/476,960
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 09/851,520
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
; US-10-476-960-4

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      822 GCCTCTCATGACCCAGGAA 840
Db      1 GCCACTCCAGACCCAGGAA 19

RESULT 364
US-10-484-442-73
; Sequence 73, Application US/10484442
; Publication No. US20040254359A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
```

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; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL?COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH?0695
; CURRENT APPLICATION NUMBER: US/10/484,442
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-484-442-73

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      814 TGAAGCAGGCGCTCTCATGA 832
Db      2 TCAAGCAGGCGCATCTGATGA 20

RESULT 365
US-10-858-500-205
; Sequence 205, Application US/10858500
; Publication No. US20050014257A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: BIOL0014US
; CURRENT APPLICATION NUMBER: US/10/858,500
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 09/912,724
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/475,272
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/540,042
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 627
; SEQ ID NO 205
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-858-500-205

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      56 CCCAGTTCGGGAGACATGG 74
Db      2 CCCATTTCAGGAGACCTGG 20

RESULT 366
US-10-858-500-381/c
; Sequence 381, Application US/10858500
; Publication No. US20050014257A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: BIOL0014US
; CURRENT APPLICATION NUMBER: US/10/858,500
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 09/912,724
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/475,272
```

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; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/540,042
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 627
; SEQ ID NO 381
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-858-500-381

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      56 CCCAGTTCGGGAGACATGG 74
      ||||| ||| ||||| |||||
Db      19 CCCATTTCAGGAGACCTGG 1

RESULT 367
US-10-643-775-1061
; Sequence 1061, Application US/10643775
; Publication No. US20050026156A1
; GENERAL INFORMATION:
; APPLICANT: Lie, Oystein
; APPLICANT: Slettan, Audun
; APPLICANT: Hoyum, Morten
; APPLICANT: Lingaas, Frode
; TITLE OF INVENTION: Verification of Food Origin Based on
; TITLE OF INVENTION: Nucleic Acid Pattern Recognition
; FILE REFERENCE: 66849-019
; CURRENT APPLICATION NUMBER: US/10/643,775
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US 60/404,200
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1061
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Oreochromis niloticus
US-10-643-775-1061

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      782 CTTGGGGATGTGCTTGGAG 800
      ||||| ||| ||||| |||||
Db      2 CTTGGGTTTGAGCTTGGAG 20

RESULT 368
US-10-619-253-73
; Sequence 73, Application US/10619253
; Publication No. US20050043256A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590US.P1
; CURRENT APPLICATION NUMBER: US/10/619,253
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US 09/918,187
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 418
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

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US-10-619-253-73

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      814 TGAAGCAGGCCCTCTCATGA 832
      ||||| ||||| ||||| |||||
Db      2 TCAAGCAGGCATCTGATGA 20

RESULT 369
US-10-477-173-310/c
; Sequence 310, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul
; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: US/10/477,173
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-173-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCCCACAGAC 900
      ||| ||||| ||||| |||||
Db      19 AATATTGTGGCCCCACACAC 1

RESULT 370
US-10-831-901A-10393/c
; Sequence 10393, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
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Fri Aug 19 11:00:02 2005

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; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10393
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10393

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      407 ATTCAGGGTTTTCCTTA 425
      ||| |||| | |||||
Db      19 ATTAAGGTTCTTTCCTTA 1

RESULT 371
US-10-831-901A-10394/c
; Sequence 10394, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10394

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      407 ATTCAGGGTTTTCCTTA 425
      ||| |||| | |||||
Db      19 ATTAAGGTTCTTTCCTTA 1

RESULT 371
US-10-831-901A-10394/c
; Sequence 10394, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10394

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      407 ATTCAGGGTTTTCCTTA 425
      ||| |||| | |||||
Db      19 ATTAAGGTTCTTTCCTTA 1

RESULT 371
US-10-831-901A-10394/c
; Sequence 10394, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-10394

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      407 ATTCAGGGTTTTCCTTA 425
      ||| |||| | |||||
Db      19 ATTAAGGTTCTTTCCTTA 2

RESULT 372
US-10-831-901A-11295
; Sequence 11295, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11295
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11295

Query Match          1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1014 AGAAGCATCATCAGAGA 1032
      || ||||| ||||| |||
Db      1 AGCAGCATCATCAAAACA 19

RESULT 373
US-10-831-901A-11296
; Sequence 11296, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
```

Best Local Similarity 84.2%; Pred. No. 2.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 407 ATTCAGGGTTTTCCTTA 425
 ||| |||| | |||||
Db 20 ATTAAGGTTCTTTCCTTA 2

RESULT 372
US-10-831-901A-11295
; Sequence 11295, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11295
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11295

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1014 AGAAGCATCATCAGAGA 1032
 || ||||| ||||| |||
Db 1 AGCAGCATCATCAAAACA 19

RESULT 373
US-10-831-901A-11296
; Sequence 11296, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.

```
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11296
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11296

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1014 AGAAGCATCATCAGAGA 1032
Db      2 ACAGCATCATCATAACA 20

RESULT 374
US-10-831-901A-12114
; Sequence 12114, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12115

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1014 AGAAGCATCATCAGAGA 1032
Db      2 ACAGCATCATCATAACA 20

RESULT 374
US-10-831-901A-12114
; Sequence 12114, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12115
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12114

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      596 TTTAAGAAAGACTTCATAA 614
Db      1 TTTGAGAACGACTTCAGAA 19

RESULT 375
US-10-831-901A-12115
; Sequence 12115, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-12115

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      596 TTTAAGAAAGACTTCATAA 614
Db      2 TTTGAGAACGACTTCAGAA 20

RESULT 376
US-10-831-901A-14584
; Sequence 14584, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
```

Fri Aug 19 11:00:02 2005

```
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14584
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14584

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1006 AAAGTTTGAGAAGCATCAT 1024
      |||||||
Db      1 ACAGTTTGAAAAGCAACAT 19

RESULT 377
US-10-831-901A-14587
; Sequence 14587, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15628

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14587
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-14587

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1004 TGAAGTTTGAGAAGCATC 1022
      |||
Db      2 TGACAGTTTGAAAAGCAAC 20

RESULT 378
US-10-831-901A-15628
; Sequence 15628, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-15628

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1017 AGCATCATCATAGAGAAGT 1035
      |||
Db      1 AGAATCATCATGGAGAAAT 19
```

```
RESULT 379
US-10-831-901A-26183/c
; Sequence 26183, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/469,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26183
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26183

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      318 GATTTCCTGTTATTCTTGC 336
      ||||| ||||| ||||| |||||
Db      19 GCTTCGTGGTATTCTTGC 1

RESULT 380
US-10-831-901A-26188/c
; Sequence 26188, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
```

```
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26188

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      322 TCCTGTTATTCTTGCCTCGT 340
      ||||| ||||| ||||| |||||
Db      20 TCGTGGTATTCTTGCCTAGT 2

RESULT 381
US-10-831-901A-26488/c
; Sequence 26488, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26488
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-26488

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
```


Fri Aug 19 11:00:02 2005

Matches16;Conservative0;Mismatches3;Indels0;Gaps0;

QY658TAGATTATGTTACTCAAAAT676

Db19TGGATTATGTTACTACAAT1

RESULT382

US-10-831-901A-26896

Sequence26896,ApplicationUS/10831901A

PublicationNo.US20050100885A1

GENERALINFORMATION:

APPLICANT:Crooke,StanleyT.

APPLICANT:Ecker,DavidJ.

APPLICANT:Sampath,Rangarajan

APPLICANT:Freier,SusanM.

APPLICANT:Massire,Christian

APPLICANT:Hofstadler,StevenA.

APPLICANT:Lowery,KristinSannes

APPLICANT:Swayze,Eric

APPLICANT:Baker,BrendaF.

APPLICANT:Bennett,C.Frank

TITLEOFINVENTION:CompositionsAndMethodsForTheTreatmentOfSevere

FILEREFERENCE:ISIS0083-100(BIOL0008US)

CURRENTAPPLICATIONNUMBER:US/10/831,901A

CURRENTFILINGDATE:2004-04-26

PRIORAPPLICATIONNUMBER:60/466,426

PRIORFILINGDATE:2003-04-28

PRIORAPPLICATIONNUMBER:60/468,562

PRIORFILINGDATE:2003-05-06

PRIORAPPLICATIONNUMBER:60/467,770

PRIORFILINGDATE:2003-04-30

PRIORAPPLICATIONNUMBER:60/468,627

PRIORFILINGDATE:2003-05-06

PRIORAPPLICATIONNUMBER:60/477,637

PRIORFILINGDATE:2003-06-10

PRIORAPPLICATIONNUMBER:60/483,579

PRIORFILINGDATE:2003-06-27

NUMBEROFSEQIDNOS:30063

SOFTWARE:FastSEQforWindowsVersion4.0

SEQIDNO26896

LENGTH:20

TYPE:DNA

ORGANISM:ArtificialSequence

FEATURE:

OTHERINFORMATION:Antisensecompound

US-10-831-901A-26897

QueryMatch1.3%;Score14.2;DB1;Length20;

BestLocalSimilarity84.2%;Pred.No.2.7e+02;

Matches16;Conservative0;Mismatches3;Indels0;Gaps0;

QY699ATGTAGTCACGGTGCTCTC717

Db2ATGTAGCCACAGTGATCTC20

RESULT384

US-10-476-264-189/c

Sequence189,ApplicationUS/10476264

PublicationNo.US20050123910A1

GENERALINFORMATION:

APPLICANT:Cookson,WilliamOsmondCharlesMichael

APPLICANT:Moffat,MiriamFleur

APPLICANT:Allen,Maxine

APPLICANT:Lench,Nick

TITLEOFINVENTION:EnzymeandSNPmarkerfordisease

FILEREFERENCE:16721-002US1

CURRENTAPPLICATIONNUMBER:US/10/476,264

CURRENTFILINGDATE:2003-10-24

PRIORAPPLICATIONNUMBER:PCT/GB02/01887

PRIORFILINGDATE:2002-04-24

PRIORAPPLICATIONNUMBER:GB0110044.5

PRIORFILINGDATE:2001-04-24

PRIORAPPLICATIONNUMBER:GB0110046.0

PRIORFILINGDATE:2001-04-24

PRIORAPPLICATIONNUMBER:GB0124594.3

PRIORFILINGDATE:2001-10-12

PRIORAPPLICATIONNUMBER:GB0124575.2

PRIORFILINGDATE:2001-10-12

NUMBEROFSEQIDNOS:421

SOFTWARE:PatentInversion3.1

SEQIDNO189

LENGTH:20

TYPE:DNA

ORGANISM:ArtificialSequence

FEATURE:

OTHERINFORMATION:Primer

US-10-476-264-189

QueryMatch1.3%;Score14.2;DB1;Length20;

BestLocalSimilarity84.2%;Pred.No.2.7e+02;

Matches16;Conservative0;Mismatches3;Indels0;Gaps0;

QY699ATGTAGTCACGGTGCTCTC717

Db1ATGTAGCCACAGTGATCTC19

RESULT383

US-10-831-901A-26897

Sequence26897,ApplicationUS/10831901A

PublicationNo.US20050100885A1

GENERALINFORMATION:

APPLICANT:Crooke,StanleyT.

APPLICANT:Ecker,DavidJ.

APPLICANT:Sampath,Rangarajan

APPLICANT:Freier,SusanM.

APPLICANT:Massire,Christian

APPLICANT:Hofstadler,StevenA.

APPLICANT:Lowery,KristinSannes

APPLICANT:Swayze,Eric

APPLICANT:Baker,BrendaF.

APPLICANT:Bennett,C.Frank

TITLEOFINVENTION:CompositionsAndMethodsForTheTreatmentOfSevere

FILEREFERENCE:ISIS0083-100(BIOL0008US)

CURRENTAPPLICATIONNUMBER:US/10/831,901A

CURRENTFILINGDATE:2004-04-26

PRIORAPPLICATIONNUMBER:60/466,426

PRIORFILINGDATE:2003-04-28

PRIORAPPLICATIONNUMBER:60/468,562

PRIORFILINGDATE:2003-05-06

PRIORAPPLICATIONNUMBER:60/477,637

PRIORFILINGDATE:2003-06-10

PRIORAPPLICATIONNUMBER:60/483,579

PRIORFILINGDATE:2003-06-27

NUMBEROFSEQIDNOS:30063

SOFTWARE:FastSEQforWindowsVersion4.0

SEQIDNO26896

LENGTH:20

TYPE:DNA

ORGANISM:ArtificialSequence

FEATURE:

OTHERINFORMATION:Antisensecompound

US-10-831-901A-26896

QueryMatch1.3%;Score14.2;DB1;Length20;

BestLocalSimilarity84.2%;Pred.No.2.7e+02;

Matches16;Conservative0;Mismatches3;Indels0;Gaps0;

QY 472 TATTCTGATTACAGTGCAT 490
| | | | | | | | | | | | | | |
Db 19 TGTCTGGTTACAATGCAT 1

RESULT 385
US-10-834-377-310/c
; Sequence 310, Application US/10834377
; Publication No. US20050142617A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/10/834,377
; CURRENT FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US/09/543,771B
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-834-377-310

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
| | | | | | | | | | | | | | |
Db 19 AATATTGTGGCCACAC 1

RESULT 386
US-10-980-850-1
; Sequence 1, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer for GOS2 gene
US-10-980-850-1

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 798 GAGAGGCAGATAACGCTGA 816
| | | | | | | | | | | | | | |
Db 1 GAGAGGAGGAGACGCTGA 19

RESULT 387
US-11-039-629-125/c
; Sequence 125, Application US/11039629
; Publication No. US20050164271A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0532US
; CURRENT APPLICATION NUMBER: US/11/039,629
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: 60/538,173
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/550,191
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-11-039-629-125

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1075 ACCACTTAACCTCTCTGGG 1093
| | | | | | | | | | | | | | |
Db 20 ACAACTTGACTTCTCTGGG 2

RESULT 388
US-10-774-721-43
; Sequence 43, Application US/10774721
; Publication No. US20050009042A1
; GENERAL INFORMATION:
; APPLICANT: JOCKERS, Ralf
; APPLICANT: COUTURIER, Cyril
; APPLICANT: UHLMANN, Eugen
; TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP Protein
; TITLE OF INVENTION: And Method For Detecting Compounds Which Modify The Interaction
; TITLE OF INVENTION: Between Proteins Of the OB-RGRP Family And The Leptin Receptor
; FILE REFERENCE: FRV2003/0005 US NP
; CURRENT APPLICATION NUMBER: US/10/774,721
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/461,005
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 0301543
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-774-721-43

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CCGTGGCAGGAAGC 39
| | | | | | | | | | | | | | |

| | | | | |
|-----------------------|---------|-----------|----------|------------|
| Query Match | 1.3%; | Score 14; | DB 1; | Length 19; |
| Best local Similarity | 100.0%; | Pred. No. | 2.6e+02; | |

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1060 CTTTCCAGTGGCTA 1073
Db 1 CTTTCCAGTGGCTA 14

RESULT 393
US-09-802-669-156/c
; Sequence 156, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-802-669-156

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
Db 18 AGATGAGTTTATT 5
RESULT 394
US-10-172-911-55
; Sequence 55, Application US/10172911
; Publication No. US20030232434A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN12 EXPRESSION
; FILE REFERENCE: PTS-0016
; CURRENT APPLICATION NUMBER: US/10/172,911
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-172-911-55

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 345 CTGTGATCAAAATGG 358
Db 1 CTGTGATCAAAATGG 14

RESULT 395

US-10-349-143-4185/c
; Sequence 4185, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,
US-10-349-143-4185

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTAATA 575
Db 19 TGGGTTTTTTAATA 6

RESULT 396
US-10-349-143-5624
; Sequence 5624, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5624
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-5681 for SEQ 1690,
US-10-349-143-5624

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY      324 CTGTTATTCTTGCT 337
      |||||
Db      4 CTGTTATTCTTGCT 17

RESULT 397
US-10-619-220-156/c
; Sequence 156, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-619-220-156

      Query Match      1.3%; Score 14; DB 1; Length 20;
      Best Local Similarity 100.0%; Pred. No. 2.9e+02;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AGATGAGTTTTATT 633
      |||||
Db      18 AGATGAGTTTTATT 5

RESULT 398
US-10-831-901A-18964
; Sequence 18964, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18964
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18964

      Query Match      1.3%; Score 14; DB 1; Length 20;
      Best Local Similarity 100.0%; Pred. No. 2.9e+02;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      311 GCCTTTGGATTTC 324
      |||||
Db      1 GCCTTTGGATTTC 14

RESULT 399
US-10-831-901A-18965
; Sequence 18965, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18965
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18965

      Query Match      1.3%; Score 14; DB 1; Length 20;
      Best Local Similarity 100.0%; Pred. No. 2.9e+02;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      311 GCCTTTGGATTTC 324
      |||||
Db      2 GCCTTTGGATTTC 15
```

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RESULT 400
US-10-831-901A-18966
; Sequence 18966, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18966
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18966

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      311 GCCTTTGGATTTC 324
      |||||
Db      3 GCCTTTGGATTTC 16

RESULT 401
US-10-831-901A-18967
; Sequence 18967, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
```

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; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18967
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18967

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      311 GCCTTTGGATTTC 324
      |||||
Db      4 GCCTTTGGATTTC 17

RESULT 402
US-10-831-901A-18968
; Sequence 18968, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18968
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18968

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      311 GCCTTTGGATTTC 324
      |||||
Db      3 GCCTTTGGATTTC 16

RESULT 403
US-10-831-901A-18969
; Sequence 18969, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18969
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18969

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      311 GCCTTTGGATTTC 324
      |||||
Db      3 GCCTTTGGATTTC 16

RESULT 404
US-10-831-901A-18970
; Sequence 18970, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
```

```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 311 GCCTTTGGATTTC 324
Db 5 GCCTTTGGATTTC 18

RESULT 403
US-10-831-901A-18969
; Sequence 18969, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18969
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18969

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 GCCTTTGGATTTC 324
Db 5 GCCTTTGGATTTC 18

RESULT 404
US-10-831-901A-18970
; Sequence 18970, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
```

```
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18970
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-18970

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 GCCTTTGGATTTC 324
Db 7 GCCTTTGGATTTC 20

RESULT 405
US-09-866-108-2563/c
; Sequence 2563, Application US/098666108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2563
```

```
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 745 GCAGCTGCCACCTTATG 761
Db 17 GCAGCTGCCGCCTTCTG 1
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RESULT 406

```
US-09-866-108-2564/c
; Sequence 2564, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
```

```
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2564
```

```
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 744 GCAGCTGCCACCTTAT 760
Db 17 GCAGCTGCCGCCTTCT 1
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RESULT 407

```
US-09-866-108-6749
; Sequence 6749, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6749
```

```
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      836 AGGAAGCCGGGGTGA 852
      |||||
Db      1 AGGAAGCCGTGGAGGA 17

RESULT 408
US-09-780-533A-2567/c
; Sequence 2567, Application US/09780533A
; Publication No. US2003006011A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowli, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2567

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      413 GGGTTTTTCCTTATTT 429
      | |||||
Db      17 GAGTTTTTCCTTATTT 1

RESULT 409
US-09-848-754A-3616/c
; Sequence 3616, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3616
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3616

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      499 TTAGAACTCATACTATC 515
      |||||
Db      17 TTAGGGCTCATACTATC 1

RESULT 410
US-09-978-600-140/c
; Sequence 140, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
```

```

; PARKER, WILLIAM D.
; DAVIS, ROBERT
; MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; Animal Models for Diseases Associated With Mitochondrial
; Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/978,600
; FILING DATE: 15-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-978-600-140

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      562 TGGGTTTTTAAATACCT 578
      |||||
Db      17 TGGTTTTTCTAATACCT 1

RESULT 411
US-09-978-600-151/c
; Sequence 151, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; PARKER, WILLIAM D.
; DAVIS, ROBERT
; MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; Animal Models for Diseases Associated With Mitochondrial
; Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
```

STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 151:
US-09-978-600-151

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTAATACCT 578
||| ||| ||| ||| ||| ||| |||
Db 17 TGGTTTCTTAATACCT 1

RESULT 412
US-09-978-600-185/c
Sequence 185, Application US/09978600
Publication No. US20030087858A1
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated with Mitochondrial
Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-978-600-185
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 562 TGGGTTTTTTAATACCT 578
||| ||| ||| ||| ||| ||| |||
Db 17 TGGTTTCTTAATACCT 1
RESULT 413
US-09-978-600-186/c
Sequence 186, Application US/09978600
Publication No. US20030087858A1
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated with Mitochondrial
Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
FILING DATE: 15-Oct-2001

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 AGCGTCCCGGGCCGTG 30
|||||
Db 17 AGCGCGCCAGGCCGTG 1

RESULT 417
US-09-792-818-603
; Sequence 603, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 603
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-603

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 105 TCAGTGGGGCTATTGGA 121
:|||||: |||
Db 1 UCAGUGGGGCGUGGGA 17

RESULT 418
US-10-060-756A-4243
; Sequence 4243, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4243

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 673 AAATTATGTTACTTGT 689
|||||
Db 1 AGATTATGTTCTTGT 17

RESULT 419
US-10-339-782-270
; Sequence 270, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-0001100S
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-270

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 898 GACCAAGAGCCTCAACA 914
|||||
Db 1 GATCAAGACCTCAACA 17

RESULT 420
US-10-240-046A-64
; Sequence 64, Application US/10240046A
; Publication No. US20030190639A1
; GENERAL INFORMATION:
; APPLICANT: HUGOT, JEAN-PIERRE
; APPLICANT: THOMAS, GILLES
; APPLICANT: ZOULALI, MOHAMED
; APPLICANT: LESAGE, SUZANNE
; APPLICANT: CHAMAILLARD, MATHIAS
; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 37991-0009
; CURRENT APPLICATION NUMBER: US/10/240,046A
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: PCT/FR 01/00935
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: FR 00/03832
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-240-046A-64

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 GCCATCTCCCCCATCCC 213
|||||
Db 1 GCCATCTCCCCAAGCCC 17

US-10-430-882-217/c
; Sequence 217, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 217
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-217

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GGCTGCCCGGCCGTGG 31
||| |||| |||||
Db 17 GGCGGCCCGGCCGTGG 1

RESULT 422
US-10-430-882-888/c
; Sequence 888, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-430-882-888

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 AGGCTGCCCGGCCGTG 30
||||| ||||| |||||
Db 17 AGCGGCCCGGCCGTG 1

RESULT 423
US-10-297-068-894
; Sequence 894, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 894
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-894

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 404 ACAATTCAAGGGTTTTT 420
||||| ||||| |||||
Db 1 ACAATTACAGGGTTTTT 17

RESULT 424
US-10-723-361-2563/c
; Sequence 2563, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2563

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATG 761
Db      17 GCAGCTGCCGCCTTCG 1

RESULT 425
US-10-723-361-2564/c
; Sequence 2564, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2564
```

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Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      744 GGCAGCTGCCACCTTAT 760
Db      17 GGCAGCTGCCGCCTTCT 1

RESULT 426
US-10-723-361-6749
; Sequence 6749, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 6749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6749

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      836 AGGAAGCGCGGGTGGA 852
Db      1 AGGAAGCGCGTGAGGA 17

RESULT 427
US-10-890-776A-4243
; Sequence 4243, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
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Fri Aug 19 11:00:02 2005

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; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4243

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      673 AAATTATGTTTACTTGTT 689
Db      1 AGATTATGTTTCTTGTT 17

RESULT 428
US-09-468-147-6
; Sequence 6, Application US/09468147A
; Publication No. US20030049601A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: HEPATITIS E VIRUS
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/09/468,147A
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/173,141
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/061,199
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer C375
US-09-468-147-6

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1035 TAAACATCACACCCCAAC 1051
Db      2 TGAACATCACGCCCAAC 18

; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4243

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      673 AAATTATGTTTACTTGTT 689
Db      1 AGATTATGTTTCTTGTT 17

RESULT 428
US-09-468-147-6
; Sequence 6, Application US/09468147A
; Publication No. US20030049601A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: HEPATITIS E VIRUS
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/09/468,147A
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/173,141
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/061,199
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer C375
US-09-468-147-6

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1035 TAAACATCACACCCCAAC 1051
Db      2 TGAACATCACGCCCAAC 18
```

```

RESULT 429
US-09-888-625-17
; Sequence 17, Application US/09888625
; Publication No. US20030064365A1
; GENERAL INFORMATION:
; Sequencing List
; APPLICANT: Kwangmyung Sungae Medical Foundation
; TITLE OF INVENTION: GAP VECTOR FOR E. COLI STOP CODON ASSAY AND METHOD FOR DETECTING
; TITLE OF INVENTION: HETEROZYGOUS MUTATION USING THE SAME
; FILE REFERENCE: Sungae-1
; CURRENT APPLICATION NUMBER: US/09/888,625
; CURRENT FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer BV-b5
US-09-888-625-17

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 CACATGAAAGTTTGAGA 1016
Db      1 CACATGCAAGTTTGAAA 17

RESULT 430
US-10-265-689-37/c
; Sequence 37, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-265-689-37

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      201 TCTCCCCCATCCCCCAT 217
Db      17 TCTCACCCCTCCCCCAT 1
```

```
RESULT 431
US-10-319-745-6
; Sequence 6, Application US/10319745
; Publication No. US20030211467A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/10/319,745
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US/09/468,147A
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/173,141
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/061,199
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer C375
US-10-319-745-6

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1035 TAAACATCACACCCCAAC 1051
Db      2 TGAACATCACGCCCAAC 18
      |||||
      |||||

RESULT 432
US-10-108-260A-5064/c
; Sequence 5064, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5064
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-10-108-260A-5064

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      295 TGAATTTGTTGTTCTG 311
Db      18 TGGTATTGTTGTGCTG 2
      |||||
      |||||

RESULT 433
US-10-349-143-4732/c
; Sequence 4732, Application US/10349143
```

```
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4732
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798,
US-10-349-143-4732

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      905 AGCCTCAACATTTCCTA 921
Db      17 AGCCTCAGCATTTCATA 1
      |||||
      |||||

RESULT 434
US-10-349-143-6041
; Sequence 6041, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6041
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-10-349-143-6041

Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      942 AATCTGAAGCCCCCACTC 958
```


Fri Aug 19 11:00:02 2005

Db 2 AATCTCAACCCCACTC 18
RESULT 435
US-10-349-143-11352/c
; Sequence 11352, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11352
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-4448 for SEQ 3487, in compleme
US-10-349-143-11352
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 CCCCCATCCCCCATTC 220
Db 18 CCTCCATCCCCCACTC 2
RESULT 436
US-10-443-545-10
; Sequence 10, Application US/10443545
; Publication No. US20040038266A1
; GENERAL INFORMATION:
; APPLICANT: Neo Gen Screening, Inc.
; TITLE OF INVENTION: Advancing the Detection of Hearing Loss in Newborns through
; TITLE OF INVENTION: Parallel Genetic Analysis
; FILE REFERENCE: 2175
; CURRENT APPLICATION NUMBER: US/10/443,545
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: 60/370762
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-443-545-10
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 196 CGCCATCTCCCCATCC 212
Db 1 CCCCATCTCCCATCC 17

RESULT 437
US-10-486-319A-275
; Sequence 275, Application US/10486319A
; Publication No. US20050064410A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/486,319A
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 275
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for PGR
US-10-486-319A-275

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 TAGGAGATGAGTTTAT 632
Db 2 TAGGAGATGAGATTTT 18

RESULT 438
US-10-486-319A-277/c
; Sequence 277, Application US/10486319A
; Publication No. US20050064410A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/486,319A
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 277
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for PGR
US-10-486-319A-277

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 TAGGAGATGAGTTTAT 632
Db 17 TAGGAGATGAGATTTT 1

RESULT 439
US-10-352-179-63/c
; Sequence 63, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63

```
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-63

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      414 GGTTTTCCTTATATT 430
      ||||| ||| |||||
Db      19 GGTTTTCCTTGTTT 3

RESULT 440
US-10-444-795B-599/c
; Sequence 599, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 599
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - hTCTP1.5
US-10-444-795B-599

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      343 GGCTGTGATCAAAATGGG 359
      | ||||| ||| |||||
Db      18 GACTGTGATCATATGGG 2

RESULT 441
US-10-444-795B-600
; Sequence 600, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 600
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA - hTCTP1.5
US-10-444-795B-600

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      343 GGCTGTGATCAAAATGGG 359
      | | : | : | : | : | : |
```

```
Db      2 GACUGUGAUCAUUGGG 18

RESULT 442
US-10-735-461-89
; Sequence 89, Application US/10735461
; Publication No. US20050014264A1
; GENERAL INFORMATION:
; APPLICANT: CZECH, Michael P.
; APPLICANT: ZHOU, Qionglin
; APPLICANT: JIANG, Zhen
; TITLE OF INVENTION: METHOD OF INTRODUCING siRNA INTO
; TITLE OF INVENTION: ADIPOCYTES
; FILE REFERENCE: UMY-055
; CURRENT APPLICATION NUMBER: US/10/735,461
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/432427
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-735-461-89

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1097 TACCTGCTCATTGTTT 1113
      |||| | ||||| |||||
Db      3 TACCACCTCATTGTTT 19

RESULT 443
US-10-735-461-90
; Sequence 90, Application US/10735461
; Publication No. US20050014264A1
; GENERAL INFORMATION:
; APPLICANT: CZECH, Michael P.
; APPLICANT: ZHOU, Qionglin
; APPLICANT: JIANG, Zhen
; TITLE OF INVENTION: METHOD OF INTRODUCING siRNA INTO
; TITLE OF INVENTION: ADIPOCYTES
; FILE REFERENCE: UMY-055
; CURRENT APPLICATION NUMBER: US/10/735,461
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/432427
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-735-461-90

Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1097 TACCTGCTCATTGTTT 1113
      |||| | ||||| |||||
Db      2 TACCACCTCATTGTTT 18

RESULT 444
US-10-918-896-222/c
; Sequence 222, Application US/10918896
; Publication No. US20050164966A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
```

```

; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leo
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
; TITLE OF INVENTION: Growth Factor Receptor (IGF-1R) Gene Expression Using Short,
; TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/203 (MBHB03-195-B)
; CURRENT APPLICATION NUMBER: US/10/918,896
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: PCT/US03/05044
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 680
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA se
; US-10-918-896-222

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; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 680
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 499
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-918-896-499

Query Match          1.2%;      Score 13.8;  DB 1;      Length 19;
Best Local Similarity 82.4%;      Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      22  CGGGCCGTGGCAGGAAG 38
        ||||| |:||||| ||
Db      3   CGGGCAGUGGCAGGGAG 19

RESULT 446
US-10-923-329-124/c
; Sequence 124, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/225 (MBHB04-672)
; CURRENT APPLICATION NUMBER: US/10/923,329
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA

```

US-10-923-329-124

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 452 TGGGAGCAGTGGTAGCA 468
:|||||:|||||
Db 19 TGGGAGCAGAGGCAGCA 3

RESULT 447

US-10-923-329-320

; Sequence 320, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
; FILE REFERENCE: 400/225 (MBHB04-672)
; CURRENT APPLICATION NUMBER: US/10/923,329
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 320
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-923-329-320

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 452 TGGGAGCAGTGGTAGCA 468
:|||||:|||||
Db 1 UGGGAGCAGAGGCAGCA 17

RESULT 448

US-09-916-466-24/c

; Sequence 24, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Related

; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-916-466-24

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 380 GCAGGCAATGCAGTC 394
:|||||:|||||
Db 15 GCAGGCAAAGCAGTC 1

RESULT 449

US-10-277-494-24/c

; Sequence 24, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; FILE REFERENCE: MBHB00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-277-494-24

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 380 GCAGGCAATGCAGTC 394
:|||||:|||||
Db 15 GCAGGCAAAGCAGTC 1

RESULT 450

US-10-339-674-1179/c

; Sequence 1179, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1179
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1357006)...(1357020)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1542

US-10-339-674-1179

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1034 GTAAACATCACACCC 1048
 ||||| |||||

Db 15 GTAAACAGCACACCC 1

RESULT 451
US-10-339-674-3197/c
; Sequence 3197, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 3197
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (4276408)...(4276422)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4240
US-10-339-674-3197

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1034 GTAAACATCACACCC 1048
 ||||| |||||

Db 15 GTAAACAGCACACCC 1

RESULT 452
US-10-342-450-3/c
; Sequence 3, Application US/10342450
; Publication No. US20040091880A1
; GENERAL INFORMATION:
; APPLICANT: Wiebusch, Heiko
; APPLICANT: Schmitt-John, Thomas
; APPLICANT: Weidner, Jurgen
; TITLE OF INVENTION: A Method For Direct Genetic Analysis of
; TARGET CELLS BY USING FLUORESCENCE PROBES
; FILE REFERENCE: 3515.1000-000
; CURRENT APPLICATION NUMBER: US/10/342,450
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/EP01/08202
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: EP 00115268.5
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-342-450-3

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 GAAGCAGCCGCGGCC 56
 ||||| |||||

Db 15 GAAGCAGCCGCGGCC 1

RESULT 453
US-10-255-120-466

; Sequence 466, Application US/10255120
; Publication No. US20040091865A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori, strain J99 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/255,120
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 903
; SOFTWARE: Proprietary
; SEQ ID NO 466
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Helicobacter pylori, strain J99 complete genome.
; FEATURE:
; LOCATION: (821578)...(821593)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 703,
US-10-255-120-466

Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTTAGCTGGGA 456
 ||||| |||||

Db 1 TGGTTT TAGCTGGGA 15

RESULT 454
US-10-255-120-890
; Sequence 890, Application US/10255120
; Publication No. US20040091865A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori, strain J99 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/255,120
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 903
; SOFTWARE: Proprietary
; SEQ ID NO 890
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Helicobacter pylori, strain J99 complete genome.
; FEATURE:
; LOCATION: (1618564)...(1618579)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 135,
US-10-255-120-890

Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 442 TGATTTTAGCTGGGA 456
 ||||| |||||

Db 1 TGGTTT TAGCTGGGA 15

RESULT 455
US-09-866-108-2567/c
; Sequence 2567, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108

```
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2567
```

```
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCGCCT 1
```

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RESULT 456
US-09-866-108-6287
; Sequence 6287, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6287
```

```
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 21 CCGGGCCGTGGCAGG 35
Db 3 CCGGGCTGTGGCAGG 17
```

```
RESULT 457
US-09-866-108-6288
; Sequence 6288, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6288
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6288

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
      ||||| |||||
Db      1 CCGGGCTGTGGCAGG 15

RESULT 458
US-09-866-108-6289
; Sequence 6289, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6288
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6288

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
      ||||| |||||
Db      2 CCGGGCTGTGGCAGG 16

RESULT 459
US-09-780-533A-818
; Sequence 818, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 818
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-818

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      49 CCGCGGCCCCAGTTC 63
      ||||| |||||
Db      2 CCGCGGCCCCAGUGC 16

RESULT 460
US-09-780-533A-819
; Sequence 819, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 819
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

US-09-780-533A-819

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCCAGTTC 63
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCGCGGCCCCCAGUGC 15

RESULT 461

US-09-780-533A-2566/c

; Sequence 2566, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2566
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-780-533A-2566

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GTTTTCCTTATTT 429
| | | | | | | | | | | | | | | | | | | | | |
Db 16 GTTTTCCTTATTT 2

RESULT 462

US-09-777-478-949

; Sequence 949, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus

US-09-777-478-1483

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATA 583
::||:|::|:
Db 3 UUAUAUGCCUUUAUA 17

RESULT 464

US-10-060-756A-4244

; Sequence 4244, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177

; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus

US-09-877-478-949

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 570 TTAATACCTTTATAT 584
::||:|::|:
Db 1 UUAUAUGCCUUUAUA 15

RESULT 463

US-09-877-478-1483

; Sequence 1483, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus

US-09-877-478-1483

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATA 583
::||:|::|:
Db 3 UUAUAUGCCUUUAUA 17

RESULT 464

US-10-060-756A-4244

; Sequence 4244, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177

; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4244
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4244

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 675 ATTATGTTACTTGT 689
| | | | | | | | | |
Db 2 ATTATGTTTCTTGT 16

RESULT 465
US-10-060-756A-4245
; Sequence 4245, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4245
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4245

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 675 ATTATGTTACTTGT 689
| | | | | | | | | |
Db 1 ATTATGTTTCTTGT 15

RESULT 466
US-10-339-782-483/c
; Sequence 483, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 483
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-483

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
| | | | | | | | | |
Db 17 ATGTTCACTTGAAGA 3

RESULT 467
US-10-342-902-949
; Sequence 949, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-949

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 570 TTAATACCTTTATAT 584
::||: ||::|:|:
Db 1 UUAAGCCUUAUAU 15

RESULT 468
US-10-342-902-1483
; Sequence 1483, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-1483

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTAATACCTTTATA 583
::||: ||::|:|:
Db 3 UUAAGCCUUAUA 17

RESULT 469
US-10-138-674-4443/C
; Sequence 4443, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4443

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTATTCTCAGCA 640
||||| |||||
Db 15 GTTTATGCTCAGCA 1

RESULT 470
US-10-138-674-9117/C
; Sequence 9117, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9117
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-9117

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 817 AGCAGGCCTCTCATG 831
||||| |||||
Db 15 AGCAGACCTCTCATG 1

RESULT 471
US-10-287-949A-4443/C
; Sequence 4443, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4443

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTATTCTCAGCA 640
||||| |||||
Db 15 GTTTATGCTCAGCA 1

Fri Aug 19 11:00:02 2005

```

; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-949

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      570 TTAATACCTTTATAT 584
Db      1 UUAAGCCUUUAUAU 15

RESULT 474
US-10-669-841-1483
; Sequence 1483, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-1483

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      569 TTTAATACCTTTATA 583
Db      3 UUUAAUGCCUUUAUA 17

RESULT 473
US-10-669-841-949
; Sequence 949, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-9117

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      817 AGCAGGCCTCTCATG 831
Db      15 AGCAGACCTCTCATG 1

RESULT 472
US-10-287-949A-9117/c
; Sequence 9117, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9117
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-9117
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Remaining Prior Application data removed - See File Wrapper or PALM.

```
RESULT 475
US-10-723-361-2567/c
; Sequence 2567, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2567

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACCT 757
Db      15 AGGCAGCTGCCGCT 1
|||||

RESULT 476
US-10-723-361-6287
; Sequence 6287, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2567

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACCT 757
Db      15 AGGCAGCTGCCGCT 1
|||||

RESULT 477
US-10-723-361-6288
; Sequence 6288, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6287

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
Db      3 CCGGGCTGTGGCAGG 17
|||||

RESULT 477
US-10-723-361-6288
; Sequence 6288, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6287
```


Fri Aug 19 11:00:02 2005

```
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6288
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6288

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
      ||||| |||||
Db      2 CCGGGCTGTGGCAGG 16

RESULT 478
US-10-723-361-6289
; Sequence 6289, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6289
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6289

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CCGGGCCGTGGCAGG 35
      ||||| |||||
Db      1 CCGGGCTGTGGCAGG 15

RESULT 479
US-10-712-633-348/c
```

```
; Sequence 348, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-348

Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTATTCTCAGCA 640
      ||||| |||||
Db      15 GTTTATGCTCAGCA 1

RESULT 480
US-10-712-633-4385/c
; Sequence 4385, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACI
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
```

; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4385
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-4385

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 817 AGCAGGCCTCTCATG 831
| | | | | | | | | |
Db 15 AGCAGACCTCTCATG 1

RESULT 481
US-10-494-343-812/c
; Sequence 812, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 812
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-812

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
| | | | | | | | | |
Db 17 TCATTTTCCTTTCAA 3

RESULT 482
US-10-494-343-813/c
; Sequence 813, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 813

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-813

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
| | | | | | | | | |
Db 16 TCATTTTCCTTTCAA 2

RESULT 483
US-10-494-343-814/c
; Sequence 814, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 814
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-814

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
| | | | | | | | | |
Db 15 TCATTTTCCTTTCAA 1

RESULT 484
US-10-890-776A-4244
; Sequence 4244, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761

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; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4244
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4244

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      675 ATTATGTTTCTTGTT 689
Db      2 ATTATGTTTCTTGTT 16

RESULT 485
US-10-890-776A-4245
; Sequence 4245, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4245
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-4245

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      675 ATTATGTTTCTTGTT 689
Db      1 ATTATGTTTCTTGTT 15

RESULT 486
US-10-704-513-258/c
; Sequence 258, Application US/10704513
; Publication No. US20050170500A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: KAMMERER, STEFAN M.
```

```
; APPLICANT: BRAUN, ANDREAS
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4062-UT
; CURRENT APPLICATION NUMBER: US/10/704,513
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 60/489,703
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 60/424,475
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 774
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 258
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
US-10-704-513-258

Query Match          1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      702 TAGTCACGGTGCTCT 716
Db      16 TAGTCACGGTGCTCT 2

RESULT 487
US-09-969-373-3260
; Sequence 3260, Application US/09969373
; Patent No. US2002013852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3260
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3260

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      994 TGTATGCACATGAAA 1008
Db      1 TGGATGCACATGAAA 15

RESULT 488
US-09-816-814-2
; Sequence 2, Application US/09816814
; Publication No. US20030027136A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
```



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; PRIOR APPLICATION NUMBER: US 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: US 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: US 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: US 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: US 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-368-643-43

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 2.8e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      48  GCCGCGGCCCCAGTT 62
      ||||| ||||| |||||
Db      2  GCCGCGGCCCCAGTT 16

RESULT 493
US-10-349-143-5495/c
; Sequence 5495, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5495
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-4677 for SEQ 1561,
; US-10-349-143-5495

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 2.8e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1060 CTTTCCAGTGGCTAA 1074
      ||| ||||| |||||
Db      18  CTTACCAGTGGCTAA 4

RESULT 494
US-10-349-143-5744
; Sequence 5744, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
```

```
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5744
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6557 for SEQ 1810,
; US-10-349-143-5744

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 2.8e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      612 TAAGTAGGAGATGAG 626
      ||||| ||||| |||||
Db      3  TAAGTAAGAGATGAG 17

RESULT 495
US-10-764-238-81
; Sequence 81, Application US/10764238
; Publication No. US20040219616A1
; GENERAL INFORMATION:
; APPLICANT: Eirx Therapeutics Ltd.
; APPLICANT: Seery, Liam
; APPLICANT: Hayes, Ian
; APPLICANT: Murphy, Finbarr
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
; FILE REFERENCE: 8912/2012
; CURRENT APPLICATION NUMBER: US/10/764,238
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/457,533
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: UK 0301566.5
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: QPCR Reverse Primer (Bcl2)
; US-10-764-238-81

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 2.8e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      199 CATCTCCCCCATCCC 213
      ||||| ||||| |||||
Db      3  CATCTCCCGCATCCC 17

RESULT 496
US-10-861-520-43
; Sequence 43, Application US/10861520
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; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-901-484A-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 500
US-09-853-526-372/c
; Sequence 372, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-853-526-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 501
US-10-349-143-4387/c
; Sequence 4387, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
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; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4387
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453,
US-10-349-143-4387
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Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1
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RESULT 502
US-10-349-143-11326
; Sequence 11326, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11326
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-4233 for SEQ 3461, in compleme
US-10-349-143-11326
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Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 CATTTCCTTACAAT 408
Db 4 CATTTCCTTACAAT 18

RESULT 503
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Db 5 GUUUUCCUGUAU 19

RESULT 507

US-10-863-973-799/c

; Sequence 799, Application US/10863973

; Publication No. US2005014333A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Richards, Ivan

; APPLICANT: Polisky, Barry

; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and

; TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering

; TITLE OF INVENTION: Nucleic Acid (siNA)

; FILE REFERENCE: 400/163 (MBHB03-084-D)

; CURRENT APPLICATION NUMBER: US/10/863,973

; CURRENT FILING DATE: 2004-06-09

; PRIOR APPLICATION NUMBER: PCT/US03/04566

; PRIOR FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: PCT/US04/16390

; PRIOR FILING DATE: 2004-05-24

; PRIOR APPLICATION NUMBER: US 10/826,966

; PRIOR FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: US 10/757,803

; PRIOR FILING DATE: 2004-01-14

; PRIOR APPLICATION NUMBER: US 10/720,448

; PRIOR FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: US 10/693,059

; PRIOR FILING DATE: 2003-10-23

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1832

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 799

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-863-973-799

Query Match 1.2%; Score 13.4; DB 1; Length 19;

Best Local Similarity 93.3%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GTTTTCCTTATTT 429

Db 15 GTTTTCCTTGTTT 1

RESULT 508

US-10-923-522-1371

; Sequence 1371, Application US/10923522

; Publication No. US20050159381A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: McSwiggen, James

; APPLICANT: Chowrira, Bharat

; APPLICANT: Beigelman, Leonid

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Chromosome Translocation

; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)

; FILE REFERENCE: 400/192 (MBHB03-026-B)

; CURRENT APPLICATION NUMBER: US/10/923,522

; CURRENT FILING DATE: 2004-08-20

; PRIOR APPLICATION NUMBER: PCT/US 03/05234

QY 958 CTGGACCCAGGACAT 972

Db 5 CUGGACUCAGGACAU 19

RESULT 509

US-10-923-522-1547/c

; Sequence 1547, Application US/10923522

; Publication No. US20050159381A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: McSwiggen, James

; APPLICANT: Chowrira, Bharat

; APPLICANT: Beigelman, Leonid

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Chromosome Translocation

; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)

; FILE REFERENCE: 400/192 (MBHB03-026-B)

; CURRENT APPLICATION NUMBER: US/10/923,522

; CURRENT FILING DATE: 2004-08-20

; PRIOR APPLICATION NUMBER: PCT/US 03/05234

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/439,922

; PRIOR FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: US 60/404,039

; PRIOR FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: PCT/US 04/16390

; PRIOR FILING DATE: 2004-05-24

; PRIOR APPLICATION NUMBER: US 10/826,966

; PRIOR FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: US 10/757,803

; PRIOR FILING DATE: 2004-01-14

; PRIOR APPLICATION NUMBER: US 10/720,448

; PRIOR FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: US 10/693,059

; PRIOR FILING DATE: 2003-10-23

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1779
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1547
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-522-1547

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 958 CTGGACCCAGGACAT 972
Db 15 CTGGACTCAGGACAT 1

RESULT 510
US-10-864-044-66/c
; Sequence 66, Application US/10864044
; Publication No. US20050171040A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfe
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic A
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 04-466-B (400/161)
; CURRENT APPLICATION NUMBER: US/10/864,044
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-864-044-66

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 370 CCTTGTGTTGGCAGG 384
Db 18 CCTTGTGTTGGCAGG 4

RESULT 511
US-10-864-044-166
; Sequence 166, Application US/10864044
; Publication No. US20050171040A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Cholesteryl Ester Transfe
; TITLE OF INVENTION: Protein (CEPT) Gene Expression Using Short Interfering Nucleic ;
; TITLE OF INVENTION: (siNA)
; FILE REFERENCE: 04-466-B (400/161)
; CURRENT APPLICATION NUMBER: US/10/864,044
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target/siNA sense
US-10-864-044-166

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 370 CCTTGTGTTGGCAGG 384
Db 2 CCUUGUUUUGGCAGG 16

Search completed: August 19, 2005, 10:59:40
Job time : 13 secs

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:54:17 ; Search time 6 Seconds
(without alignments)
2.738 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctgcttgccaggtgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 422 seqs, 7374 residues

Total number of hits satisfying chosen parameters: 844

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 471 summaries

Database : issdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 19 | 1.7 | 19 | 1 | US-08-803-346-51 |
| 2 | 18.8 | 1.7 | 25 | 1 | US-09-396-196G-107033 |
| 3 | 18.6 | 1.7 | 25 | 1 | US-09-396-196G-125800 |
| 4 | 18 | 1.6 | 18 | 1 | US-08-803-346-50 |
| 5 | 18 | 1.6 | 18 | 1 | US-08-780-562-30 |
| 6 | 18 | 1.6 | 18 | 1 | US-08-780-562-31 |
| 7 | 17.6 | 1.6 | 25 | 1 | US-09-396-196G-20048 |
| 8 | 16.2 | 1.5 | 21 | 1 | US-08-222-177A-296 |
| 9 | 16.2 | 1.5 | 21 | 1 | US-08-117-952-600 |
| 10 | 15.8 | 1.4 | 20 | 1 | US-08-836-261A-72 |
| 11 | 15.8 | 1.4 | 21 | 1 | US-09-816-814-7 |
| 12 | 15.8 | 1.4 | 22 | 1 | US-09-792-024-382 |
| 13 | 15.4 | 1.4 | 18 | 1 | US-09-422-978-11660 |
| 14 | 15.4 | 1.4 | 19 | 1 | US-09-696-791-3309 |
| 15 | 15.4 | 1.4 | 19 | 1 | PCT-US94-06331A-65 |
| 16 | 15.4 | 1.4 | 20 | 1 | US-08-486-408-14 |
| 17 | 15.4 | 1.4 | 20 | 1 | US-08-975-570-14 |
| 18 | 15.2 | 1.4 | 20 | 1 | US-09-428-584-11 |
| 19 | 15.2 | 1.4 | 20 | 1 | US-09-198-452A-6064 |
| 20 | 15.2 | 1.4 | 20 | 1 | US-09-980-052-219 |
| 21 | 15.2 | 1.4 | 21 | 1 | US-09-657-472-690 |
| 22 | 14.8 | 1.3 | 20 | 1 | US-09-280-799-152 |
| 23 | 14.8 | 1.3 | 20 | 1 | US-09-277-020-16 |
| 24 | 14.8 | 1.3 | 20 | 1 | US-08-875-847B-9 |
| 25 | 14.8 | 1.3 | 20 | 1 | US-09-378-842-9 |
| 26 | 14.8 | 1.3 | 20 | 1 | US-09-858-152B-9 |
| 27 | 14.8 | 1.3 | 21 | 1 | US-09-657-472-1733 |
| 28 | 14.4 | 1.3 | 17 | 1 | US-09-866-108A-2565 |
| 29 | 14.4 | 1.3 | 17 | 1 | US-09-866-108A-2566 |
| 30 | 14.4 | 1.3 | 19 | 1 | US-09-544-398B-588 |
| 31 | 14.4 | 1.3 | 19 | 1 | US-09-696-791-3308 |
| 32 | 14.4 | 1.3 | 19 | 1 | US-09-543-771B-588 |
| 33 | 14.4 | 1.3 | 20 | 1 | US-09-422-978-6795 |

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| C | 34 | 14.4 | 1.3 | 20 | 1 | US-09-198-452A-1803 | Sequence 1803, Ap |
| | 35 | 14.4 | 1.3 | 20 | 1 | US-09-953-318-37 | Sequence 37, Appl |
| C | 36 | 14.4 | 1.3 | 20 | 1 | US-09-917-963-91 | Sequence 91, Appl |
| | 37 | 14.2 | 1.3 | 20 | 1 | US-08-105-483-336 | Sequence 336, App |
| C | 38 | 14.2 | 1.3 | 20 | 1 | US-08-389-067-9 | Sequence 9, Appli |
| | 39 | 14.2 | 1.3 | 20 | 1 | US-08-709-209-336 | Sequence 336, App |
| | 40 | 14.2 | 1.3 | 20 | 1 | US-08-458-101-336 | Sequence 336, App |
| C | 41 | 14.2 | 1.3 | 20 | 1 | US-08-478-178A-86 | Sequence 86, Appl |
| C | 42 | 14.2 | 1.3 | 20 | 1 | US-08-488-177-86 | Sequence 86, Appl |
| C | 43 | 14.2 | 1.3 | 20 | 1 | US-08-634-350-24 | Sequence 24, Appl |
| C | 44 | 14.2 | 1.3 | 20 | 1 | US-08-481-072A-86 | Sequence 86, Appl |
| C | 45 | 14.2 | 1.3 | 20 | 1 | US-08-664-336-86 | Sequence 86, Appl |
| C | 46 | 14.2 | 1.3 | 20 | 1 | US-08-481-066A-86 | Sequence 86, Appl |
| C | 47 | 14.2 | 1.3 | 20 | 1 | US-08-578-615A-94 | Sequence 94, Appl |
| C | 48 | 14.2 | 1.3 | 20 | 1 | US-09-392-580-12 | Sequence 12, Appl |
| C | 49 | 14.2 | 1.3 | 20 | 1 | US-09-433-699-36 | Sequence 36, Appl |
| C | 50 | 14.2 | 1.3 | 20 | 1 | US-08-829-637A-86 | Sequence 86, Appl |
| | 51 | 14.2 | 1.3 | 20 | 1 | US-09-851-520-4 | Sequence 4, Appli |
| | 52 | 14.2 | 1.3 | 20 | 1 | US-09-792-594-57 | Sequence 57, Appl |
| | 53 | 14.2 | 1.3 | 20 | 1 | US-09-668-313A-208 | Sequence 208, App |
| C | 54 | 14.2 | 1.3 | 20 | 1 | US-09-422-978-9409 | Sequence 9409, Ap |
| C | 55 | 14.2 | 1.3 | 20 | 1 | US-10-025-139-86 | Sequence 86, Appl |
| | 56 | 14.2 | 1.3 | 20 | 1 | US-09-198-452A-2125 | Sequence 2125, Ap |
| | 57 | 14.2 | 1.3 | 20 | 1 | US-09-198-452A-4121 | Sequence 4121, Ap |
| | 58 | 14.2 | 1.3 | 20 | 1 | US-09-198-452A-5159 | Sequence 5159, Ap |
| | 59 | 14.2 | 1.3 | 20 | 1 | US-09-198-452A-5166 | Sequence 5166, Ap |
| | 60 | 14.2 | 1.3 | 20 | 1 | US-09-198-452A-6581 | Sequence 6581, Ap |
| | 61 | 14.2 | 1.3 | 20 | 1 | US-10-054-225-12 | Sequence 12, Appl |
| | 62 | 14.2 | 1.3 | 20 | 1 | US-09-771-357-79 | Sequence 79, Appl |
| C | 63 | 14.2 | 1.3 | 20 | 1 | US-09-544-398B-310 | Sequence 310, App |
| C | 64 | 14.2 | 1.3 | 20 | 1 | US-09-543-771B-310 | Sequence 310, App |
| | 65 | 14.2 | 1.3 | 20 | 1 | US-10-059-579A-79 | Sequence 79, Appl |
| C | 66 | 14.2 | 1.3 | 20 | 1 | PCT-US94-07770-94 | Sequence 94, Appl |
| | 67 | 14 | 1.3 | 15 | 1 | US-08-319-492B-460 | Sequence 460, App |
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Fri Aug 19 10:59:59 2005

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ALIGNMENTS

RESULT 1
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; Sequence 51, Application US/08803346
; Patent No. 6281346
; GENERAL INFORMATION:
; APPLICANT: HESS, JOHN W.
; APPLICANT: CASKEY, C. THOMAS
; APPLICANT: LIU, QINGYUN
; APPLICANT: PHILLIPS, MICHAEL SEAN
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,346
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GIESSER, JOANNE M
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19642Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3046
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-803-346-51

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RESULT 2
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; Sequence 107033, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1


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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107033
; LENGTH: 25
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US-09-396-196G-107033

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RESULT 3
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-125800

Query Match      1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      864 GTTGAGTCCATGCTATTAAAGTG 888
Db      1 GCTGACTCATGCTGTTAAAGTG 25

RESULT 4
US-08-803-346-50
; Sequence 50, Application US/08803346
; Patent No. 6281346
; GENERAL INFORMATION:
; APPLICANT: HESS, JOHN W.
; APPLICANT: CASKEY, C. THOMAS
; APPLICANT: LIU, QINGYUN
; APPLICANT: PHILLIPS, MICHAEL SEAN
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,346
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GIESSER, JOANNE M
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19642Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3046
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-803-346-50

Query Match      1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      131 CTTATGCTGGGATGTGCC 148
Db      1 CTTATGCTGGGATGTGCC 18

RESULT 5
US-08-780-562-30/c
; Sequence 30, Application US/08780562
; Patent No. 6541604
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/
; FILING DATE: 01/08/97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:

```


TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-780-562-30

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153
| | | | | | | | | | | | | | | | | |
Db 18 GCTGGGATGTCCTTAGA 1

RESULT 6
US-08-780-562-31
; Sequence 31, Application US/08780562
; Patent No. 6541604
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/97
; PRIOR APPLICATION DATA: 60/
; APPLICATION NUMBER: 60/
; FILING DATE: 01/08/97
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-780-562-31

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCTGGGATGTCCTTAGA 153
| | | | | | | | | | | | | | | | | |

TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-780-562-30

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 957 TCTGGACCCAGGACATTTTGATGA 980
| | | | | | | | | | | | | | | | | |
Db 25 TCTTGACCCAGACACTTTGGTGA 2

RESULT 8
US-08-222-177A-296
; Sequence 296, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 296:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTGCACATG 533
|||||
DB 1 ATCTGTATATATGTGTACCTG 21

RESULT 9
US-08-117-952-600
; Sequence 600, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-117-952-600

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTGCACATG 533
|||||
DB 1 ATCTGTATATATGTGTACCTG 21

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd90p2
US-08-222-177A-296

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTGCACATG 533
|||||
DB 1 ATCTGTATATATGTGTACCTG 21

RESULT 10
US-08-836-261A-72
; Sequence 72, Application US/08836261A
; Patent No. 6221582
; GENERAL INFORMATION:
; APPLICANT: GIESENDORF, BELINDA
; APPLICANT: QUINT, WILHELMUS
; APPLICANT: VAN DOORN, LEENDERT-JAN
; TITLE OF INVENTION: NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF PROKARYOTIC ORGANISMS
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,261A
; FILING DATE: 25 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04264
; FILING DATE: 30 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870171.9
; FILING DATE: 28 Oct 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:005
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-836-261A-72

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 TAGAAATGCAGAATCTGAA 949
|||||
DB 2 TAGCAATGCAGAATCTGCA 20

RESULT 11
US-09-816-814-7/c
; Sequence 7, Application US/09816814
; Patent No. 6818406
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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Fri Aug 19 10:59:59 2005

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; OTHER INFORMATION: primer for PCR
US-09-816-814-7

Query Match      1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 GCCGGAAGCAGCCGCGCC 56
Db 21 GCTGGAAGCAGCCGCGTGGCC 3

RESULT 12
US-09-792-024-382/c
; Sequence 382, Application US/09792024
; Patent No. 6783985
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Targets Discovery
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/09/792,024
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer
US-09-792-024-382

Query Match      1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAA 355
Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 13
US-09-422-978-11660
; Sequence 11660, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11660
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-21246 for SEQ 3795, in complem
US-09-422-978-11660

; OTHER INFORMATION: primer for PCR
US-09-816-814-7

Query Match      1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 TTCAATGGGGCTATTGG 120
Db 2 TTCAATGGGGCTATTGG 18

RESULT 14
US-09-696-791-3309/c
; Sequence 3309, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3309
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cycilin B1 ribozyme binding site
US-09-696-791-3309

Query Match      1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 790 TGTGCTTGGAGAGGCAG 806
Db 18 TGGGCTTGGAGAGGCAG 2

RESULT 15
PCT-US94-06331A-65/c
; Sequence 65, Application PC/TUS9406331A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF FIBROSIS AND
; TITLE OF INVENTION: FIBROUS TISSUE DISEASE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06331A
; FILING DATE: June 2, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; none
```

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; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-584-11

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 TCGGGAGACATGCGGGCGT 81
    ||||| ||||| ||||| |||||
Db 20 TCGGGCAACATGCGGGGTGT 1

RESULT 19
US-09-198-452A-6064/c
; Sequence 6064, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6819
; SEQ ID NO 6064
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6064

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 459 AGTGGTAGCATTATTCTG 478
    ||||| ||||| ||||| |||||
Db 20 AGCGGTAGCAGTTTCTCTG 1

RESULT 20
US-09-980-052-219
; Sequence 219, Application US/09980052
; Patent No. 6670130
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 219

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```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
US-09-980-052-219

Query Match      1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 998 TGCACATGAAAGTTTGAGAA 1017
    ||||| ||||| ||||| |||||
Db 1 TGCACACAAACTTTGAGAA 20

RESULT 21
US-09-657-472-690/c
; Sequence 690, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 690
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-690

Query Match      1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 733 GCAGTCTTGTAGGCAGCTGC 752
    ||||| ||||| ||||| |||||
Db 20 GCAGTCATTAGGCAGCTGC 1

RESULT 22
US-09-280-799-152
; Sequence 152, Application US/09280799
; Patent No. 6136603
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA

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Fri Aug 19 10:59:59 2005

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; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US94-06331A-65

Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1077 CACTTAACCTCTCTGGG 1093
Db 18 CCCTTAACCTCTCTGGG 2

RESULT 16
US-08-486-408-14/c
; Sequence 14, Application US/08486408
; Patent No. 5716846
; GENERAL INFORMATION:
; APPLICANT: Brown, Steven Joel
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Naidu, Yathi M.
; TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
; TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
; TITLE OF INVENTION: mRNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,408
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CBI009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-486-408-14

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-08-486-408-14
```

```

Qy 32 CAGGAAGCCGGAAGCAG 48
Db 18 CAGGAAGCCGGAAGCAG 2

RESULT 17
US-08-975-570-14/c
; Sequence 14, Application US/08975570
; Patent No. 5945336
; GENERAL INFORMATION:
; APPLICANT: Brown, Steven Joel
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Naidu, Yathi M.
; TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
; TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
; TITLE OF INVENTION: mRNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,570
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CBI009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-570-14

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 32 CAGGAAGCCGGAAGCAG 48
Db 18 CAGGAAGCCGGAAGCAG 2

RESULT 18
US-09-428-584-11/c
; Sequence 11, Application US/09428584
; Patent No. 6136604
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF METHIONINE AMINOPEPTIDASE 2 EXPRESSION
; FILE REFERENCE: RTS-0114
; CURRENT APPLICATION NUMBER: US/09/428,584
; CURRENT FILING DATE: 1999-10-27
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-280-799-152

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1050 ACTTCCTTATCTTTCCAG 1067
Db      2 ACTTCCTTACCTTTCTG 19

RESULT 23
US-09-277-020-16
; Sequence 16, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; TITLE OF INVENTION: of mRNA Processing.
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-277-020-16

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1050 ACTTCCTTATCTTTCCAG 1067
Db      2 ACTTCCTTACCTTTCTG 19

RESULT 24
US-08-875-847B-9/c
; Sequence 9, Application US/08875847B
; Patent No. 6255105
; GENERAL INFORMATION:
; APPLICANT: The Government of the United
; APPLICANT: States of America as represented by the
; APPLICANT: Secretary, Department of Health and Human
; APPLICANT: Services; Callahan, Robert; Marchetti,
; APPLICANT: Antonio; Buttitta, Fiamma; Smith, Gilbert H.
; TITLE OF INVENTION: Nucleotide And Deduced
; TITLE OF INVENTION: Amino Acid Sequences Of A New Tumor Gene,
; TITLE OF INVENTION: Int6, And the Use Of Reagents Derived From
; TITLE OF INVENTION: These Sequences In Diagnostic Assays,
; TITLE OF INVENTION: Vaccines, Immunotherapy And Gene Therapy
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; NAME: William S. Feiler
```

```

; SOFTWARE: MS WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,847B
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,998
; FILING DATE: 09-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: William S. Feiler
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4179PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-875-847B-9

Query Match      1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      926 CTTATTAGAAATGCAGAA 943
Db      20 CTAATTAAATGCAGAA 3

RESULT 25
US-09-378-842-9/c
; Sequence 9, Application US/09378842
; Patent No. 6342392
; GENERAL INFORMATION:
; APPLICANT: The Government of the United
; APPLICANT: States of America as represented by the
; APPLICANT: Secretary, Department of Health and Human
; APPLICANT: Services; Callahan, Robert; Marchetti,
; APPLICANT: Antonio; Buttitta, Fiamma; Smith, Gilbert H.
; TITLE OF INVENTION: Nucleotide And Deduced
; TITLE OF INVENTION: Amino Acid Sequences Of A New Tumor Gene,
; TITLE OF INVENTION: Int6, And the Use Of Reagents Derived From
; TITLE OF INVENTION: These Sequences In Diagnostic Assays,
; TITLE OF INVENTION: Vaccines, Immunotherapy And Gene Therapy
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,842
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,847
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: 08/385,998
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: William S. Feiler
```

Fri Aug 19 10:59:59 2005

```

;
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4179PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-378-842-9

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 CTTATTAGAAATGCAGAA 943
Db 20 CTAATTAAAAATGCAGAA 3

RESULT 26
US-09-858-152B-9/c
; Sequence 9, Application US/09858152B
; Patent No. 6737251
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Marchetti, Antonio
; APPLICANT: Buttitta, Fiamma
; APPLICANT: Smith, Gilbert H.
; APPLICANT: Callahan, Robert
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6
; FILE REFERENCE: 4239-59122
; CURRENT APPLICATION NUMBER: US/09/858,152B
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/858,152
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-858-152B-9

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 CTTATTAGAAATGCAGAA 943
Db 20 CTAATTAAAAATGCAGAA 3

RESULT 27
US-09-657-472-1733/c
; Sequence 1733, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
```

```

;
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1733
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-657-472-1733

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTGGCTTGGGCGAGCTGCCC 22
Db 21 CTGCCTGGGGYAGGCTGTCC 2
```

```

RESULT 28
US-09-866-108A-2565/c
; Sequence 2565, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2565
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-866-108A-2565
```

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 89;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
|||||
Db 17 AGGCAGCTGCCGCCTT 2

RESULT 29

US-09-866-108A-2566/c
; Sequence 2566, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2566
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108A-2566

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
|||||
Db 16 AGGCAGCTGCCGCCTT 1

RESULT 30

US-09-544-398B-588
; Sequence 588, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013

; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-588

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTTCT 310
|||||
Db 1 TCGAATTGTTGTCT 16

RESULT 31

US-09-696-791-3308/c
; Sequence 3308, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3308
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cyclin B1 ribozyme binding site
US-09-696-791-3308

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 791 GTGCTTGGAGAGGCAG 806
|||||
Db 19 GGGCTTGGAGAGGCAG 4

RESULT 32

US-09-543-771B-588
; Sequence 588, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13


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; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-543-771B-588

```

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 295 TCGAATTGTTGTTTCT 310
|||
Db 1 TCGAATTGTTGTTGTTCT 16

RESULT 33

US-09-422-978-6795
; Sequence 6795, Application US/09422978
; Patent No. 6537751

```

Query Match          1.3%;      Score 14.4;  DB 1;  Length 20;
Best Local Similarity 93.8%;      Pred. No. 92;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 218 TTCATTGCCAAAGAG 233
 ||| ||||| |||||
Db 5 TTCTTTGCCAAAGAG 20

RESULT 34

US-09-198-452A-1803/c
; Sequence 1803, Application US/09198452A
; Patent No. 6559294

; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1803

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1; Indels

Qy
287 TTCACTACTGGAATTG 302

Dd
19 TTCACTACGGGAATTG 4

RESULT 35

US-09-953-318-37
; Sequence 37, Application US/09953318
; Patent No. 6710174

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 626 GTTTTATTCTCAGCA 641
|||||

p6 4 GTTTTATGCTCAGCA 19

RESULT 36

US-09-917-963-91/c
; Sequence 91, Application US/09917963
; Patent No. 6767739

; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection

QY 130 TCTTATGCTGGCATGT 145
|||
Db 18 TCTTATGCTGGCATGT 3

RESULT 37

```
US-08-105-483-336
; Sequence 336, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,483
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-105-483-336

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 394 CATTTCTCTTACAATTCAA 412
||| ||||| ||||| |||||
Db 1 CATGTTCTCTTCAAGTCAA 19

RESULT 38
US-08-389-067-9/c
; Sequence 9, Application US/08389067
; Patent No. 5714312
; GENERAL INFORMATION:
; APPLICANT: NUNO BARDOSA NOLASCO, Gustavo
; APPLICANT: DE BLAS BEORLEGUI, Carmen
; APPLICANT: BORJA TOME, Maria Jose
; APPLICANT: PONS ASCASO, Fernando
; APPLICANT: TORRES PASCUAL, Vicente
; TITLE OF INVENTION: PROCEDURE FOR THE DETECTION AND
; TITLE OF INVENTION: IDENTIFICATION OF VIRAL AND SUBVIRAL PATHOGENS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
```

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US-08-105-483-336
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,067
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,729
; FILING DATE: 02-JUN-1993
; APPLICATION NUMBER: ES 9201232
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: FA-1849 (613-54)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-389-067-9

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 857 TCTTTGTGTTGTAGTCCAT 875
||||| ||||| ||||| |||||
Db 19 TCTTTGTGTTGTGTCGTCAT 1

RESULT 39
US-08-709-209-336
; Sequence 336, Application US/08709209
; Patent No. 5762938
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,209
; FILING DATE: 21-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,483
; FILING DATE: 12-AUG-1993
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 336:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-336
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 394 CATTTTCCTTACAATTCAA 412
Db 1 CATGTTCCCTTCAAGTCAA 19
RESULT 40
US-08-458-101-336
Sequence 336, Application US/08458101
Patent No. 5766599
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: No. 5766599ton, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 336:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-336

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 394 CATTTTCCTTACAATTCAA 412
Db 1 CATGTTCCCTTCAAGTCAA 19
RESULT 41
US-08-478-178A-86/c
Sequence 86, Application US/08478178A
Patent No. 5882927
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5882927ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,178A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-478-178A-86
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 434 ACAGGAGATGATTTTAGCT 452
Db 19 ACAGAAGAGGATTTTGCT 1
RESULT 42
US-08-488-177-86/c
Sequence 86, Application US/08488177
Patent No. 5885970
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein Kinase C
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:

Kinase C

;; ADDRESSEE: Woodcock Washburn Kurtz
;; ADDRESSEE: Mackiewicz & No. 5885970ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,177
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 852,852
;; FILING DATE: March 16, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul K. Legaard
;; REGISTRATION NUMBER: 38,534
;; REFERENCE/DOCKET NUMBER: ISIS-1995
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 86:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: yes
;; US-08-488-177-86

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
Db 19 AGAGAAGAGGATTTGGCT 1

RESULT 43
US-08-634-350-24/c
; Sequence 24, Application US/08634350
; Patent No. 5911982
; GENERAL INFORMATION:
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: HZ-1 VIRUS PERSISTENCE-ASSOCIATED
; TITLE OF INVENTION: GENE 1(pag1) PROMOTER, USES
; TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING SAME OR PRODUCTS
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,350
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

;; NAME: Lawrence, William F.
;; REGISTRATION NUMBER: 28,029
;; REFERENCE/DOCKET NUMBER: 516450-2008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 840-3333
;; TELEFAX: (212) 840-0712
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-634-350-24

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 566 TTTTAAATACCTTTATAT 584
Db 19 TTGTTAAATACCTTTGTTT 1

RESULT 44
US-08-481-072A-86/c
; Sequence 86, Application US/08481072A
; Patent No. 5916807
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5916807ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,072A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-481-072A-86

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Kinase C

Fri Aug 19 10:59:59 2005

Qy
nb

434 AGAGGAGATGATTTTAGCT 452
19 AGAGAAGAGGGATTTTGGCT 1

RESULT 45

US-08-664-336-86/c
; Sequence 86, Application US/08664336
; Patent No. 5922686
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5922686ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,336
FILING DATE: herewith
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 852,852
 FILING DATE: March 16, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 089,996
 FILING DATE: July 9, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul K. Legaard
 REGISTRATION NUMBER: 38,534
 REFERENCE/DOCKET NUMBER: ISIS-2345
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ANTI-SENSE: yes
 US-08-664-336-86

| | | | | |
|--------------------------|--------|------------------|-----------|------------|
| Query Match | 1.3%; | Score 14.2; | DB 1; | Length 20; |
| Best Local Similarity | 84.2%; | Pred. No. 1e+02; | | |
| Matches 16; Conservative | 0; | Mismatches 3; | Indels 0; | Gaps 0; |

QY 434 AGAGGAGATGATTTTAGCT 452

nb 19 AGAGAAGAGGATTTTGGCT 1

RESULT 46

US-08-481-066A-86/c
; Sequence 86, Application US/08481066A
; Patent No. 5959096
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5959096ris
;

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481, 066A
 FILING DATE: herewith
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 852,852
 FILING DATE: March 16, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Rebecca Ralph Gaumond
 REGISTRATION NUMBER: 35,152
 REFERENCE/DOCKET NUMBER: ISIS-11544
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100

TELEPHONE: (215) 568-3439
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-066A-86

| | | | | |
|-----------------------|--------|------------------|-------|---------------|
| Query Match | 1.3%; | Score 14.2; | DB 1; | Length 20; |
| Best Local Similarity | 84.2%; | Pred. No. 1e+02; | | |
| Matches | 16: | Conservative | 0; | Mismatches 3; |
| | | Indels | 0; | Gaps 0; |

QY
434 AGAGGAGATGATTTTAGCT 452

n6
19 AGAGAAGAGGATTTTGGCT 1

RESULT 47

US-08-578-615A-94/c
; Sequence 94, Application US/08578615A
; Patent No. 6015892
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein KinaseC
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,615A
; FILING DATE: 11-JAN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: 16-MAR-1992
; APPLICATION NUMBER: 08/089,996
; FILING DATE: 09-JUL-1993
; APPLICATION NUMBER: 08/199,779
; FILING DATE: 22-FEB-1994

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1568
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-578-615A-94

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
Db 19 AGAGAAGAGGATTTGGCT 1
||||| ||| ||||| |||

RESULT 48
US-09-392-580-12/c
; Sequence 12, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-580-12

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 426 TATTTGAAGAGGAGATGA 444
Db 20 TATTTCAAGAGAAGATGA 2
||||| ||| ||||| |||

RESULT 49
US-09-433-699-36/c
; Sequence 36; Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; FILE REFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433,699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
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```

US-09-433-699-36

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 800 GAGCAGATAACGCTGAAG 818
Db 19 GAGGAAGATGACTCTGAAG 1
||||| ||| ||||| |||

RESULT 50
US-08-829-637A-86/c
; Sequence 86, Application US/08829637A
; Patent No. 6339066
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Phillip Dan Cook
; APPLICANT: Nicholas Dean
; APPLICANT: Glenn Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES WHICH HAVE
; TITLE OF INVENTION: PHOSPHOROTHIOATE LINKAGES OF HIGH CHIRAL PURITY AND
; TITLE OF INVENTION: WHICH MODULATE ai, aii, , k, n, AND ISOFORMS OF
; TITLE OF INVENTION: PROTEIN KINASE C
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Caldwell (28,937) Woodcock
; ADDRESSEE: Washburn Kurtz Mackiewicz & No. 6339066ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,637A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,066
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,129
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,851
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,569
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/089,996
; FILING DATE: 09-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/058,023
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,007
; FILING DATE: 16-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,760
; FILING DATE: 15-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,852
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00243
; FILING DATE: 11-JAN-1991
; PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: US 07/566,977
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA: US 07/436,358
; APPLICATION NUMBER: US 07/436,358
; FILING DATE: 11-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: ISIS-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-829-637A-86

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTAGCT 452
||| ||| ||| ||| ||| ||| |||
Db 19 AGAGAAGAGGATTTTGCT 1

RESULT 51
US-09-851-520-4
; Sequence 4, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
; FILE REFERENCE: RTS-0241
; CURRENT APPLICATION NUMBER: US/09/851,520
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-851-520-4

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 822 GCCTCTCATGACCCAGGAA 840
||| ||| ||| ||| ||| ||| |||
Db 1 GCCACTCCAGACCCAGGAA 19

RESULT 52
US-09-792-594-57
; Sequence 57, Application US/09792594
; Patent No. 6436706
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL4 EXPRESSION
; FILE REFERENCE: RTS-0209
; CURRENT APPLICATION NUMBER: US/09/792,594
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 57
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-792-594-57

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GGCAGGCTGCCCCGGCCG 28
||| ||| ||| ||| ||| ||| |||
Db 1 GGCAGGCTGCCCCGTCACG 19

RESULT 53
US-09-668-313A-208/c
; Sequence 208, Application US/09668313A
; Patent No. 6503756
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF SYNTAXIN 4 INTERACTING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0127
; CURRENT APPLICATION NUMBER: US/09/668,313A
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 247
; SEQ ID NO 208
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-668-313A-208

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 932 AGAAATGCAGAAATCTGAAG 950
||| ||| ||| ||| ||| ||| |||
Db 19 AGAACTCCAGAAATGTGAAG 1

RESULT 54
US-09-422-978-9409/c
; Sequence 9409, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complem
US-09-422-978-9409

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 427 ATTTGGAAGAGGAGATGAT 445
Db 19 AGTTGGAGGGGAGATGAT 1

RESULT 55
US-10-025-139-86/c
; Sequence 86, Application US/10025139
; Patent No. 6537973
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Holmlund, Jon T.
; APPLICANT: Dorr, F. Andrew
; TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
; FILE REFERENCE: ISIS4954
; CURRENT APPLICATION NUMBER: US/10/025,139
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 08/829,637
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: US 08/478,178
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/089,996
; PRIOR FILING DATE: 1993-07-09
; PRIOR APPLICATION NUMBER: US 07/852,852
; PRIOR FILING DATE: 1992-03-16
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-025-139-86
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTAGCT 452
Db 19 AGAGAAGAGGATTTGGCT 1

RESULT 56
US-09-198-452A-2125
; Sequence 2125, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-2125
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 940 AGAATCTGAAGCCCCACTC 958
Db 1 AGAATCGGAACCCCCACGC 19

RESULT 57
US-09-198-452A-4121
; Sequence 4121, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4121
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 771 GAAACCTTTTGTGGGA 789
Db 1 GAGACCTTTTCTTGGGA 19

RESULT 58
US-09-198-452A-5159
; Sequence 5159, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-5159
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 291 CTACTGGAATTGTTGTTTC 309
Db 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 59
US-09-198-452A-5166
; Sequence 5166, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24

Fri Aug 19 10:59:59 2005

```

; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5166

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      291 CTACTGGGATTTGTTTTC 309
      ||||| ||||| ||||| |||||
Db      2 CTTCTGGAGTCGTGTTTC 20

RESULT 60
US-09-198-452A-6581
; Sequence 6581, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6581
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6581

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      460 GTGGTAGCACTTTATTCTG 478
      ||||| ||||| ||||| |||||
Db      2 GTGGTAGCACTATAACCTG 20

RESULT 61
US-10-054-225-12
; Sequence 12, Application US/10054225
; Patent No. 6623931
; GENERAL INFORMATION:
; APPLICANT: Saint Jude Children's Research Hospital
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Atkinson, Robyn M
; TITLE OF INVENTION: Diagnostic Assay for Antibiotic Tolerance
; FILE REFERENCE: SJ-01-0022
; CURRENT APPLICATION NUMBER: US/10/054,225
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)..(20)
; OTHER INFORMATION: reverse PCR primer sequence about 30 bp downstream of VncS SNP
US-10-054-225-12

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      489 ATTGAATTTCTTAGAACTC 507

; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5166

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      291 CTACTGGGATTTGTTTTC 309
      ||||| ||||| ||||| |||||
Db      2 CTTCTGGAGTCGTGTTTC 20

RESULT 62
US-09-771-357-79
; Sequence 79, Application US/09771357
; Patent No. 6756200
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William
; APPLICANT: DAVIDSON, Nancy
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHUI630
; CURRENT APPLICATION NUMBER: US/09/771,357
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-09-771-357-79

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      149 TTAGAGGATTATGGCGTTT 167
      ||||| ||||| ||||| |||||
Db      1 TTCGAAGTTTATGGCGTTT 19

RESULT 63
US-09-544-398B-310/c
; Sequence 310, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11ql3.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-310

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      882 AAAAGTGTGGCCACACAG 900
      ||||| ||||| ||||| |||||
Db      19 AATATTGTGGCCACACAC 1
```

RESULT 64

US-09-543-771B-310/c
; Sequence 310, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-310

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 882 AAAAGTGTGGCCACAGAC 900
||| ||||| ||||| |||
Db 19 AATATTGTGGCCACAC 1

RESULT 65

US-10-059-579A-79
; Sequence 79, Application US/10059579A
; Patent No. 6835541
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: FACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR sense primer
US-10-059-579A-79

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 149 TTAGAGGATTATGGCGTTT 167
||| ||||| ||||| |||
Db 1 TTCGAAGTTATGGCGTTT 19

RESULT 66

PCT-US94-07770-94/c
; Sequence 94, Application PC/TUS9407770
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett and
; APPLICANT: Russell T. Boggs
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07770
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; APPLICATION NUMBER: 08/089,996
; FILING DATE: July 9, 1993
; APPLICATION NUMBER: 08/199,779
; FILING DATE: February 22, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1546
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
PCT-US94-07770-94

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTTAGCT 452
||| ||| ||| ||| ||| |||
Db 19 AGAGAAGAGGATTTTGCT 1

RESULT 67

US-08-319-492B-460
; Sequence 460, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

iss.res

Fri Aug 19 10:59:59 2005

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
;
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 460:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-319-492B-460

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 6; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 123 TGACTTTTCTTATG 136
Db 1 UGACUUUUUUUAUG 14

RESULT 68
US-09-422-978-5553
; Sequence 5553, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5553
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 460:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-319-492B-460

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 6; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 123 TGACTTTTCTTATG 136
Db 1 UGACUUUUUUUAUG 14

RESULT 68
US-09-422-978-5553
; Sequence 5553, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5553
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18

; OTHER INFORMATION: upstream amplification primer 99-5186 for SEQ 1619,
US-09-422-978-5553

Query Match 1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ATCTCCCCCATCCC 213
Db 5 ATCTCCCCCATCCC 18

RESULT 69
US-09-422-978-4185/c
; Sequence 4185, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,
US-09-422-978-4185

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAAATA 575
Db 19 TGGGTTTTTAAATA 6

RESULT 70
US-09-422-978-5624
; Sequence 5624, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5624
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
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```
;
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-5681 for SEQ 1690,
US-09-422-978-5624

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      324 CTGTTATTCTTGCT 337
Db      4 CTGTTATTCTTGCT 17

RESULT 71
US-09-665-615B-156/c
; Sequence 156, Application US/096665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-665-615B-156

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AGATGAGTTTATT 633
Db      18 AGATGAGTTTATT 5

RESULT 72
US-10-172-911-55
; Sequence 55, Application US/10172911
; Patent No. 6743909
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN12 EXPRESSION
; FILE REFERENCE: PTS-0016
; CURRENT APPLICATION NUMBER: US/10/172,911
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-172-911-55

Query Match      1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 CTGTGATCAATGG 358
```

```
Db      1 CTGTGATCAATGG 14

RESULT 73
US-08-219-842-12/c
; Sequence 12, Application US/08219842
; Patent No. 5565323
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herinstdt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,842
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-219-842-12

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      562 TGGGTTTTTTAATACCT 578
Db      17 TGGTTTTTCTAATACCT 1

RESULT 74
US-08-451-096-12/c
; Sequence 12, Application US/08451096
; Patent No. 5760205
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herinstdt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,096
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-451-096-12

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAATACCT 578
||| ||||| ||||| |||||
Db 17 TGGTTTTTCTAATACCT 1

RESULT 75
US-08-810-599-64/c
; Sequence 64, Application US/08810599
; Patent No. 5976798
; GENERAL INFORMATION:
; APPLICANT: PARKER, W. Davis
; APPLICANT: HERRNSTADT, Corinna
; APPLICANT: GHOSH, Soumitra S.
; APPLICANT: FAHY, Eoin
; TITLE OF INVENTION: Methods for Detecting Mitochondrial Mutations
; TITLE OF INVENTION: Diagnostic for Alzheimer's Disease and Methods for Determining
; TITLE OF INVENTION: of Mitochondrial Nucleic Acid
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,599
; FILING DATE: Concurrent Herewith
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/757,438
; FILING DATE: 27 No. 5976798 1996
; APPLICATION NUMBER: US 08/614,072
; FILING DATE: 12 Mar 1996
; APPLICATION NUMBER: US 08/536,036
; FILING DATE: 29 Sep 1995
; APPLICATION NUMBER: US 08/414,969
; FILING DATE: 31 Mar 1995
; APPLICATION NUMBER: US 08/413,740

FILING DATE: 30 Mar 1995
APPLICATION NUMBER: US 08/410,658
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: US 08/397,808
FILING DATE: 3 Mar 1995
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2105/17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: No
ANTI-SENSE: No
US-08-810-599-64
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAATACCT 578
||| ||||| ||||| |||||
Db 17 TGGTTTTTCTAATACCT 1

RESULT 76
US-08-413-740A-140/c
; Sequence 140, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-413-740A-140

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 77
US-08-413-740A-151/c
; Sequence 151, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO

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; ANTI-SENSE: YES
US-08-413-740A-151

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 78
US-08-413-740A-185/c
; Sequence 185, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-413-740A-185

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

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Fri Aug 19 10:59:59 2005

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RESULT 79
US-08-413-740A-186/c
; Sequence 186, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-413-740A-186

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTTAATACCTT 579
||| ||||| ||||| |||||
Db 17 GGGTTTTTCTAATACCTT 1

RESULT 80
US-08-413-740A-188/c
; Sequence 188, Application US/08413740A
; Patent No. 6171859
; GENERAL INFORMATION:
; APPLICANT: HERRNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT W.
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
```

```
;
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,740A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: 08/413,740
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-413-740A-188

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTTAATACCTT 579
||| ||||| ||||| |||||
Db 17 GGGTTTTTCTAATACCTT 1

RESULT 81
US-09-866-108A-2563/c
; Sequence 2563, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
```

```
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2563

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATG 761
      ||||| ||||| ||||| ||
Db      17 GCAGCTGCCGCCTTCTG 1

RESULT 82
US-09-866-108A-2564/c
; Sequence 2564, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2564/c

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTTATG 761
      ||||| ||||| ||||| ||
Db      17 GCAGCTGCCGCCTTCTG 1

RESULT 82
US-09-866-108A-2564/c
; Sequence 2564, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
```

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; Patent No. 6686188
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2564

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      744 GCAGCTGCCACCTTAT 760
      ||||| ||||| ||||| ||
Db      17 GCAGCTGCCGCCTTCT 1

RESULT 83
US-09-866-108A-6749
; Sequence 6749, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6749

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      836 AGGAAGGCCGGGTGGA 852
      ||||| ||||| ||||| ||
Db      1 AGGAAGGCCGTGGAGGA 17

RESULT 84
PCT-US95-04063-140/c
```


iss.res

Fri Aug 19 10:59:59 2005

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; Sequence 140, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US95-04063-140

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 85
PCT-US95-04063-151/c
; Sequence 151, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US95-04063-140

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 85
PCT-US95-04063-151/c
; Sequence 151, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
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```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; PCT-US95-04063-151

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 86
PCT-US95-04063-185/c
; Sequence 185, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-185

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      562 TGGGTTTTTTTAATACCT 578
Db      17 TGGTTTTTCTAATACCT 1

RESULT 87
PCT-US95-04063-186/c
; Sequence 186, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-186

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      563 GGGTTTTTTTAATACCTT 579
Db      17 GGTTCCTTAATACCTT 1

RESULT 88
PCT-US95-04063-186/c
; Sequence 186, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-186
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PCT-US95-04063-188/c
; Sequence 188, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04063
; FILING DATE: 30-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonham, David B.
; REGISTRATION NUMBER: 34297
; REFERENCE/DOCKET NUMBER: 2105/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04063-188

Query Match      1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      563 GGGTTTTTTTAATACCTT 579
Db      17 GGTTCCTTAATACCTT 1

RESULT 89
US-08-219-842-23/c
; Sequence 23, Application US/08219842
; Patent No. 5565323
; GENERAL INFORMATION:
; APPLICANT: Parker, W. D.
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
; TITLE OF INVENTION: for Alzheimer's Disease
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,842
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-AG 9504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1, "")
; OTHER INFORMATION: /note= "N = fluorescein"
;
US-08-219-842-23

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTAATACCT 578
Db 18 TGGTTTTTCTAATACCT 2

RESULT 91
US-08-634-350-23/c
; Sequence 23, Application US/08634350
; Patent No. 5911982
; GENERAL INFORMATION:
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: H2-1 VIRUS PERSISTENCE-ASSOCIATED
; TITLE OF INVENTION: GENE 1(pag1) PROMOTER, USES
; TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING SAME OR PRODUCTS
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,350
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, William F.
; REGISTRATION NUMBER: 28,029
; REFERENCE/DOCKET NUMBER: 516450-2008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-634-350-23

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 566 TTTTAAATACCTTTAT 582
Db 17 TTGTTAATACCTTTGT 1

RESULT 92
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```
US-09-422-978-4732/c
; Sequence 4732, Application US/094222978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4732
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798,
US-09-422-978-4732
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      905 AGCCTCAACATTTCCTA 921
      ||||| ||||| ||||| ||
Db      17 AGCCTCAGCATTTTCATA 1

RESULT 93
US-09-422-978-6041
; Sequence 6041, Application US/094222978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6041
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-09-422-978-6041
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      942 AATCTGAAGCCCCCACTC 958
      ||||| ||||| ||||| ||
Db      2 AATCTCAACCCCCCACTC 18
```

```
RESULT 94
US-09-422-978-11352/c
; Sequence 11352, Application US/094222978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11352
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-4448 for SEQ 3487, in complem
US-09-422-978-11352
Query Match      1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      204 CCCCCATCCCCCATTC 220
      ||||| ||||| ||||| ||
Db      18 CCTCCATCCCCCATCTC 2

RESULT 95
US-09-696-791-649/c
; Sequence 649, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 649
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk6 ribozyme binding site
US-09-696-791-649
Query Match      1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      603 AAGACTTCATAAGTAGG 619
      ||||| ||||| ||||| ||
Db      19 AACACTTCAGAGTAGG 3

RESULT 96
US-09-696-791-1039/c
```


Db 16 TAGCTGGGAACAGTG 2

RESULT 99

US-08-373-124A-1915/c
; Sequence 1915, Application US/08373124A
; Patent No. 5646042

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627

ADDRESSEE: Lyon & Lyonn
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: word perfect 5.1
?

```

CURRENT REFLECTION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

```

;
; INFORMATION FOR SEQ ID NO: 1915:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 17 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
US-08-373-124A-1915

```

; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4443

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 626 GTTTTATTCTCAGCA 640
Db 15 GTTTATGCTCAGCA 1

RESULT 102
US-09-866-108A-2567/c
; Sequence 2567, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2567

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCGCCT 1

RESULT 103
US-09-866-108A-6287
; Sequence 6287, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6287

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
Db 3 CCGGGCTGTGGCAGG 17

RESULT 104
US-09-866-108A-6288
; Sequence 6288, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6288
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6288

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGCGCGTGGCAGG 35
||||| |||||
Db 2 CCGGCGTGTGGCAGG 16

RESULT 105
US-09-866-108A-6289
; Sequence 6289, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6289
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6289

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGCGCGTGGCAGG 35
||||| |||||
Db 1 CCGGCGTGTGGCAGG 15

RESULT 106
US-09-135-021-41
; Sequence 41, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-021-41

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCCAGTT 62
||||| |||||
Db 2 GCCGCGGCCCCAGTT 16

RESULT 107
US-09-135-020-43
; Sequence 43, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN mink WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068


```

; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-020-43

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 1.4e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      48 GCCGCGGCCCCAGTT 62
Db      2 GCCGCGGCCCCAGTT 16

RESULT 108
US-09-135-010A-43
; Sequence 43, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-010A-43

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 1.4e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      48 GCCGCGGCCCCAGTT 62
Db      2 GCCGCGGCCCCAGTT 16

RESULT 109
US-09-444-871-43
; Sequence 43, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; APPLICANT: Igor
```

```

; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-871-43

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 1.4e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      48 GCCGCGGCCCCAGTT 62
Db      2 GCCGCGGCCCCAGTT 16

RESULT 110
US-09-662-402A-6
; Sequence 6, Application US/09662402A
; Patent No. 6420117
; GENERAL INFORMATION:
; APPLICANT: Wessler, Susan R
; APPLICANT: Casa, Alexandra M
; TITLE OF INVENTION: MINIATURE INVERTED REPEAT TRANSPOSABLE ELEMENTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 235.00230101
; CURRENT APPLICATION NUMBER: US/09/662,402A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/153,812
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer
US-09-662-402A-6

Query Match      1.2%;   Score 13.4;   DB 1;   Length 18;
Best Local Similarity 93.3%;   Pred. No. 1.4e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      909 TCAACATTTCTCTAGA 923
Db      1 TCAACGTTTCTCTAGA 15

RESULT 111
US-09-597-735-43
; Sequence 43, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
```

; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-735-43

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
||||| |||||
Db 2 GCCGCGGCCCCAGTT 16

RESULT 112
US-09-444-295-43
; Sequence 43, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,295
; CURRENT FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-295-43

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
||||| |||||
Db 2 GCCGCGGCCCCAGTT 16

RESULT 113
US-09-597-732-43
; Sequence 43, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-732-43

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
||||| |||||
Db 2 GCCGCGGCCCCAGTT 16

RESULT 114
US-09-422-978-5495/c
; Sequence 5495, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5495
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind

iss.res

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```
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-4677 for SEQ 1561,
US-09-422-978-5495

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1060 CTTTCCAGTGGCTAA 1074
Db 18 CTTACCAGTGGCTAA 4

RESULT 115
US-09-422-978-5744
; Sequence 5744, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5744
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6557 for SEQ 1810,
US-09-422-978-5744

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 TAAGTAGGAGATGAG 626
Db 3 TAAGTAAGAGATGAG 17

RESULT 116
US-09-597-731-43
; Sequence 43, Application US/09597731
; Patent No. 6582913
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,731
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
```

```
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-731-43

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCCGCGGCCCCAGTT 62
Db 2 GCCGCGGCCCCAGTT 16

RESULT 117
US-09-816-814-2
; Sequence 2, Application US/09816814
; Patent No. 6818406
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-816-814-2

Query Match          1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 277 GGCATATTTCTTCAC 291
Db 1 GGCATGTTTCTTCAC 15

RESULT 118
US-09-338-907-372/c
; Sequence 372, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
```

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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-338-907-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 351 TCAAAATGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 119
US-09-218-207-372/c
; Sequence 372, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-218-207-372

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 351 TCAAAATGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 120
US-09-228-302-23
; Sequence 23, Application US/09228302
; Patent No. 6399370
; GENERAL INFORMATION:
; APPLICANT: WILSON, James M
; APPLICANT: GOLDMAN, Mitchell
; APPLICANT: BALS, Robert
; APPLICANT: STOLZENBERG, Ethan D
; APPLICANT: ANDERSON, Mark
; APPLICANT: ZASLOFF, Michael
; APPLICANT: KARI, Prasad
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE OF DEFENSIN
; FILE REFERENCE: 209596.0161/16U2
; CURRENT APPLICATION NUMBER: US/09/228,302
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/023,424
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 60/027,334
```

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; PRIOR FILING DATE: 1996-10-01
; PRIOR APPLICATION NUMBER: US 08/915,011
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Forward Primer
US-09-228-302-23

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 954 CACTCTGGACCCAGG 968
Db 3 CACTCTGGACCCCTGG 17

RESULT 121
US-09-422-978-4387/c
; Sequence 4387, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4387
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453,
US-09-422-978-4387

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 351 TCAAAATGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 122
US-09-422-978-11326
; Sequence 11326, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
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Fri Aug 19 10:59:59 2005

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;
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11326
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-4233 for SEQ 3461, in compleme
US-09-422-978-11326

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      394 CATTTCCTTACAAT 408
      ||||| ||||| |||||
Db      4 CATTGCCTTACAAT 18

RESULT 123
US-09-818-780-80/c
; Sequence 80, Application US/09818780
; Patent No. 6677146
; GENERAL INFORMATION:
; APPLICANT: Mchenry, Charles
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
; FILE REFERENCE: 1794.0030004
; CURRENT APPLICATION NUMBER: US/09/818,780
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,736
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse/antisense ATG primer #P133-A1237
US-09-818-780-80

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      835 CAGGAAGGCCGGGGT 849
      | ||||| ||||| |||||
Db      15 CTGGAAGGCCGGGGT 1

RESULT 124
US-09-696-791-3671
; Sequence 3671, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3671
; LENGTH: 19
; TYPE: DNA
```

```
;
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3671

Query Match          1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      238 CTATGACTCAGATGC 252
      ||||| ||||| |||||
Db      2 CTATCACTCAGATGC 16

RESULT 125
US-08-802-547-12/c
; Sequence 12, Application US/08802547
; Patent No. 5780611
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attilla
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
; TITLE OF INVENTION: COLLAGEN GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,547
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 24129-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816-474-9050
; TELEFAX: 816-474-9057
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; POSITION IN GENOME:
; UNITS: bp
; US-08-802-547-12

Query Match          1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      202 CTCCTCCATCCCCCATTT 219
      ||||| ||||| |||||
Db      18 CTCCTCCCTCCTCCCTTT 1

RESULT 126
US-08-800-751-34/c
```

; Sequence 34, Application US/08800751
; Patent No. 5807730
; GENERAL INFORMATION:
; APPLICANT: ITO, Kiyoshi
; APPLICANT: YAMAKI, Toshifumi
; APPLICANT: ARII, Teruo
; APPLICANT: TSURUOKA, Miyuki
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,751
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-027004
; FILING DATE: 14-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 028022-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; US-08-800-751-34

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 17 CTGCGCGCGCGTGGCAG 34
Db 18 CTGCTCGTGGCGGGCAG 1

RESULT 127
US-08-712-357-12/c
; Sequence 12, Application US/08712357
; Patent No. 5808037
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT
; TITLE OF INVENTION: EXPRESSION OF COLLAGEN GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.

; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,357
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; POSITION IN GENOME:
; UNITS: bp
; US-08-712-357-12

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 202 CTCCTCCCATCCCCCATTT 219
Db 18 CTCCTCCCATCTCTCCCTTT 1

RESULT 128
US-08-525-849C-3
; Sequence 3, Application US/08525849C
; Patent No. 5866411
; GENERAL INFORMATION:
; APPLICANT: Pederson, Finn S
; APPLICANT: Lund, Anders H
; APPLICANT: Lovmand, Jette
; APPLICANT: Jorgensen, Poul
; APPLICANT: Duch, Mogens
; TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
; TITLE OF INVENTION: SYSTEM FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
; TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Building, 310 East Michigan.
; STREET: Avenue
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,849C
; FILING DATE: 08-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: BNRIAS 100

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Fri Aug 19 10:59:59 2005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: tRNA
US-08-525-849C-3
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 192 TCCACGCCATCTCCCCA 209
Db 1 UCCCCGGCAUCCACCA 18
RESULT 129
US-08-749-495A-3
Sequence 3, Application US/08749495A
Patent No. 5886166
GENERAL INFORMATION:
APPLICANT: Pederson, Finn S
APPLICANT: Lund, Anders H
APPLICANT: Lovmand, Jette
APPLICANT: Jorgensen, Poul
APPLICANT: Duch, Mogens
TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
TITLE OF INVENTION: SYSTEM FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Building, 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,495A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/525,849
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: BNRIAS 100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: tRNA
US-08-749-495A-3
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 192 TCCACGCCATCTCCCCA 209
Db 1 UCCCCGGCAUCCACCA 18
RESULT 130
US-08-990-818-34/c
Sequence 34, Application US/08990818
Patent No. 5910432
GENERAL INFORMATION:
APPLICANT: ITO, Kiyoshi
APPLICANT: YAMAKI, Toshifumi
APPLICANT: ARII, Teruo
APPLICANT: TSURUOKA, Miyuki
APPLICANT: NAKAMURA, Takeshi
TITLE OF INVENTION: NOVEL NITRILE HYDRATASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,818
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,751
FILING DATE:
APPLICATION NUMBER: JP 8-027004
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 028022-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-990-818-34
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 CTGCCCGGGCGGTGGCAG 34
Db 18 CTGCTCGTCCGGGGCAG 1
RESULT 131
US-09-205-204-37/c
Sequence 37, Application US/09205204
Patent No. 5958772
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann

APPLICANT: Lex M. Cowbert
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRESS
FILE REFERENCE: RTS-0020
CURRENT APPLICATION NUMBER: US/09/205,204
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 37
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-204-37

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 974 TTGATGAGATCCAAAGGA 991
Db 18 TTGATGAGATTCAAGGTA 1

RESULT 132

US-09-169-078-3
Sequence 3, Application US/09169078
Patent No. 6037172

GENERAL INFORMATION:

APPLICANT: Pederson, Finn S
APPLICANT: Lund, Anders H
APPLICANT: Lovmand, Jette
APPLICANT: Jorgensen, Poul
APPLICANT: Duch, Mogens

TITLE OF INVENTION: A RETROVIRAL VECTOR, A REPLICATION
TITLE OF INVENTION: SYSTEM FOR SAID VECTOR AND AVIAN OR MAMMALIAN CELLS
TITLE OF INVENTION: TRANSFECTED WITH SAID VECTOR
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Building, 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,078

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/525,849

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: BNRIAS 100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
TELEFAX: 616-382-2030

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: tRNA

US-09-169-078-3

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 192 TCCACGCCCATCTCCCCCA 209
Db 1 UCCCCGGCAUCUCCACCA 18

RESULT 133

US-08-434-511-2/c
Sequence 2, Application US/08434511
Patent No. 6057114

GENERAL INFORMATION:

APPLICANT: Akong, Anthony
APPLICANT: Harpold, Michael
APPLICANT: Velicelebi, Gonul
APPLICANT: Brust, Paul

TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY
TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,511
FILING DATE: 04-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/244,985
FILING DATE: 20-JUN-1994
APPLICATION NUMBER: PCT/US92/11090
FILING DATE: 18-DEC-1992
APPLICATION NUMBER: 07/812,254
FILING DATE: 20-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9738
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-434-511-2

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 695 GTTCATGTAGTCACGGTG 712
Db 18 GTTCATGAATTCAGGTG 1

Fri Aug 19 10:59:59 2005

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; CURRENT FILING DATE: 1994-04-18
; EARLIER APPLICATION NUMBER: 07/812,254
; EARLIER FILING DATE: 1991-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for screening of products having
; OTHER INFORMATION: EcoRI site adjacent to initiation codon of human
; OTHER INFORMATION: HM1 coding region
US-08-229-150-2
Query Match      1.2%;   Score 13.2;   DB 1;   Length 18;
Best Local Similarity 83.3%;   Pred. No. 1.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      695 GTTCATGTAGTCACGGTG 712
      ||||| ||||| |||||
Db      18 GTTCATGAATTCAGGTG 1

RESULT 136
US-09-182-145-131
; Sequence 131, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 131
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-18
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-131
Query Match      1.2%;   Score 13.2;   DB 1;   Length 18;
Best Local Similarity 83.3%;   Pred. No. 1.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      897 AGACCAAGAGCCTCAACA 914
      ||||| ||||| |||||
Db      1 AGTCCAAGAGTCTCAGCA 18

RESULT 137
US-09-422-978-5708
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; CURRENT FILING DATE: 1994-04-18
; EARLIER APPLICATION NUMBER: 07/812,254
; EARLIER FILING DATE: 1991-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for screening of products having
; OTHER INFORMATION: EcoRI site adjacent to initiation codon of human
; OTHER INFORMATION: HM1 coding region
US-08-229-150-2
Query Match      1.2%;   Score 13.2;   DB 1;   Length 18;
Best Local Similarity 83.3%;   Pred. No. 1.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      695 GTTCATGTAGTCACGGTG 712
      ||||| ||||| |||||
Db      18 GTTCATGAATTCAGGTG 1

RESULT 136
US-09-182-145-131
; Sequence 131, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 131
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-18
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-131
Query Match      1.2%;   Score 13.2;   DB 1;   Length 18;
Best Local Similarity 83.3%;   Pred. No. 1.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      897 AGACCAAGAGCCTCAACA 914
      ||||| ||||| |||||
Db      1 AGTCCAAGAGTCTCAGCA 18

RESULT 137
US-09-422-978-5708
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; Sequence 5708, Application US/094222978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5708
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6298 for SEQ 1774,
US-09-422-978-5708

Query Match          1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      871  TCCATGCTATTAAAGTG 888
Db      1    TCCATGCTCTTACCAGTG 18
          ||||| ||| ||| |||

RESULT 138
US-09-422-978-9959
; Sequence 9959, Application US/094222978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9959
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-8478 for SEQ 2094, in compleme
US-09-422-978-9959

Query Match          1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      209  ATCCCCCATTTTCATTGCC 226
Db      1    ATCCCCCTCTTTCATTCC 18
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RESULT 139
US-09-533-494A-29/c
; Sequence 29, Application US/095333494A
; Patent No. 6586581
; GENERAL INFORMATION:
; APPLICANT: Bancroft, F. Carter
; APPLICANT: Fliss, Maikiko
; APPLICANT: Taylor, Clelland, Catherine L.
; TITLE OF INVENTION: PROLACTIN REGULATORY ELEMENT BINDING
; FILE REFERENCE: AP31818 070165.0497
; CURRENT APPLICATION NUMBER: US/09/533,494A
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
US-09-533-494A-29

Query Match          1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      279  CATATTTCTTCTACTACTG 296
Db      18  CACATTTCTTCTCTGCTG 1
          || ||||| ||| ||| |||

RESULT 140
US-09-404-912-16/c
; Sequence 16, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
; APPLICANT: John Landers
; APPLICANT: David Houseman
; APPLICANT: Barbara Jordan
; APPLICANT: Alain Charest
; TITLE OF INVENTION: Methods and Products Related to
; TITLE OF INVENTION: Genotyping and DNA Analysis
; FILE REFERENCE: M0656/7045(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/404,912
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,757
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22283
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-16

Query Match          1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      568  TTTTAATACCTTTATATA 585
Db      18  TTTTATACCTTCATAAA 1
          ||||| ||||| ||| |||

RESULT 141
PCT-US91-05625-4/c
; Sequence 4, Application PC/TUS9105625
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael M.
; APPLICANT: Brust, Paul
; TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS FOR DETECTING
```

iss.res

Fri Aug 19 10:59:59 2005

;; TITLE OF INVENTION: AND EVALUATING THE INTRACELLULAR TRANSDUCTION
;; TITLE OF INVENTION: OF AN EXTRACELLULAR SIGNAL
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fitch Even Tabin & Flannery
;; STREET: 135 So. LaSalle Street, Suite 900
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/05625
;; FILING DATE: 19910807
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/563,751
;; FILING DATE: 07-AUG-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 1838-51826
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-552-1311
;; TELEFAX: 619-552-0095
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 7..12
;; OTHER INFORMATION: /function= "EcoRI restriction
;; OTHER INFORMATION: recognition sequence"
;; OTHER INFORMATION: /label= EcoRI
;; PCT-US91-05625-4

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 695 GTTCATGTAGTCACGGTG 712
||||| | | | | | | |
Db 18 GTTCATGAATTCAGGTG 1

RESULT 142
5401629-3/c
; Patent No. 5401629
; APPLICANT: HARPOLD, MICHAEL M.; BRUST, PAUL
; TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS USEFUL
; FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/563,751
; FILING DATE: 07-AUG-1990
; SEQ ID NO: 3:
; LENGTH: 18
; 5401629-3

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 695 GTTCATGTAGTCACGGTG 712
||||| | | | | | | |

Db 18 GTTCATGAATTCAGGTG 1

RESULT 143
US-08-657-884-16/c
; Sequence 16, Application US/08657884
; Patent No. 5858981
; GENERAL INFORMATION:
; APPLICANT: SCHREIBER, ALAN D.
; APPLICANT: PARK, JONG-GU
; TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,884
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 555-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-657-884-16

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGC 79
||||| | | | | | | |
Db 16 AGACATGGCGGC 4

RESULT 144
US-09-158-980-16/c
; Sequence 16, Application US/09158980
; Patent No. 6242427
; GENERAL INFORMATION:
; APPLICANT: SCHREIBER, ALAN D.
; APPLICANT: PARK, JONG-GU
; TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,980
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/657,884
; APPLICATION NUMBER: 08/657,884
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 555-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-158-980-16

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 AGACATGGCGGGC 79
Db 16 AGACATGGCGGGC 4

RESULT 145
US-09-811-492-16/c
; Sequence 16, Application US/09811492
; Patent No. 6638764
; GENERAL INFORMATION:
; APPLICANT: SCHREIBER, ALAN D.
; PARK, JONG-GU
; TITLE OF INVENTION: METHODS OF INHIBITING PHAGOCYTOSIS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/811,492
; FILING DATE: 19-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/657,884
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 555-46
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-811-492-16

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 AGACATGGCGGGC 79
Db 16 AGACATGGCGGGC 4

RESULT 146
US-09-014-065-4/c
; Sequence 4, Application US/09014065
; Patent No. 6033854
; GENERAL INFORMATION:
; APPLICANT: Kurnit, David M.
; APPLICANT: Chiang, Pei-Wen
; APPLICANT: Wang, Chang-Ning J.
; TITLE OF INVENTION: METHOD FOR DETERMINING THE COPY NUMBER OF A NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 06498/004001
; CURRENT APPLICATION NUMBER: US/09/014,065
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 08/434,474
; EARLIER FILING DATE: 1995-05-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-014-065-4

Query Match 1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 746 CAGCTGCCACCTT 758
Db 13 CAGCTGCCACCTT 1

RESULT 147
US-07-988-194A-6
; Sequence 6, Application US/07988194A
; Patent No. 5359046
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Weiss, Arthur
; APPLICANT: Irving, Brian A.
; APPLICANT: Roberts, Margo R.
; APPLICANT: Zsebo, Krisztina
; TITLE OF INVENTION: Chimeric Chains for Receptor
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton &
; ADDRESSEE: Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,194A
```


iss.res

Fri Aug 19 10:59:59 2005

;; FILING DATE: December 9, 1992
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland, Bertram I.
;; REGISTRATION NUMBER: 20015
;; REFERENCE/DOCKET NUMBER: A-55107-1 CELL-0051
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-781-1989
;; TELEFAX: 415-398-3249
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-07-988-194A-6

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AGTTCGGGAGACATGG 74
Db 1 AGTTGGGAGACAGGG 16

RESULT 148
US-08-757-024-750
; Sequence 750, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 750:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-750

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 GGGAGACATGGCGGC 79

Db 1 GGGCGCATGGCGGC 16

RESULT 149
US-08-582-776C-35/c
; Sequence 35, Application US/08582776C
; Patent No. 6077510
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. I.
; APPLICANT: Briese, Thomas
; APPLICANT: Kliche, Stefanie
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Stitz, Lothar
; APPLICANT: Schneemann, Anette
; TITLE OF INVENTION: Borna Disease Viral Sequences,
; TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
; TITLE OF INVENTION: System Diseases
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 865 South Figueroa Street, 29th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017-2576
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS NT
; SOFTWARE: ASCII DOS TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,776C
; FILING DATE: 04-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,822
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,831
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Churchill, Margaret A.
; REGISTRATION NUMBER: 39,944
; REFERENCE/DOCKET NUMBER: 1279-194C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/680-4518
; TELEFAX: 213/892-9200
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-582-776C-35

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 CGGCGGTGGCAGGAA 37
Db 16 CGGCGGTGGCAGGAA 1

RESULT 150
US-08-611-587-16/c
; Sequence 16, Application US/08611587
; Patent No. 6150091
; GENERAL INFORMATION:

APPLICANT: PANDOLFO, MASSIMO
APPLICANT: MONTERMINI, LAURA
APPLICANT: MOLTO, MARIA D.
APPLICANT: Koenig, Michael
APPLICANT: Campuzano, Victoria
APPLICANT: Cossee, Mireille
TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,587
FILING DATE: 03-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Brashers-Macatee, Sarah J.
REGISTRATION NUMBER: 38,087
REFERENCE/DOCKET NUMBER: D-5901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5620
TELEFAX: 713-651-5246
TELEX: 76-2829
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
POSITION IN GENOME:
UNITS: bp
US-08-611-587-16
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 39 CCGGAAGCAGCCGCGG 54
Db 16 CCGGAACAGCCGCGG 1
RESULT 151
US-08-479-737-6
Sequence 6, Application US/08479737
Patent No. 6319494
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J
Weiss, Arthur
Irving, Brian A
Roberts, Margo R
Zeebo, Krisztina
TITLE OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR ASSOCIATED
SIGNAL TRANSDUCTION PATHWAYS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 Lakeside Drive
CITY: Foster City
STATE: California

COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,737
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,405
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralytn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: Cell 5.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-9600
TELEFAX: (415) 358-0803
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-479-737-6
Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 59 AGTTCGGGAGACATGG 74
Db 1 AGTTGGGAGACAGGG 16
RESULT 152
US-08-475-442A-6
Sequence 6, Application US/08475442A
Patent No. 6407221
GENERAL INFORMATION:
APPLICANT: CAPON, DANIEL J
APPLICANT: WEISS, ARTHUR
APPLICANT: IRVING, BRIAN A
APPLICANT: ROBERTS, MARGO R
APPLICANT: ZEEBO, KRISZTINA
TITLE OF INVENTION: CHIMERIC CHAINS FOR
RECEPTOR-ASSOCIATED SIGNAL TRANSDUCTION PATHWAYS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,442A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,405
FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CCTGTTATTCTTGCTC 338
||||| ||| |||||
Db 2 CCTGTTTTCTTGCTC 17

RESULT 155

US-08-390-850-478/c
; Sequence 478, Application US/08390850
; Patent No. 5612215

; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 478:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-390-850-478

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 904 GAGCCTCAACATTTC 919
||||| ||| |||||
Db 16 GAGCCAAACATTTC 1

RESULT 156

US-08-435-634-478/c

; Sequence 478, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 478:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-478

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 904 GAGCCTCAACATTTC 919
||||| ||| |||||
Db 16 GAGCCAAACATTTC 1

RESULT 157

US-08-758-306-65/c
; Sequence 65, Application US/08758306
; Patent No. 5807743

; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH

TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
 NUMBER OF SEQUENCES: 1379
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/758,306
 FILING DATE: December 3, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 212/132
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 65:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-758-306-65

Qy 1073 AAACCACTTAACCTCT 1088
||| ||| ||| ||| |||
pb 17 AAACACCTGAACCTCT 2

RESULT 158
 US-08-758-306-577
 ; Sequence 577, Application US/08758306
 ; Patent No. 5807743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: McSwiggen, James A.
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: TREATMENT OF DISEASES
 ; TITLE OF INVENTION: ASSOCIATED WITH
 ; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
 ; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
 ; NUMBER OF SEQUENCES: 1379
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ;
 ;
 ;

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Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 1.8e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

RESIST 159

US-08-758-306-631/c
; Sequence 631, Application US/08758306
; Patent No. 5807743

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:

ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeg Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 631:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-631

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1073 AAACCACTTAACCTCT 1088
Db 17 AAAGCACTGAACCTCT 2

RESULT 160
US-08-770-234-2
Sequence 2, Application US/08770234
Patent No. 5840556
GENERAL INFORMATION:
APPLICANT: BRIGGS, ROBERT E.
APPLICANT: TATUM, FRED M.
TITLE OF INVENTION: MOLECULAR GENETIC CONSTRUCTION OF
TITLE OF INVENTION: VACCINE STRAINS OF PASTEURRELLACEAE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER AND WITCOFF, LTD.
STREET: 1001 G STREET, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,234
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0295.56516
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508 9100
TELEFAX: 202 508 9299

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pasteurella haemolytica
STRAIN: serotype 1/pd70
US-08-770-234-2

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 323 CCTGTATTCTTGCTC 338

Db 2 CCTGTTTTCCTGCTC 17
RESULT 161
US-08-757-024-731
Sequence 731, Application US/08757024
Patent No. 6025339
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 731:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-731

Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 GGGAGACATGGCGGC 79
Db 2 GGGCGCATGGCGGC 17

RESULT 162
US-08-757-024-749
Sequence 749, Application US/08757024
Patent No. 6025339
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

iss.res

Fri Aug 19 10:59:59 2005

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 749:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-749

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      64 GGGAGACATGGCGGGC 79
      ||||| ||||| |||||
Db      1 GGGCGCATGGCGGGC 16

RESULT 163
US-09-442-143A-40/c
; Sequence 40, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-442-143A-40

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      202 CTCCTCCCATCCCCCAT 217
      ||||| ||||| |||||
Db      16 CTCCTCCCATCCCCCAT 1

RESULT 164
US-09-474-432B-368
; Sequence 368, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
```

```

; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleo
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 368
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-368

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.8e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      12 GCAGGCTGCCCGGGCC 27
      ||||| :|| |||||
Db      2 GCCGGCUGCACGGGCC 17

RESULT 165
US-09-474-432B-578
; Sequence 578, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucle
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-578

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      359 GGAGCCTGCGGCCTTG 374
      ||||| ||||| :||
```

Db 2 GGAGCUGGCGCCUUG 17

RESULT 166

US-09-474-432B-579

; Sequence 579, Application US/09474432B

; Patent No. 6528640

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Belgelman, Leo

; APPLICANT: Burgin, Alex

; APPLICANT: Beaudry, Amber

; APPLICANT: Karpeisky, Alex

; APPLICANT: Adamic, Jasenka

; APPLICANT: Sweedler, David

; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot

; FILE REFERENCE: MBHB00-831-B (247/276)

; CURRENT APPLICATION NUMBER: US/09/474,432B

; CURRENT FILING DATE: 1999-12-19

; PRIOR APPLICATION NUMBER: US 60/064,866

; PRIOR FILING DATE: 1997-11-05

; PRIOR APPLICATION NUMBER: US 60/084,727

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: US 09/186,675

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: US 09/301,511

; PRIOR FILING DATE: 1999-04-28

; NUMBER OF SEQ ID NOS: 1526

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 579

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-474-432B-579

Query Match 1.1%; Score 12.8; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 1.8e+02;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 361 AGCCTGCGGCTTG 376

Db 1 AGCUGCGCCUUG 16

RESULT 167

US-09-371-772B-6170/c

; Sequence 6170, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; FILE REFERENCE: MBHB00,876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6170

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-371-772B-6170

Query Match 1.1%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 288 TCACTACTGGAATTGT 303

Db 17 TCACTTTTGGAAATTGT 2

RESULT 168

US-09-371-772B-6171/c

; Sequence 6171, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R

; FILE REFERENCE: MBHB00,876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6171

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-371-772B-6171

Query Match 1.1%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 288 TCACTACTGGAATTGT 303

Db 16 TCACTTTTGGAAATTGT 1

RESULT 169

US-09-589-560B-3/c

; Sequence 3, Application US/09589560B

; Patent No. 6605451

; GENERAL INFORMATION:

; APPLICANT: Marmaro, Jeffery M.

; APPLICANT: Gerdes, John C.

; TITLE OF INVENTION: Methods and Devices for Multiplexing Amplification Reactions

; FILE REFERENCE: XTR005

; CURRENT APPLICATION NUMBER: US/09/589,560B

; CURRENT FILING DATE: 2000-06-06

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-589-560B-3

Query Match 1.1%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 340 TGTGGCTGTGATCAAA 355

Db 17 TGTGGCTCTGATTAA 2

RESULT 170

Fri Aug 19 10:59:59 2005

```
; ORGANISM: Homo sapiens
US-09-476-387-367

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.8e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 367
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-367

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.8e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      12 GCAGGCTGCCGGGCC 27
      |||:|||||
DB      2 GCCGGCUGCACGGGCC 17

RESULT 171
US-09-476-387-577
; Sequence 577, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-577

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      359 GGAGCCTGGCGCCTTG 374
      ||||| |||||:|
DB      2 GGAGCUGGCGCCUUG 17

RESULT 172
US-09-476-387-578
; Sequence 578, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-578

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.8e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      361 AGCCTGGCGCCTGTG 376
      ||| |||||:|
DB      1 AGCUGGCGCCUUGUG 16

RESULT 173
US-09-827-998-515/c
; Sequence 515, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
```

```
; ORGANISM: Homo sapiens
US-09-476-387-577

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      359 GGAGCCTGGCGCCTTG 374
      ||||| |||||:|
DB      2 GGAGCUGGCGCCUUG 17

RESULT 172
US-09-476-387-578
; Sequence 578, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-578

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.8e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      361 AGCCTGGCGCCTGTG 376
      ||| |||||:|
DB      1 AGCUGGCGCCUUGUG 16

RESULT 173
US-09-827-998-515/c
; Sequence 515, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
```

```
; SEQ ID NO 515
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-515

Query Match          1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 310 TGCCTTTGGATTTCCT 325
Db 17 TTCCCTTTGAATTTCCT 2

RESULT 174
US-09-827-998-516/c
; Sequence 516, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 516
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-516

Query Match          1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 310 TGCCTTTGGATTTCCT 325
Db 16 TTCCCTTTGAATTTCCT 1

RESULT 175
US-09-866-108A-2562/c
; Sequence 2562, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6308
; LENGTH: 17
; TYPE: DNA
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2562
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2562

Query Match          1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 746 CAGCTGCCACCTTATG 761
Db 17 CAGCTGCCGCCTTCTG 2

RESULT 176
US-09-866-108A-6308/c
; Sequence 6308, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6308
; LENGTH: 17
; TYPE: DNA
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Fri Aug 19 10:59:59 2005

; ORGANISM: Homo sapiens
US-09-866-108A-6308
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTGCCCTT 150
Db 17 TGCTGGGAGGTGCCCT 2

RESULT 177
US-09-866-108A-6309/c
; Sequence 6309, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6748
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6748
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 836 AGGAAGGCCGGGTGG 851
Db 2 AGGAAGGCCGTGGAGG 17

RESULT 179
US-09-866-108A-6750
; Sequence 6750, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; ORGANISM: Homo sapiens
US-09-866-108A-6308
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTGCCCTT 150
Db 17 TGCTGGGAGGTGCCCT 2

RESULT 177
US-09-866-108A-6309/c
; Sequence 6309, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6309
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6309
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTGCCCTT 150
Db 16 TGCTGGGAGGTGCCCT 1

RESULT 178
US-09-866-108A-6748
; Sequence 6748, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6750
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6750

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      837 GGAAGCGCGGGTGA 852
Db      1 GGAAGCGCGTGGAGGA 16

RESULT 180
US-09-866-108A-7017/c
; Sequence 7017, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7017
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7017/c

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      837 GGAAGCGCGGGTGA 852
Db      1 GGAAGCGCGTGGAGGA 16

RESULT 180
US-09-866-108A-7017/c
; Sequence 7017, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7017
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7017/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7017

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      743 AGGAGCTGCCACCTT 758
Db      17 AAGCAGCTGCCACCAT 2

RESULT 181
US-09-866-108A-7018/c
; Sequence 7018, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7018
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7018

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      743 AGGAGCTGCCACCTT 758
Db      16 AAGCAGCTGCCACCAT 1

RESULT 182
US-09-866-108A-7967/c
; Sequence 7967, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
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```

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7967
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7967

```

QY 313 CTTTGGATTTCCTGTT 328
|||
pb 17 CTCTGGATTTCCTGTT 2

RESULT 183
US-09-866-108A-7968/c
; Sequence 7968, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666

RESULT 184
US-09-866-108A-8291/c
; Sequence 8291, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8291

```

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8291

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 475 TCTGATTACAGTGCAT 490
Db 17 TCTGACAAACAGTGCAT 2

RESULT 185
US-09-866-108A-8292/c
; Sequence 8292, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8292
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8292

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 475 TCTGATTACAGTGCAT 490
Db 16 TCTGACAAACAGTGCAT 1

RESULT 186
US-09-720-435A-351/c
; Sequence 351, Application US/09720435A
; Patent No. 6803187

```

```

; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease
; TITLE OF INVENTION: gene
; FILE REFERENCE: 11362.0030.PCUS00 INNS:030
; CURRENT APPLICATION NUMBER: US/09/720,435A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/EP99/04317
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 98870143.9
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 351
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Aids-associated retrovirus
US-09-720-435A-351

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 370 CCTGTGTGGCAGGC 385
Db 17 CCTATGTTGACAGGC 2

RESULT 187
US-09-902-563-40/c
; Sequence 40, Application US/09902563
; Patent No. 6805863
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; PRIOR APPLICATION NUMBER: 2002-09-09
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-902-563-40

Query Match      1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 202 CTCCTCCCATCCCCCAT 217
Db 16 CTCCTCCCATGCCCAT 1

RESULT 188
US-09-093-972C-731
; Sequence 731, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury

```

Fri Aug 19 10:59:59 2005

STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 731:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 731:
US-09-093-972C-731
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 GGGAGACATGGCGGC 79
||| |||||
Db 2 GGGCGGCATGGCGGC 17
RESULT 189
US-09-093-972C-749
Sequence 749, Application US/09093972C
Patent No. 6825174
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 749:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 749:
US-09-093-972C-749
Query Match 1.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 GGGAGACATGGCGGC 79
||| |||||
Db 1 GGGCGGCATGGCGGC 16
RESULT 190
US-08-403-634-21
Sequence 21, Application US/08403634
Patent No. 5674748
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: NOVEL HUMAN CYCLIN-DEPENDENT
KINASE-LIKE PROTEINS AND METHODS
OF USING THE SAME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSEE: No. 5674748ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,634
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,575
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100

```

; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-403-634-21

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 792 TGCTTGAGAGGCAGA 807
Db 2 TCCTGGAGAAGCAGA 17

RESULT 191
US-08-468-580-34
; Sequence 34, Application US/08468580
; Patent No. 5824642
; GENERAL INFORMATION:
; APPLICANT: Attie, Kenneth
; APPLICANT: Carlsson, Lena
; APPLICANT: Gesundheit, Neil
; APPLICANT: Goddard, Audrey
; TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,580
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/410452
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224982
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P0884PIC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-468-580-34

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1080 TTAACCTCTCTGGTG 1095
```

```

Db 1 TTAACCTCTGTGGCTG 16

RESULT 192
US-08-816-693A-25/c
; Sequence 25, Application US/08816693A
; Patent No. 5874241
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S
; APPLICANT: Turek, Fred W
; APPLICANT: Pinto, Lawrence H
; TITLE OF INVENTION: Clock Gene and Gene Product
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,693A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5874241thrup, Thomas E
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-816-693A-25

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1048 CAACTTCCTTATCTTT 1063
Db 16 CAACTACCTTATCTGT 1

RESULT 193
US-09-212-771-42/c
; Sequence 42, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-212-771-42
```



```

Query Match      1.1%;      Score 12.8;  DB 1;      Length 18;
Best Local Similarity 87.5%;      Pred. No. 1.8e+02;
Marches 14: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 661 ATTATGTTACTCAAAT 676
|||||
Db 16 ATTATGTTGTTCAAAT 1

RESULT 194
US-09-213-768-39/c
; Sequence 39, Application US/09213768
; Patent No. 5985664
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowsest
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47

```
Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 282 ATTTCTTCACTACTGG 297
||| ||| ||| ||| ||| |||
pb 16 ATTACTTCACTCCTGG 1

| | |
|---|--|
| RESULT 195 | |
| US-09-161-244-74 | |
| ; Sequence 74, Application US/09161244 | |
| ; Patent No. 6004814 | |
| ; GENERAL INFORMATION: | |
| ; APPLICANT: Bennett, C. Frank | |
| ; APPLICANT: Cowser, Lex M. | |
| ; TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION | |
| ; FILE REFERENCE: RTS-0007 | |
| ; CURRENT APPLICATION NUMBER: US/09/161,244 | |
| ; CURRENT FILING DATE: 1998-09-25 | |
| ; NUMBER OF SEQ ID NOS: 91 | |
| ; SEQ ID NO 74 | |
| ; LENGTH: 18 | |
| ; TYPE: DNA | |
| ; ORGANISM: Artificial Sequence | |
| ; FEATURE: | |
| ; OTHER INFORMATION: Antisense Oligonucleotide | |
| US-09-161-244-74 | |

```
Query Match      1.1%;      Score 12.8;  DB 1;   Length 18;
Best Local Similarity 87.5%;
Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 216 ATTTCAATGCCAAAAG 231
|||
ph 1 ATCTCAGTGCCAAAAG 16

RESULT 196
US-09-255-888-35/c
; Sequence 35, Application US/09255888
; Patent No. 6013787
; GENERAL INFORMATION:

```

; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD4 EXPRESSION
; FILE REFERENCE: RTS-0041
; CURRENT APPLICATION NUMBER: US/09/255,888
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-255-888-35

```

```

Query Match          1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred.No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 123 TGACTTTTCTTATGCT 138
| | | | | | | | | |
Dh 18 TCACCTTTTCTTCTGCT 3

RESULT 197
US-08-757-024-711
; Sequence 711, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 711:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-711

| | | | | |
|-----------------------|--------|--------------------|-----------|------------|
| Query Match | 1.1%; | Score 12.8; | DB 1; | Length 18; |
| Best Local Similarity | 87.5%; | Pred. No. 1.8e+02; | | |
| Conservative | 0; | Mismatches 2; | Indels 0; | Gaps 0; |

QY 64 GGGAGACATGGCGGC 79
||| | |||||
ph 3 GGGCGGCATGGCGGC 18

```

RESULT 198
US-08-757-024-730
; Sequence 730, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 730:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-730

```

```

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      64 GGGAGACATGGCGGGC 79
      ||| | ||| ||| |||
Db      2 GGGCGGCATGGCGGGC 17

```

```

RESULT 199
US-08-757-024-748
; Sequence 748, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024

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; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 748:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-748

```

```

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      64 GGGAGACATGGCGGGC 79
      ||| | ||| ||| |||
Db      1 GGGCGGCATGGCGGGC 16

```

```

RESULT 200
US-08-885-291-25/c
; Sequence 25, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A
; EARLIER FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-885-291-25

```

```

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1048 CAACTTCCTTATCTTT 1063
      ||| | ||| ||| |||
Db      16 CAACTACCTTATCTGT 1

```

```

RESULT 201
US-08-913-441B-21
; Sequence 21, Application US/08913441B
; Patent No. 6162612
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; TITLE OF INVENTION: No. 6162612el Human Cyclin-Dependent Kinase-Like Proteins and
; FILE REFERENCE: 8321-76 C11
; CURRENT APPLICATION NUMBER: US/08/913,441B
; CURRENT FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 08/403,634
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/US96/03557

```

iss.res

Fri Aug 19 10:59:59 2005

```

; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-08-913-441B-21
    Query Match          1.1%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 1.8e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      792 TGCTTGGAGAGGAGCA 807
      | ||||| ||||| |||||
Db      2 TCCTTGGAGAGGAGCA 17

RESULT 202
US-08-643-212-56
; Sequence 56, Application US/08643212
; Patent No. 6207640
; GENERAL INFORMATION:
; APPLICANT: Attie, Kenneth
; APPLICANT: Carlsson, Lena
; APPLICANT: Gesundheit, Neil
; APPLICANT: Goddard, Audrey
; TITLE OF INVENTION: Treatment of Partial Growth Hormone
; TITLE OF INVENTION: Insensitivity Syndrome
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,212
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,982
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63292-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-643-212-56
    Query Match          1.1%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 1.8e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1080 TTAACCTCTCTGGTG 1095

; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-08-913-441B-21
    Query Match          1.1%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 1.8e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      792 TGCTTGGAGAGGAGCA 807
      | ||||| ||||| |||||
Db      2 TCCTTGGAGAGGAGCA 17

RESULT 203
US-09-496-672-25/c
; Sequence 25, Application US/09496672
; Patent No. 6291429
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/09/496,672
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/885,291
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 08/816,693
; PRIOR FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-496-672-25
    Query Match          1.1%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 1.8e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1048 CCACTTCCTTATCTT 1063
      ||||| ||||| |||||
Db      16 CCACTACCTTATCTGT 1

RESULT 204
US-09-496-694B-116
; Sequence 116, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 116
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-116
    Query Match          1.1%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 1.8e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      953 CCACTCTGGACCCAGG 968
      ||||| ||||| |||||
Db      1 CCACTCTGGACCCAGG 16

RESULT 205
```

```

US-09-167-109-184
; CURRENT APPLICATION NUMBER: US/09167109
; Sequence 184, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 184
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-184

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      267 GTCGGGAAGTGGCATA 282
Db      2 GTAGGGAAGTGGCATA 17
      |||||
RESULT 206
US-09-506-768-2
; Sequence 2, Application US/09506768
; Patent No. 6448059
; GENERAL INFORMATION:
; APPLICANT: Hou, Ya-Ming
; TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities
; FILE REFERENCE: JEFF-0229
; CURRENT APPLICATION NUMBER: US/09506,768
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/026,094
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: US 08/928,362
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yeast D stem-loop
US-09-506-768-2

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      454 GGAGCAGTGGTAGCAC 469
Db      2 GGCGCAGUGGUAGCGC 17
      |||||
US-09-475-947A-340
; Sequence 340, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
US-09-475-947A-340
; CURRENT APPLICATION NUMBER: US/09475,947A
; Sequence 340, Application US/09475947A
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 184
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-184

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      267 GTCGGGAAGTGGCATA 282
Db      2 GTAGGGAAGTGGCATA 17
      |||||
RESULT 206
US-09-506-768-2
; Sequence 2, Application US/09506768
; Patent No. 6448059
; GENERAL INFORMATION:
; APPLICANT: Hou, Ya-Ming
; TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities
; FILE REFERENCE: JEFF-0229
; CURRENT APPLICATION NUMBER: US/09506,768
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/026,094
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: US 08/928,362
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yeast D stem-loop
US-09-506-768-2

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      454 GGAGCAGTGGTAGCAC 469
Db      2 GGCGCAGUGGUAGCGC 17
      |||||
US-09-475-947A-340
; Sequence 340, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
US-09-475-947A-340
; CURRENT APPLICATION NUMBER: US/09475,947A
; Sequence 340, Application US/09475947A
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 184
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-184

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      267 GTCGGGAAGTGGCATA 282
Db      2 GTAGGGAAGTGGCATA 17
      |||||
RESULT 206
US-09-506-768-2
; Sequence 2, Application US/09506768
; Patent No. 6448059
; GENERAL INFORMATION:
; APPLICANT: Hou, Ya-Ming
; TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities
; FILE REFERENCE: JEFF-0229
; CURRENT APPLICATION NUMBER: US/09506,768
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/026,094
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: US 08/928,362
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yeast D stem-loop
US-09-506-768-2

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      454 GGAGCAGTGGTAGCAC 469
Db      2 GGCGCAGUGGUAGCGC 17
      |||||
US-09-475-947A-340
; Sequence 340, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
US-09-475-947A-340
; CURRENT APPLICATION NUMBER: US/09475,947A
; Sequence 340, Application US/09475947A
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 184
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-184

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      267 GTCGGGAAGTGGCATA 282
Db      2 GTAGGGAAGTGGCATA 17
      |||||
RESULT 206
US-09-506-768-2
; Sequence 2, Application US/09506768
; Patent No. 6448059
; GENERAL INFORMATION:
; APPLICANT: Hou, Ya-Ming
; TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities
; FILE REFERENCE: JEFF-0229
; CURRENT APPLICATION NUMBER: US/09506,768
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/026,094
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: US 08/928,362
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yeast D stem-loop
US-09-506-768-2

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      454 GGAGCAGTGGTAGCAC 469
Db      2 GGCGCAGUGGUAGCGC 17
      |||||
US-09-475-947A-340
; Sequence 340, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
US-09-475-947A-340
; CURRENT APPLICATION NUMBER: US/09475,947A
; Sequence 340, Application US/09475947A
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 184
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-184

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      267 GTCGGGAAGTGGCATA 282
Db      2 GTAGGGAAGTGGCATA 17
      |||||
RESULT 206
US-09-506-768-2
; Sequence 2, Application US/09506768
; Patent No. 6448059
; GENERAL INFORMATION:
; APPLICANT: Hou, Ya-Ming
; TITLE OF INVENTION: Methods And Compositions For Inhibition Of tRNA Activities
; FILE REFERENCE: JEFF-0229
; CURRENT APPLICATION NUMBER: US/09506,768
; CURRENT FILING DATE: 200
```


iss.res

Fri Aug 19 10:59:59 2005

```
US-09-856-662-80
Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      811 CGCTGAAGCAGGCCTCTC 828
      ||| ||| ||| ||| ||| ||| ||| |||
Db      18 CGATGAAGCGGGGCTCYC 1

RESULT 212
US-09-720-435A-349/c
; Sequence 349, Application US/09720435A
; Patent No. 6803187
; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease
; FILE REFERENCE: 11362.0030.PCUS00 INNS:030
; CURRENT APPLICATION NUMBER: US/09/720,435A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/EP99/04317
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 98870143.9
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 349
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Aids-associated retrovirus
US-09-720-435A-349

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      370 CCTTGTGTGGCAGGC 385
      ||| ||| ||| ||| ||| ||| |||
Db      18 CCTTATGTGACAGGC 3

RESULT 213
US-09-571-985C-21
; Sequence 21, Application US/09571985C
; Patent No. 6822080
; GENERAL INFORMATION:
; APPLICANT: Antonio Giordano
; TITLE OF INVENTION: No. 6822080el Human Cyclin-Dependent Kinase-Like
; TITLE OF INVENTION: Proteins and Methods of Using Same
; FILE REFERENCE: 8321-76 D11
; CURRENT APPLICATION NUMBER: US/09/571,985C
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 08/913,441
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 08/403,634
; PRIOR FILING DATE: 1995-03-14
; PRIOR APPLICATION NUMBER: PCT/US96/035557
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-571-985C-21

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-856-662-80/c
; Sequence 80, Application US/09856662
; Patent No. 6790616
; GENERAL INFORMATION:
; APPLICANT: MORIBE, Toyoki et al.
; TITLE OF INVENTION: Method for typing HLA class 1 genes
; FILE REFERENCE: 0032-0261P
; CURRENT APPLICATION NUMBER: US/09/856,662
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: JP P1998-335151
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA probe 134-9
```

```
US-09-856-662-80
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7460
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-49 for SEQ 3526,
US-09-422-978-7460

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      308 TCTGCCTTTGGATTTC 323
      ||| ||| ||| ||| ||| ||| |||
Db      17 TCTGACTGTGGATTTC 2

RESULT 210
US-09-696-791-4204/c
; Sequence 4204, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Hammerhead ribozyme recognition site for cdc 2 kinase
US-09-696-791-4204

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      424 TATATTGGAAGAGGA 439
      ||| ||| ||| ||| ||| ||| |||
Db      17 TATATTGGATGACGA 2

RESULT 211
US-09-856-662-80/c
; Sequence 80, Application US/09856662
; Patent No. 6790616
; GENERAL INFORMATION:
; APPLICANT: MORIBE, Toyoki et al.
; TITLE OF INVENTION: Method for typing HLA class 1 genes
; FILE REFERENCE: 0032-0261P
; CURRENT APPLICATION NUMBER: US/09/856,662
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: JP P1998-335151
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA probe 134-9
```

```

QY      792 TGCTTGAGAGGCGA 807
Db      2 TCCTTGAGAGGCGA 17

RESULT 214
US-09-093-972C-711
; Sequence 711, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 711:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 711:
US-09-093-972C-711

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      64 GGGAGACATGGCGGC 79
Db      3 GGGCGCATGGCGGC 18

RESULT 215
US-09-093-972C-730
; Sequence 730, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:

```

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; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 730:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 730:
US-09-093-972C-730

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      64 GGGAGACATGGCGGC 79
Db      2 GGGCGCATGGCGGC 17

RESULT 216
US-09-093-972C-748
; Sequence 748, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA

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Query Match          1.1%;      Score 12.8;   DB 1;   Length 18;
Best Local Similarity 87.5%;      Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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64 GGGAGACATGGCGGC 79
||| | |||||
1 GGGCGCATGGCGGC 16

```

RESULT 217
US-09-918-186A-116
; Sequence 116, Application US/09918186A
; Patent No. 6838283
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 116
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
;
US-09-918-186A-116

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| | | | | |
|-----------------------|--------------|--------------------|---------------|------------|
| Query Match | 1.1%; | Score 12.8; | DB 1; | Length 18; |
| Best Local Similarity | 87.5%; | Pred. No. 1.8e+02; | | |
| Matches 14; | Conservative | 0; | Mismatches 2; | Indels 0; |
| | | | | Gaps 0; |

QY 953 CCACCTCTGGACCCAGG 968
| | | | | | | | | |
nb 1 CCACCTCTGGGACCAGG 16

RESULT 218
PCT-US95-03731-34
; Sequence 34, Application PC/TUS9503731
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Treatment of Partial Growth Hormone Insensitivity Syndrome
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03731
; FILING DATE:
; CLASSIFICATION:

```

Query Match      1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. NO. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1080 TTAACCTCTCTGGGTG 1095
pb 1 TTAACCTCTGTGGCTG 16

RESULT 219
US-08-785-750-2/c
; Sequence 2, Application US/08785750
; Patent No. 5846528
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
;

STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,355
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-785-750-2

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 740 TGTAGGCAGCTGCC 753
||| ||||| |||||
Db 14 TGCAGGCAGCTGCC 1

RESULT 220
US-08-588-355-1/c
Sequence 1, Application US/08588355
Patent No. 5858351
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KESSLER, PAUL D.
APPLICANT: BYRNE, BARRY J.
APPLICANT: KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,355
FILING DATE: 18-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-588-355-1

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 740 TGTAGGCAGCTGCC 753
||| ||||| |||||
Db 14 TGCAGGCAGCTGCC 1

RESULT 221
US-09-116-780-5/c
Sequence 5, Application US/09116780
Patent No. 5945335
GENERAL INFORMATION:
APPLICANT: Colosi, Peter
TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences
FILE REFERENCE: 2555.2.2
CURRENT APPLICATION NUMBER: US/09/116,780
CURRENT FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 08/745,957
EARLIER FILING DATE: 1996-11-07
EARLIER APPLICATION NUMBER: 60/006,402
EARLIER FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-116-780-5

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 740 TGTAGGCAGCTGCC 753
||| ||||| |||||
Db 14 TGCAGGCAGCTGCC 1

RESULT 222
US-08-812-102-1/c
Sequence 1, Application US/08812102
Patent No. 5952221
GENERAL INFORMATION:
APPLICANT: KURTZMAN, GARY J.
APPLICANT: COLOSI, PETER C.
APPLICANT: YOSHIDA, JUN
APPLICANT: MIZUNO, MASAOKI
APPLICANT: OKADA, HIDEHO
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
TITLE OF INVENTION: TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:


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Qy      740 TGTAGGCAGCTGCC 753
Db      14 TGCAGGCAGCTGCC 1

RESULT 225
US-08-646-789A-13/c
; Sequence 13, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-646-789A-13

Query Match      1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      499 TTAGAACTCATACT 512
Db      14 TTAGAACTCAAACT 1

RESULT 226
US-08-646-789A-83/c
; Sequence 83, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-646-789A-83

Query Match      1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      499 TTAGAACTCATACT 512
Db      14 TTAGAACTCAAACT 1

RESULT 227
US-09-309-042-1/c
; Sequence 1, Application US/09309042
; Patent No. 6211163
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,042
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-309-042-1

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Query Match      1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 740 TGTAGGCAGCTGCC 753
||| ||| ||| ||| |||
pb 14 TGCAGGCAGCTGCC 1

RESULT 228
US-09-205-337-2/c
; Sequence 2, Application US/09205337
; Patent No. 632598
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; .
; .
; .

```
,  
,  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
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CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/205,337
 FILING DATE: 04-Dec-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/785,750
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MCCracken, THOMAS P.
 REGISTRATION NUMBER: 38,548
 REFERENCE/DOCKET NUMBER: 0800-0000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 325-7812
 TELEFAX: (415) 325-7823
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-205-337-2

RESULT 229
US-09-406-362-1/c

Sequence 1, Application US/09406362
Patent No. 6335011
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
KESSLER, PAUL D.
BYRNE, BARRY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/406,362
 FILING DATE: 28-Sep-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/784,757
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MCCracken, Thomas P.
 REGISTRATION NUMBER: 38,548
 REFERENCE/DOCKET NUMBER: 0800-000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 325-7812
 TELEFAX: (415) 325-7823
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-406-362-1

RESULT 230
US-09-755-734-1/c
; Sequence 1, Application US/09755734
; Patent No. 6391858
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.

QY 740 TGTAGGCAGCTGCC 753
|||
pb 14 TGCAGGCAGCTGCC 1

RESULT 229
US-09-406-362-1/c

```
;
;
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/755,734
; FILING DATE: 04-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,355
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-755-734-1

Query Match          1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      740 TGTAGGCAGCTGCC 753
Db      14 TGCAGGCAGCTGCC 1

RESULT 231
US-09-406-363-1/c
; Sequence 1, Application US/09406363
; Patent No. 6482633
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
; RECOMBINANT AAV VIRION PRODUCTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,363
; FILING DATE: 28-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,957
; FILING DATE: 11-Jul-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
```

```
;
;
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-406-363-1

Query Match          1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      740 TGTAGGCAGCTGCC 753
Db      14 TGCAGGCAGCTGCC 1

RESULT 232
US-09-649-890-1/c
; Sequence 1, Application US/09649890
; Patent No. 6531456
; GENERAL INFORMATION:
; APPLICANT: KURTZMAN, GARY J.
; COLOSI, PETER C.
; YOSHIDA, JUN
; MIZUNO, MASAOKI
; OKADA, HIDEHO
; TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
; TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/649,890
; FILING DATE: 28-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,102
; FILING DATE: 05-MAR-1997
; APPLICATION NUMBER: US 60/013,209
; FILING DATE: 06-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-649-890-1

Query Match          1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
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Fri Aug 19 10:59:59 2005

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCAGCTGCC 753
Db 14 TGCAGGCAGCTGCC 1

RESULT 233
US-09-969-204A-1/c
; Sequence 1, Application US/09969204A
; Patent No. 6610290
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS
; VIRIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,204A
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,362
; FILING DATE: 28-Sep-1999
; APPLICATION NUMBER: 08/784,757
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-969-204A-1

Query Match 1.1%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGTAGGCAGCTGCC 753
Db 14 TGCAGGCAGCTGCC 1

RESULT 234
US-08-182-968A-118
; Sequence 118, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
```

```
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-118

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 683 ACTTGTTGGCTGT 696
Db 2 ACUGGUUGGCUGU 15

RESULT 235
US-08-182-968A-119
; Sequence 119, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
```

;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-119

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 683 ACTGTGTTGGCTGT 696
||:|::|||:|:
Db 1 ACUGGUUGGCGUGU 14

RESULT 236
US-08-373-124A-94
; Sequence 94, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327

;
;
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-94

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 294 CTGGAATTGTTGTT 307
|:|||||:|:|:
Db 1 CUGGAUUUGUGCU 14

RESULT 237
US-08-435-628-94
; Sequence 94, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 94:

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Fri Aug 19 10:59:59 2005

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-94

Query Match          1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      294 CTGGAATTGTTGT 307
Db      1 CUGGAUUGUUGCU 14

RESULT 238
US-08-774-306A-118
; Sequence 118, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-118

Query Match          1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      683 ACTTGTTGGCTGT 696
Db      2 ACUGGUUUGGCGU 15

RESULT 239
US-08-774-306A-119
; Sequence 119, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-119

Query Match          1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      683 ACTTGTTGGCTGT 696
Db      1 ACUGGUUUGGCGU 14

RESULT 240
US-08-667-939A-10
; Sequence 10, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LJO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-667-939A-10

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 455 GAGCAGTGGTAGCA 468
|||||
Db 1 GAGCAGTGGCAGCA 14

RESULT 241

US-08-667-939A-21/c
; Sequence 21, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-11 VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-667-939A-21

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 455 GAGCAGTGGTAGCA 468
|||||
Db 15 GAGCAGTGGCAGCA 2

RESULT 242

US-09-284-782-13/c
; Sequence 13, Application US/09284782
; Patent No. 6057111
; GENERAL INFORMATION:
; APPLICANT: ENTERPRISES, LTD., QBI
; APPLICANT: Deiss, Louis P.
; APPLICANT: Yehiely, Fruma
; APPLICANT: Efimova, Elena
; APPLICANT: Vasquez-Iaslop, No. 6057111a C.
; APPLICANT: Einat, Paz
; TITLE OF INVENTION: GENE IDENTIFICATION METHOD
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6057111thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 0168-00022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
US-09-284-782-13

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 841 GGCCGGGGTGGATC 854
|||||
Db 14 GGCCGAGGTGGATC 1

RESULT 243

US-09-064-156A-118
; Sequence 118, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:


```
RESULT 246
US-08-584-040-8484
; Sequence 8484, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8484:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-8484

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATATA 1028
Db 1 GAAGCAUCAGCAUA 14

RESULT 247
US-08-433-123-10
; Sequence 10, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
```

```
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-433-123-10

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 455 GAGCAGTGGTAGCA 468
Db 1 GAGCAGTGGCAGCA 14

RESULT 248
US-08-433-123-21/c
; Sequence 21, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
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Fri Aug 19 10:59:59 2005

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-433-123-21

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 455 GAGCAGTGGTAGCA 468
Db 15 GAGCAGTGGCAGCA 2
|||||:|:|:|

RESULT 249
US-09-371-772B-4138
; Sequence 4138, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4138
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-4138

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
Db 1 GAAGCAUCAGCAUA 14
|||||:|:|:|

RESULT 250
US-09-685-664B-4138
; Sequence 4138, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
```

```
;
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4138
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-4138

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
Db 1 GAAGCAUCAGCAUA 14
|||||:|:|:|

RESULT 251
US-07-696-793A-18
; Sequence 18, Application US/07696793A
; Patent No. 5220004
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/696,793A
; FILING DATE: 19910507
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin R. Kaster
; REGISTRATION NUMBER: 32704
; REFERENCE/DOCKET NUMBER: 2598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3444
; TELEFAX: (415) 658-5239
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-07-696-793A-18

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCAACTTCC 1055
Db 1 CACACCCAGCTTCC 14
|||||:|:|:|

RESULT 252
US-07-977-694-18
; Sequence 18, Application US/07977694
```

Patent No. 5273883
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,694
; FILING DATE: 19921117
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-07-977-694-18

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1042 CACACCCAACTTCC 1055
Db 1 CACACCCAGCTTCC 14

RESULT 253
US-09-479-005A-12/c
; Sequence 12, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBHB00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-479-005A-12

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 387 ATGCAGTCATTTTC 400
Db 14 ATTCAGTCATTTTC 1

RESULT 254
US-09-410-416-19/c
; Sequence 19, Application US/09410416
; Patent No. 6743906
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Wang, Steven Siging
; APPLICANT: Esplin, Edward D.
; APPLICANT: Li, Jia Ling
; APPLICANT: Huang, Liying
; TITLE OF INVENTION: PPP2R1B is a Tumor Suppressor
; FILE REFERENCE: UTSD:574
; CURRENT APPLICATION NUMBER: US/09/410,416
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/102,952
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-410-416-19

Query Match 1.1%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 571 TAATACCTTTATAT 584
Db 14 TAATTCCTTTATAT 1

RESULT 255
US-07-696-793A-19
; Sequence 19, Application US/07696793A
; Patent No. 5220004
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/696,793A
; FILING DATE: 19910507
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

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```

; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin R. Kaster
; REGISTRATION NUMBER: 32704
; REFERENCE/DOCKET NUMBER: 2598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3444
; TELEFAX: (415) 658-5239
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-07-696-793A-19
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCAACTTCC 1055
Db 3 CACACCCAGCTTCC 16

RESULT 256
US-07-696-793A-20
; Sequence 20, Application US/07696793A
; Patent No. 5220004
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/696,793A
; FILING DATE: 19910507
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin R. Kaster
; REGISTRATION NUMBER: 32704
; REFERENCE/DOCKET NUMBER: 2598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3444
; TELEFAX: (415) 658-5239
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-07-696-793A-20
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCAACTTCC 1055
Db 3 CACACCCAGCTTCC 16

RESULT 256
US-07-696-793A-20
; Sequence 20, Application US/07696793A
; Patent No. 5220004
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/696,793A
; FILING DATE: 19910507
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin R. Kaster
; REGISTRATION NUMBER: 32704
; REFERENCE/DOCKET NUMBER: 2598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3444
; TELEFAX: (415) 658-5239
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-07-696-793A-20
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCAACTTCC 1055
Db 1 CACACCCAGCTTCC 14

RESULT 257
US-07-977-694-19
; Sequence 19, Application US/07977694
; Patent No. 5273883
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,694
; FILING DATE: 19921117
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-07-977-694-19
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CACACCCCAACTTCC 1055
Db 3 CACACCCAGCTTCC 16

RESULT 258
US-07-977-694-20
; Sequence 20, Application US/07977694
; Patent No. 5273883
; GENERAL INFORMATION:
; APPLICANT: Saiki, Randall K.
; APPLICANT: Nasarabadi, Shanavaz L.
; TITLE OF INVENTION: Methods and Reagents for G Gamma Globin
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
;
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: WordPerfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,694
; FILING DATE: 19921117
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
;
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
;
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
;
; US-07-977-694-20
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1042 CACACCCAACTTCC 1055
; Db 1 CACACCCAGCTTCC 14
;
; RESULT 259
; US-08-095-726-46/c
; Sequence 46, Application US/08095726
; Patent No. 5530188
;
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huei-Che B
;
; TITLE OF INVENTION: Beta-Carotene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
;
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,726
; FILING DATE: 21-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,566
```

```
;
; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5530188val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
;
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-095-726-46
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 20 CCGGGCCGTGGCA 33
; Db 17 CCGGGCCATGGCA 4
;
; RESULT 260
; US-08-096-043-43/c
; Sequence 43, Application US/08096043
; Patent No. 5530189
;
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huei-Che B
;
; TITLE OF INVENTION: Lycopene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
;
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,043
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,568
; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5530189val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
;
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-096-043-43
;
; Query Match 1.1%; Score 12.4; DB 1; Length 17;
; Best Local Similarity 92.9%; Pred. No. 2.1e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 572:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-572

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 294 CTGGAATTGTTGTT 307
|:|||||:|:|:
Db 2 CUGGAAUUGUUGCU 15

RESULT 264
US-08-373-124A-1611
Sequence 1611, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1611:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1611

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 294 CTGGAATTGTTGTT 307
|:|||||:|:|:
Db 2 CUGGAAUUGUUGCU 15

RESULT 265
US-08-373-124A-1917/c
Sequence 1917, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992


```

; TELEFAX: (312) 655-1501
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-08-096-623A-51

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      20 CCCGGGCGGTGGCA 33
      |||||
Db      17 CCCGGGCCATGGCA 4

RESULT 268
US-08-434-402-55/c
; Sequence 55, Application US/08434402
; Patent No. 5714581
; GENERAL INFORMATION:
; APPLICANT: KUGA, TETSURO
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: SATO, MORIYUKI
; APPLICANT: OKABE, MASAMI
; APPLICANT: MORIMOTO, MAKOTO
; APPLICANT: ITOH, SEIGA
; APPLICANT: YAMASAKI, MOTOO
; APPLICANT: YOKOO, YOSHIHARU
; APPLICANT: YAMAGUCHI, KAZUO
; APPLICANT: YOSHIDA, HAJIME
; APPLICANT: YOSHINORI, KOMATSU
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,402
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306799/86
; FILING DATE: 23-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 51357/88
; FILING DATE: 04-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 80088/88
; FILING DATE: 31-MAR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR
; REGISTRATION NUMBER: 25327
; REFERENCE/DOCKET NUMBER: 249-72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 base pairs
```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-434-402-55

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      835 CAGGAAGCCGGGG 848
      |||||
Db      17 CAGGCAGCCGGGG 4

RESULT 269
US-08-435-634-601/c
; Sequence 601, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 601:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-435-634-601

Query Match      1.1%; Score 12.4; DB 1; Length 17;
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Best Local Similarity 92.9%; Pred. No. 2.1e+02; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CCTTATTAGAAATG 938
| | | | | | | | | |
Db 17 CCTTATCAGAAATG 4

RESULT 270
US-08-783-288-55/c
; Sequence 55, Application US/08783288
; Patent No. 5795968
; GENERAL INFORMATION:

APPLICANT: KUGA, TETSURO
APPLICANT: MIYAJI, HIROMASA
APPLICANT: SATO, MORIYUKI
APPLICANT: OKABE, MASAMI
APPLICANT: MORIMOTO, MAKOTO
APPLICANT: ITOH, SEIGA
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YOKOO, YOSHIHARU
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,288
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,411
FILING DATE: 03-MAY-1995
APPLICATION NUMBER: JP 306799/86
FILING DATE: 23-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 80088/88
FILING DATE: 31-MAR-1988
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "SYNTHETIC DNA"

US-08-783-288-55
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 835 CAGGAAGGCCGGGG 848
| | | | | | | | | |
Db 17 CAGGCAGGCCGGGG 4

RESULT 271
US-08-435-628-572
; Sequence 572, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 572:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-572

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTGTT 307
| : | | | | : | : | :
Db 2 CUGGAUUGUUGCU 15

Fri Aug 19 10:59:59 2005

; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-313-185-35

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1021 TCATCATAGAGAAG 1034
|||||
Db 14 TCATCATAGGAAG 1

RESULT 275
US-08-890-640-55/c
; Sequence 55, Application US/08890640
; Patent No. 5994518
; GENERAL INFORMATION:
; APPLICANT: KUGA, TETSURO
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: SATO, MORIYUKI
; APPLICANT: OKABE, MASAMI
; APPLICANT: MORIMOTO, MAKOTO
; APPLICANT: ITOH, SEIGA
; APPLICANT: YAMASAKI, MOTOO
; APPLICANT: YOKOO, YOSHIHARU
; APPLICANT: YAMAGUCHI, KAZUO
; APPLICANT: YOSHIDA, HAJIME
; APPLICANT: YOSHINORI, KOMATSU
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
;

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,640
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,411
; FILING DATE: 03-MAY-1995
; APPLICATION NUMBER: JP 306799/86
; FILING DATE: 23-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 51357/88
; FILING DATE: 04-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 80088/88
; FILING DATE: 31-MAR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR
; REGISTRATION NUMBER: 25327
; REFERENCE/DOCKET NUMBER: 249-73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
; US-08-890-640-55

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAGGCCGGGG 848
|||||
Db 17 CAGGCAGGCCGGGG 4

RESULT 276
US-09-082-614A-35/c
; Sequence 35, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-082-614A-35

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1021 TCATCATAGAGAAG 1034
Db 14 TCATCATAGGAAG 1

RESULT 277
US-09-306-595C-27
; Sequence 27, Application US/09306595C
; Patent No. 6284506
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/306,595C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 98108210
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of genomic DNA containing MVK gene
; US-09-306-595C-27

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 TGTGTAGTCCATG 876
Db 4 TGCTGTAGTCCATG 17

RESULT 278
US-08-584-040-2568
; Sequence 2568, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
```

```

; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2568:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2568

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGGCTGTTTCATGT 702
Db 1 UUAGCUGUUGAUGU 14

RESULT 279
US-08-584-040-3886
; Sequence 3886, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
```

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3886:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-3886

| | | | | |
|--------------------------|--------|--------------------|-----------|------------|
| Query Match | 1.1%; | Score 12.4; | DB 1; | Length 17; |
| Best Local Similarity | 78.6%; | Pred. No. 2.1e+02; | | |
| Matches 11: Conservative | 2; | Mismatches 1; | Indels 0; | Gaps 0; |

QY 1015 GAAGCATCATCAT 1028
 |||||:| | | |
 2 GAAGCAUCAGCAUA 15

```

RESULT 280
US-09-634-918-1
; Sequence 1, Application US/09634918
; Patent No. 6379931
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Swiderski, Piotr M.
; TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
; FILE REFERENCE: 2124-302
; CURRENT APPLICATION NUMBER: US/09/634,918
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/148,339
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Residues 1-9 are DNA; residues 10-17 are RNA.
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: DNA/RNA ribozyme sequence
; US-09-634-918-1

```

| | | | | |
|--------------------------|--------|--------------------|-----------|------------|
| Query Match | 1.1%; | Score 12.4; | DB 1; | Length 17; |
| Best Local Similarity | 78.6%; | Pred. No. 2.1e+02; | | |
| Matches 11: Conservative | 2; | Mismatches 1; | Indels 0; | Gaps 0; |

Ov 469 CTTATTCTGATTA 482

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|||||:|:|
3 CTTTATTCTUGAUGA 16

Db

RESULT 281
US-09-634-918-3
; Sequence 3, Application US/09634918
; Patent No. 6379931
; GENERAL INFORMATION:
; APPLICANT: Rossi, John J.
; APPLICANT: Swiderski, Piotr M.
; TITLE OF INVENTION: Chimeric DNA/RNA Ribozymes Containing Propanediol
; FILE REFERENCE: 2124-302
; CURRENT APPLICATION NUMBER: US/09/634,918
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/148,339
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Residues 1-9 are DNA; residues 10-17 are RNA.
; OTHER INFORMATION: Residue 10 is cm. Residues 11 and 14 are um.
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: DNA/RNA ribozyme sequence
US-09-634-918-3

```

| | | | | |
|--------------------------|--------|--------------------|-----------|------------|
| Query Match | 1.1%; | Score 12.4; | DB 1; | Length 17; |
| Best Local Similarity | 78.6%; | Pred. No. 2.1e+02; | | |
| Matches 11: Conservative | 2; | Mismatches 1; | Indels 0; | Gaps 0; |

QY 469 CTTTATTCTGATTA 482
|||||:|
pb 3 CTTTATTCUGAUGA 16

```

RESULT 282
US-09-474-432B-475
; Sequence 475, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphat
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 475
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-475

```

```
Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 305 GTTCTGCTTGG 318
Db 3 GUUUUGCCUUUGG 16

RESULT 283
US-09-474-432B-667/c
; Sequence 667, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; PRIOR FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 667
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-667

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGCAGGCTGCCCGG 24
Db 15 GGCAGGCTGTCCGG 2

RESULT 284
US-09-371-772B-1092
; Sequence 1092, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1092
```

```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1092

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGGCTGTTTCATGT 702
Db 1 UUAGCUGUUGCAUGU 14

RESULT 285
US-09-371-772B-1653
; Sequence 1653, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1653
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1653

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
Db 2 GAAGCAUCAGCAUA 15

RESULT 286
US-09-371-772B-5446
; Sequence 5446, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5446
; LENGTH: 17
```



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; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5446

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 689 TTGGCTGTTTCATGT 702
   ::||::||::||:
Db 4 UUAGCUGUUGCAUGU 17

RESULT 287
US-09-371-772B-6259
; Sequence 6259, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6259
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6259

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
   |||||::||::||:
Db 4 GAAGCAUCAGCAUA 17

RESULT 288
US-09-371-772B-6260
; Sequence 6260, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6260
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6260

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
   |||||::||::||:
Db 4 GAAGCAUCAGCAUA 17

RESULT 289
US-09-925-388-27
; Sequence 27, Application US/09925388
; Patent No. 6586202
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/925,388
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of genomic DNA containing MVK gene
US-09-925-388-27

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 TGTGTAGTCCATG 876
   |||||::||::||:
Db 4 TGCTGTAGTCCATG 17

RESULT 290
US-09-476-387-474
; Sequence 474, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6260
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; ORGANISM: Homo sapiens
US-09-371-772B-6260

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1015 GAAGCATCATCATA 1028
   |||||::||::||:
Db 1 GAAGCAUCAGCAUA 14

RESULT 289
US-09-925-388-27
; Sequence 27, Application US/09925388
; Patent No. 6586202
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/925,388
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of genomic DNA containing MVK gene
US-09-925-388-27

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 TGTGTAGTCCATG 876
   |||||::||::||:
Db 4 TGCTGTAGTCCATG 17

RESULT 290
US-09-476-387-474
; Sequence 474, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6260
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 474
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-474

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 305 GTTCTGCTTTGG 318
Db 3 GUUUUGCCUUUGG 16

RESULT 291
US-09-476-387-666/c
; Sequence 666, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MEHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 666
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-666

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGCAGGCTGCCCGG 24
Db 15 GGCAGGCTGTCCGG 2

RESULT 292
US-09-827-998-513/c
; Sequence 513, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
```

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; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 513
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-513

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 312 CCTTTGGATTTTCCT 325
Db 17 CCTTTGAATTTTCCT 4

RESULT 293
US-09-827-998-514/c
; Sequence 514, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 514
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-514

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 312 CCTTTGGATTTTCCT 325
Db 16 CCTTTGAATTTTCCT 3

RESULT 294
US-09-866-108A-1694/c
; Sequence 1694, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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Fri Aug 19 10:59:59 2005

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1694
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-866-108A-1694

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACCTATCTGT 518
      ||||| |||||
Db      17 CTCATACCATCTGT 4

RESULT 295
US-09-866-108A-1695/c
; Sequence 1695, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1694
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-866-108A-1696/c

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACCTATCTGT 518
      ||||| |||||
Db      17 CTCATACCATCTGT 4

RESULT 296
US-09-866-108A-1696/c
; Sequence 1696, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1696
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-866-108A-1696

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACCTATCTGT 518
      ||||| |||||
Db      15 CTCATACCATCTGT 2

RESULT 297
US-09-866-108A-1697/c
```

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; Patent No. 6686188
; SEQ ID NO 1695
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1695

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACCTATCTGT 518
      ||||| |||||
Db      16 CTCATACCATCTGT 3

RESULT 296
US-09-866-108A-1696/c
; Sequence 1696, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1696
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-866-108A-1696

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACCTATCTGT 518
      ||||| |||||
Db      15 CTCATACCATCTGT 2

RESULT 297
US-09-866-108A-1697/c
```

```
; Sequence 1697, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1697
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1697

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACTATCTGT 518
          ||||| |||||
Db      14 CTCATACCATCTGT 1

RESULT 298
US-09-866-108A-2568/c
; Sequence 2568, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2568
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2568

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      743 AGGCAGCTGCCACC 756
          ||||| ||||| ||
Db      14 AGGCAGCTGCCGCC 1

RESULT 299
US-09-866-108A-6286
; Sequence 6286, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
```


; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6286
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6286

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAG 34
| | | | | | | | | | | | | | | | |
Db 4 CCGGGCTGTGGCAG 17

RESULT 300

US-09-866-108A-6290
; Sequence 6290, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 6290

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-6290

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 CCGGGCCGTGGCAG 35
| | | | | | | | | | | | | | | | |
Db 1 CCGGCTGTGGCAG 14

RESULT 301

US-09-866-108A-6310/c
; Sequence 6310, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 6310

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-6310

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 TGCTGGGATGTGCC 148
| | | | | | | | | | | | | | | | |
Db 15 TGCTGGGAGGTGCC 2

RESULT 302

US-09-866-108A-6311/c
; Sequence 6311, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6311
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6311

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      135 TGCTGGGATGTGCC 148
Db      14 TGCTGGGAGGTGCC 1

RESULT 303
US-09-866-108A-7015/c
; Sequence 7015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7016
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7016

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      135 TGCTGGGATGTGCC 148
Db      14 TGCTGGGAGGTGCC 1
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```
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7015
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7015

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTT 758
Db      17 GCAGCTGCCACCAT 4

RESULT 304
US-09-866-108A-7016/c
; Sequence 7016, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7016
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7016

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      745 GCAGCTGCCACCTT 758
Db      16 GCAGCTGCCACCAT 3
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```

RESULT 305
US-09-866-108A-7019/c
; Sequence 7019, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7019
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7019

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACC 756
Db | ||||| |||||
14 AAGCAGCTGCCACC 1

RESULT 306
US-09-866-108A-7020/c
; Sequence 7020, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7019
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7019

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACC 756
Db | ||||| |||||
15 AAGCAGCTGCCACC 2

RESULT 307
US-09-866-108A-7789/c
; Sequence 7789, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7020
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7789
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7789

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 812 GCTGAAGCAGGCCT 825
| | | | | | | | | | | | | | | | | | | | | |
Db 17 GCTGAAGCTGGCCT 4

RESULT 308
US-09-866-108A-7790/c
; Sequence 7790, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7790
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7790

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 812 GCTGAAGCAGGCCT 825
| | | | | | | | | | | | | | | | | | | | | |
Db 16 GCTGAAGCTGGCCT 3

RESULT 309
US-09-866-108A-7791/c
; Sequence 7791, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7791
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7791

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 812 GCTGAAGCAGGCCT 825
| | | | | | | | | | | | | | | | | | | | | |
Db 15 GCTGAAGCTGGCCT 2

RESULT 310
US-09-866-108A-7792/c
; Sequence 7792, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456


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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7792
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7792

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      812 GCTGAAGCAGGCCT 825
Db      14 GCTGAAGCTGGCCT 1

RESULT 311
US-09-866-108A-9275/c
; Sequence 9275, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9276
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9276

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACATCTGT 518
Db      17 CTCATAGTATCTGT 4

RESULT 312
US-09-866-108A-9276/c
; Sequence 9276, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9276
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9276

Query Match          1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      505 CTCATACATCTGT 518
Db      16 CTCATAGTATCTGT 3
```

RESULT 313
US-09-866-108A-9277/c
; Sequence 9277, Application US/098666108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEONICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9277
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9277

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 505 CTCATACTATCTGT 518
||||| |||||
Db 15 CTCATAGTATCTGT 2

RESULT 314
US-09-866-108A-9278/c
; Sequence 9278, Application US/098666108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEONICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9278
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9278

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 505 CTCATACTATCTGT 518
||||| |||||
Db 14 CTCATAGTATCTGT 1

RESULT 315
US-09-404-912-589
; Sequence 589, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
; APPLICANT: John Landers
; APPLICANT: David Houseman
; APPLICANT: Barbara Jordan
; APPLICANT: Alain Charest
; TITLE OF INVENTION: Methods and Products Related to
; TITLE OF INVENTION: Genotyping and DNA Analysis
; FILE REFERENCE: M0656/7045(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/404,912
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,757
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22283
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 589
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-589

Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 450 GCTGGGAGCAGTGG 463
||||| |||||
Db 2 GCTGGGCGCAGTGG 15

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RESULT 316
US-09-155-885A-14
; Sequence 14, Application US/09155885A
; Patent No. 6709812
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-155-885A-14
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 845 GGGGTGGATCCCTC 858
Db 2 GGGGTGGAGCCCTC 15
RESULT 317
US-09-155-885A-33/c
; Sequence 33, Application US/09155885A
; Patent No. 6709812
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-155-885A-33
Query Match 1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 845 GGGGTGGATCCCTC 858
Db 16 GGGGTGGAGCCCTC 3
RESULT 318
US-09-685-664B-1092
; Sequence 1092, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1092
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

```
US-09-685-664B-1092
Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy      689 TTGGCTGTTTCATGT 702
      ::|||::|||:
Db      1 UUAGCUGUUAUGU 14

RESULT 319
US-09-685-664B-1653
; Sequence 1653, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1653
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1653

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1015 GAAGCATCATCATA 1028
      |||||:|||||
Db      2 GAAGCAUCAGCAUA 15

RESULT 320
US-09-993-192A-5/c
; Sequence 5, Application US/09993192A
; Patent No. 6838555
; GENERAL INFORMATION:
; APPLICANT: Korea Research Institute of Bioscience and Biotechnology
; APPLICANT: Dong Kook Pharmaceutical Co.
; APPLICANT: Rhee, Sangki
; APPLICANT: Choi, Euisung
; APPLICANT: Kang, Hyunah
; APPLICANT: Sohn, Junghoon
; APPLICANT: Bae, Junghoon
; APPLICANT: Kim, Moowoong
; APPLICANT: Agaphonov, Michasel
; TITLE OF INVENTION: Hansenua polymorpha mutants and process for the preparation of
; TITLE OF INVENTION: recombinant proteins using the same
; FILE REFERENCE: 4220-116.1 US
; CURRENT APPLICATION NUMBER: US/09/993,192A
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/674,617
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
```

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR primer for S. cerevisiae PRC1 gene
US-09-993-192A-5

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      414 GGTTCCTTCTTATA 427
      |||||:|||||
Db      15 GGTTCCTCCTTATA 2

RESULT 321
5194592-80/c
; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,647
; FILING DATE: 22-DEC-1987
; SEQ ID NO:80:
; LENGTH: 17
5194592-80

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      835 CAGGAAGCCCGGG 848
      |||||:|||||
Db      17 CAGGCAGCCCGGG 4

RESULT 322
5194592-80/c
; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,647
; FILING DATE: 22-DEC-1987
; SEQ ID NO:80:
; LENGTH: 17
5194592-80

Query Match      1.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      835 CAGGAAGCCCGGG 848
      |||||:|||||
Db      17 CAGGCAGCCCGGG 4

RESULT 323
US-08-390-850-479/c
; Sequence 479, Application US/08390850
```


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Fri Aug 19 10:59:59 2005

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; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-390-850-479

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 902 AAGAGCCTCAACATTTC 918
Db 17 ATGAGCCAAACATTTC 1

RESULT 324
US-08-390-850-480/c
; Sequence 480, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-390-850-480

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 901 CAAGAGCCTCAACATTT 917
Db 17 CATGAGCCAAACATTT 1

RESULT 325
US-08-373-124A-456/c
; Sequence 456, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible

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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 456:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-456

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 598 TTAAGAAAGACTTCATAA 614
|||||
Db 17 TTAAGAAAGAAATCTATAA 1

RESULT 326
US-08-373-124A-458/c
Sequence 458, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 458:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-458
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 597 TTAAGAAAGACTTCATA 613
|||||
Db 17 TTAAGAAAGAAATCTATA 1

RESULT 327
US-08-373-124A-504
Sequence 504, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 504:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-373-124A-504
;
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTTCCTAGACC 926
Db 1 CACCAUUUCAUAGAGAC 17

RESULT 328
US-08-373-124A-716
; Sequence 716, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-373-124A-716
;
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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;
; TOPOLOGY: linear
;
US-08-373-124A-716
;
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 855 CCTCTTGTGTGTGTAGT 871
Db 1 CCUAUUUUUGUUGUGGU 17

RESULT 329
US-08-373-124A-1341/c
; Sequence 1341, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1341:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-373-124A-1341
;
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 4 TGGCTTGGCAGGCTGC 20
||||| ||||| |
```

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Db      17 TGGCTTTGGAAGGCTTC 1

RESULT 330
US-08-373-124A-1559
; Sequence 1559, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1559:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-1559

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      499 TTAGAACTCATCTATC 515
Db      1 UUAGACUCCAGCUAUC 17

RESULT 331
US-08-373-124A-2393
; Sequence 2393, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.

```

```

; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-2393

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      910 CAACATTTCTAGAGCC 926
Db      1 CACCAUUUCAUAGAGAC 17

RESULT 332
US-08-373-124A-2437
; Sequence 2437, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```


iss.res

Fri Aug 19 10:59:59 2005

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2437:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-2437

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 546 ATGAATTTTATATGCT 562
| | | | | : | | : | : | : | :
Db 1 AAGAAAUUAAUAUGGU 17

RESULT 333
US-08-373-124A-2563
; Sequence 2563, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2563:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-2563

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 499 TTAGAACTCATACTATC 515
: | | | | | : | | : | : | : | :
Db 1 UUAGAACUCCAGCUAUC 17

RESULT 334
US-08-200-232-5
; Sequence 5, Application US/08200232
; Patent No. 5721349
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,232
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-232-5

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      839 AAGCCCGGGTGGATCC 855
Db      1 AAGGCTGGTGTGGATAC 17
      ||||| ||||| ||||| |

RESULT 335
US-08-435-634-479/c
; Sequence 479, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-479
```

```

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      902 AAGAGCCTCAACATTT 918
Db      17 ATGAGCCAAACATTT 1
      ||||| ||||| ||||| |

RESULT 336
US-08-435-634-480/c
; Sequence 480, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-480

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      901 CAAGAGCCTCAACATTT 917
Db      17 CATGAGCCAAACATTT 1
      ||||| ||||| ||||| |
```

RESULT 337
US-07-936-421-22/c
; Sequence 22, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/936,421
; FILING DATE: 19920826
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-936-421-22
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 361 AGCCTGCGGCCTTGCT 377
Db 17 AGCCTGCAGCTTTGTTT 1
RESULT 338
US-08-435-628-456/c
; Sequence 456, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 456:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-456
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 598 TAAGAAAGACTTCATAA 614
Db 17 TAAGAAAGAACTCTATAA 1
RESULT 339
US-08-435-628-458/c
; Sequence 458, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California

; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-458

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 597 TTAAGAAAGACTTCATA 613
Db 17 TTAAGAAAGATCTATA 1

RESULT 340
US-08-435-628-504
; Sequence 504, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 504:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-504

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTCTAGAGCC 926
Db 1 CACCAUUUCAUAGAGAC 17

RESULT 341
US-08-435-628-716
; Sequence 716, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514


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; PRIOR APPLICATION DATA: 08/373,124
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-435-628-716

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 29.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 855 CCTCTTTGTGTGTAGT 871
Db 1 CCUAUUUUUGUGUGGU 17

RESULT 342
US-08-435-628-1341/c
; Sequence 1341, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943

```

```

; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1341:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-435-628-1341

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGGCTTGGGCAGGCTGC 20
Db 17 TGGCTTTGGAAGGCTTC 1

RESULT 343
US-08-435-628-1559
; Sequence 1559, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1559:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1559

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 499 TTGAAGCTCATCTATC 515
Db 1 UUAGAACUCCAGCUAUC 17

RESULT 344
US-08-435-628-2393
; Sequence 2393, Application US/084355628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
```

```
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-2393

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTCTAGAGCC 926
Db 1 CACCAUUUCAUAGAGAC 17

RESULT 345
US-08-435-628-2437
; Sequence 2437, Application US/084355628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-283

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTCCTAGAGCC 926
|||:|:|:|
Db 1 CAACAUCUCCGAAGCC 17

RESULT 349
US-08-985-162-337
; Sequence 337, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-283

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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 337:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-337

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCCCATCC 212
||:|:|:|
Db 1 CGAGAUCUCCUCCAUCC 17

RESULT 350
US-08-985-162-631/c
; Sequence 631, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 337:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-337

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; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 631:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-631

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 613 AAGTAGGAGATGAGTTT 629
|| ||||| |||||
Db 17 AATTAGGAGATACGTTT 1

RESULT 351
US-08-985-162-653
; Sequence 653, Application US/089885162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 653:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-653

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 654 AATTAGATTATGTTAC 670
|| :|| :|:|
Db 1 AAUAGUUUGUACU 17

RESULT 352
US-08-985-162-654
; Sequence 654, Application US/089885162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 654:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-654

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.3e+02;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 655 ATTAGATTATGTTACT 671
| :|| :|:|
Db 1 AAUAGUUUGUACU 17

RESULT 353
US-08-988-706-45
; Sequence 45, Application US/08988706
; Patent No. 6083698
; GENERAL INFORMATION:

```
; APPLICANT: OLSEN, Sheri J.
; APPLICANT: ANGELLY, Tracy S.
; APPLICANT: LAWRENCE, Tammy
; APPLICANT: LESCALLETT, Jennifer L.
; APPLICANT: MURPHY, Patricia D.
; APPLICANT: ALLEN, Antonette P.
; APPLICANT: THRUBER, Denise B.
; APPLICANT: WHITE, Marga B.
; APPLICANT: ZENG, Bin
; APPLICANT: SADZEWICZ, Lisa K.
; TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oncormed, Inc.
; STREET: 205 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,706
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TARCZA, John E.
; REGISTRATION NUMBER: 33,638
; REFERENCE/DOCKET NUMBER: PA-0108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-208-1888
; TELEFAX: 301-926-6125
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PROBE"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; STRAIN: BRCA1
US-08-988-706-45

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 927 TTATTAGAAATGCAGAA 943
Db 1 TTATTATAATTGAAGAA 17

RESULT 354
US-09-192-104-7/C
; Sequence 7, Application US/09192104B
; Patent No. 6184020
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
```

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; TITLE OF INVENTION: Polypeptides Having Aminopeptidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.200-US
; CURRENT APPLICATION NUMBER: US/09/192,104B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/069719
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: 1465/97
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: PA 1998 00670
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-192-104-7

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 797 GGAGAGGCAGATAACGC 813
Db 17 GGAGACGCATATGACGC 1

RESULT 355
US-09-275-680-7
; Sequence 7, Application US/09275680
; Patent No. 6221630
; GENERAL INFORMATION:
; APPLICANT: Hopper, James E
; TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
; TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
; TITLE OF INVENTION: Yeast
; FILE REFERENCE: 98428
; CURRENT APPLICATION NUMBER: US/09/275,680
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-275-680-7

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GCCTGTCTCGGGAACCTGCG 279
Db 1 GCCTGTTGACCAACTGGC 17

RESULT 356
US-09-324-867-24
; Sequence 24, Application US/09324867A
; Patent No. 6251632
; GENERAL INFORMATION:
; APPLICANT: Lillcrap, David
; APPLICANT: Cameron, Cherie
; APPLICANT: No. 6251632ley, Colleen
; APPLICANT: Horrocks, L. Suzanne Hoyle
; APPLICANT: Hough, Christine
; TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
; FILE REFERENCE: 1669.0010002/JAG/BJD
; CURRENT APPLICATION NUMBER: US/09/324,867A
; CURRENT FILING DATE: 1999-06-03
; EARLIER APPLICATION NUMBER: 09/035,141
; EARLIER FILING DATE: 1998-03-059
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1739:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1739

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 320 TTTCTGTATTCTTGC 336
||||| |||||
Db 17 TTTCTTCTATTATTC 1

RESULT 360
US-08-584-040-2165
; Sequence 2165, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974

; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2165

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1050 ACTTCCTTATCTTTCCA 1066
||| |:::|
Db 1 ACACCUUUAUCUUCCA 17

RESULT 361
US-08-584-040-2167
; Sequence 2167, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2167
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1054 CCTTATCTTCCAGTG 1070
| :|:|:|:| |
Db 1 CUUUAUCUUCCAUGG 17

RESULT 362
US-08-584-040-4021
; Sequence 4021, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4021:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4021
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 881 TAAAGTGTGCCACACA 897
:|:|:|:|:|
Db 1 UACAAGCUUGGCCACACA 17
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RESULT 363
US-08-584-040-5664/c
; Sequence 5664, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5664:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5664
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 421 CCTTATTTGGAGAG 437
|:|:|:|:|
Db 17 CCTTCTATTATGAGAG 1

RESULT 364
US-08-584-040-5710/c
; Sequence 5710, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
```

;; TITLE OF INVENTION: TREATMENT OF DISEASES OR
;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 8502
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;;
;; INFORMATION FOR SEQ ID NO: 5710:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-5710

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 219 TCATTGCCAAAGAGTC 235
||| ||||| |||
Db 17 TCAATTCCAAAGCGTC 1

RESULT 365
US-08-584-040-7398/C
; Sequence 7398, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;;
;; INFORMATION FOR SEQ ID NO: 7398:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-7398

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 564 GGTTTTTAAATACCTT 580
||||| ||||| |||
Db 17 GGTTTTTAAATAGCCTT 1

RESULT 366
US-08-584-040-8014
; Sequence 8014, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-8014

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 465 AGCACTTTATTCTGAT 481
DB 1 AGCACUUUAUGCUCCUU 17

RESULT 367
US-08-679-645-677
; Sequence 677, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 790:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
;
US-08-679-645-677

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 677:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-677

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 719 GAAATATATTAACGCA 735
DB 1 GAUAAUAUCUUGACGCA 17

RESULT 368
US-08-679-645-790/c
; Sequence 790, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 790:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
;
US-08-679-645-677
```

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-790

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      622 ATGAGTTTATTCTCAG 638
Db      17 ATAGGATTATTCTCAG 1

RESULT 369
US-09-371-772B-234/c
; Sequence 234, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-234

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      564 GGTTTAAATACCTTT 580
Db      17 GGTTTAAACACATTT 1

RESULT 370
US-09-371-772B-284/c
; Sequence 284, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-284
```

```

; ORGANISM: Homo sapiens
US-09-371-772B-284

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      320 TTTCCTGTTATTCTTGC 336
Db      17 TTTCCTTCTATTATTGC 1

RESULT 371
US-09-371-772B-710
; Sequence 710, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 710
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-710

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      1050 ACTTCCTTATCTTTCCA 1066
Db      1 ACACCUUUAUCUUCCA 17

RESULT 372
US-09-371-772B-712
; Sequence 712, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 712
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-712
```


Fri Aug 19 10:59:59 2005

US-09-371-772B-712

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1054 CCTTATCTTCCAGTGG 1070
| : : : : : ||
Db 1 CUUUAUCUUCCAUGGG 17

RESULT 373

US-09-371-772B-1788
; Sequence 1788, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1788
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-371-772B-1788

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 881 TAAAAGTGTGCCCCACA 897
: ||| : |||||
Db 1 UACAAGCUUGGCCACACA 17

RESULT 374

US-09-371-772B-2553/c
; Sequence 2553, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2553
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.

US-09-371-772B-2553

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 421 CCTTATATTGGAAGAG 437
||| ||| |||||
Db 17 CCTTCTATTATGAAGAG 1

RESULT 375

US-09-371-772B-2594/c
; Sequence 2594, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2594
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.

US-09-371-772B-2594

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 219 TCATTGCCAAAAGAGTC 235
||| | ||||| |||
Db 17 TCAATTCCAAAAGCGTC 1

RESULT 376

US-09-371-772B-3206/c
; Sequence 3206, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3206
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.

US-09-371-772B-3206

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 GGTTTTTAATACCTTT 580
||||| ||||| |||
Db 17 GGTTTTTAATAAGCCTT 1

RESULT 377
US-09-371-772B-3797
; Sequence 3797, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3797
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3797

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 465 AGCATTATTCTGATT 481
|||||:::|::|::|
Db 1 AGCACUUUAUGCUCCUU 17

RESULT 378
US-09-371-772B-4538/c
; Sequence 4538, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4538
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4538

Query Match 1.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1033 AGTAAACATCACACCCA 1049
||||| ||||| |||||
Db 17 AGTTAACATGAACCCA 1

RESULT 379
US-09-371-772B-4854/c
; Sequence 4854, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4854
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4854

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 TCCCTCTTGTGTGTA 869
||||| ||||| |||||
Db 17 TCGCTCTTGGTGTGTA 1

RESULT 380
US-09-371-772B-6139/c
; Sequence 6139, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6139
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6139

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;

iss.res

Fri Aug 19 10:59:59 2005

```
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 123 TGACTTTTCTTATGCTG 139
   ||||| |||||
Db 17 TGTCTTTTGTATGCTG 1

RESULT 381
US-09-401-063-157/c
; Sequence 157, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-401-063-157
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 982 ATCCAAAGGAGTTGTAT 998
   ||||| ||||| |||||
Db 17 ATCCAGAGGAGGAGTAT 1

RESULT 382
US-09-401-063-283
; Sequence 283, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
```

```
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-401-063-283
Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 910 CAACATTTTCCTAGAGCC 926
   |||||: ||| |||||
Db 1 CAACAUCUCCGAAGCC 17

RESULT 383
US-09-401-063-337
; Sequence 337, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
```

;
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 337:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-337

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCCCATCC 212
Db 1 CGAGAUCCUCCUCCAUCC 17

RESULT 384
US-09-401-063-631/c
; Sequence 631, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063

;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 631:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-401-063-631

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 613 AAGTAGGAGATGAGTTT 629
Db 17 AATTAGGAGATACGTTT 1

RESULT 385
US-09-401-063-653
; Sequence 653, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:


```

; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 653:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-401-063-653

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY      654 AATTAGATTATGTTAC 670
Db      1 AAUUAGUUUGUUUAC 17
      ||:||:||:||:||
      ||:||:||:||:||

RESULT 386
US-09-401-063-654
; Sequence 654, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 654:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-401-063-654

Query Match      1.1%; Score 12.2; DB 1; Length 17;

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```
RESULT 389
US-09-957-189-7/c
; Sequence 7, Application US/09957189
; Patent No. 6673571
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Amino peptidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.200-US
; CURRENT APPLICATION NUMBER: US/09/957,189
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/192,104
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1465/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00670
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-957-189-7

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      797 GGAGAGGCAGATAACGC 813
Db      17 GGAGAGGCATATGACGC 1

RESULT 390
US-09-866-108A-400/c
; Sequence 400, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 401
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-401

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      291 CTACTGGAATTGTTGTT 307
Db      17 CTGCTGGACTTGCTGTT 1

RESULT 391
US-09-866-108A-401/c
; Sequence 401, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 401
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-401

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 400
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-400
```

```
Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      291 CTACTGGAATTGTTGTT 307
Db      17 CTGCTGGACTTGCTGTT 1
```

```
RESULT 391
US-09-866-108A-401/c
; Sequence 401, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 401
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-401
```

```
Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Fri Aug 19 10:59:59 2005

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; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 437
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-437

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGCGCTCTCATGAC 833
    ||||| ||||| |||
Db 1 AGCAGATCTCTCAGGAC 17

RESULT 394
US-09-866-108A-733/c
; Sequence 733, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 402
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-402

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 289 CACTACTGGAATTGTTG 305
    ||||| ||||| |||||
Db 17 CACTGCTGGACTTGCTG 1

RESULT 393
US-09-866-108A-437
; Sequence 437, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```


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Fri Aug 19 10:59:59 2005

; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1487
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1487

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 32 CAGGAAGCCGGAAGCAG 48
Db 1 CAGGAAGCCGTGGGCAG 17

RESULT 398
US-09-866-108A-6438/c
; Sequence 6438, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6438
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6438

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 964 CCAGGACATTTTGATGA 980
Db 17 CCGGACCTTTTGATCA 1

RESULT 399
US-09-866-108A-6440/c
; Sequence 6440, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6440
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6440

Query Match 1.1%; Score 12.2; DB 1; Length 17;

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Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 962 ACCCAGGACATTTTGAT 978
Db 17 AGCCGGGACCTTTTGAT 1

RESULT 400
US-09-866-108A-6618/c
; Sequence 6618, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6618
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6618

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 896 CAGACCAAGAGCCTCAA 912
Db 17 CAGACGAGAGCCTCCA 1

RESULT 401
US-09-866-108A-6751
; Sequence 6751, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6618
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6618

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6751
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6751

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 838 GAAGGCCGGGTGGATC 854
Db 1 GAAGGCCGTGGAGGAGC 17

RESULT 402
US-09-866-108A-7102/c
; Sequence 7102, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6618
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6618

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7102
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7102

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853 TCCCTCTTTGTGTTGTA 869
      ||||| |||||
DB      17 TCCGTCTTAGCGTTGTA 1

RESULT 403
US-09-866-108A-7368/c
; Sequence 7368, Application US/098666108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7368
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7368
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Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      116 ATTGGACTGACTTTTCT 132
      ||||| ||||| |||||
DB      17 ATTCACACTGAATTTTCT 1

RESULT 404
US-09-866-108A-7438
; Sequence 7438, Application US/098666108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7438
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7438

Query Match      1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      345 CTGTGATCAAAATGGGGA 361
      ||||| ||||| |||||
DB      1 CTGTGCTCAGATGGAGA 17

RESULT 405
US-09-866-108A-7964/c
; Sequence 7964, Application US/098666108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7964
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7964

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 316 TGGATTTCCTGTTATTC 332
| | | | | | | | | | | | | | | | | |
Db 17 TGGATTTCCTGTTGTC 1

RESULT 406
US-09-866-108A-7969/c
; Sequence 7969, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7969
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7969

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 311 GCCTTTGGATTTCCTGT 327
| | | | | | | | | | | | | | | | | |
Db 17 GCCTCTGGATTTCCTGT 1

RESULT 407
US-09-866-108A-7970/c
; Sequence 7970, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7970
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7970

iss.res

Fri Aug 19 10:59:59 2005

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 310 TGCCTTTGGATTTCCTG 326
||| ||| ||| ||| ||| ||| |||
Db 17 TGGCTCTGGATTTCCTG 1

RESULT 408
US-09-866-108A-7971/c
; Sequence 7971, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7971
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7971

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 309 CTGCCTTTGGATTTCCT 325
||| ||| ||| ||| ||| ||| |||
Db 17 CTGGCTCTGGATTTCCT 1

RESULT 409
US-09-866-108A-9279/c
; Sequence 9279, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9279
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9279

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 501 AGAACTCATATCTG 517
||| ||| ||| ||| ||| ||| |||
Db 17 AGTCCTCATATCTG 1

RESULT 410
US-09-866-108A-9317
; Sequence 9317, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9317
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9317

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 44 AGCAGCCGCGCCCCCAG 60
||||| |||
Db 1 AGCAGCCGCATCCTCAG 17

RESULT 411
US-09-404-912-319
; Sequence 319, Application US/09404912
; Patent No. 6703228
; GENERAL INFORMATION:
; APPLICANT: John Landers
; APPLICANT: David Houseman
; APPLICANT: Barbara Jordan
; APPLICANT: Alain Charest
; TITLE OF INVENTION: Methods and Products Related to
; TITLE OF INVENTION: Genotyping and DNA Analysis
; FILE REFERENCE: M0656/7045(HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/404,912
; CURRENT FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,757
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22283
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-404-912-319

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 672 CAAATTATGTTACTTGT 688
||||| |||
Db 1 CAAATAATGTTAGTTAT 17

RESULT 412
US-09-685-664B-234/c
; Sequence 234, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-234

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 564 GGTTTTAAATACCTTT 580
||||| |||
Db 17 GGTTTTAAACACATTT 1

RESULT 413
US-09-685-664B-284/c
; Sequence 284, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-284

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 320 TTTCTGTATTCTTGC 336
||||| |||
Db 17 TTTCTTCTATTATTC 1

RESULT 414
US-09-685-664B-710
; Sequence 710, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 710
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-710

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCA 1066
|| | : : : : : ||
Db 1 ACACCUUUAUCCUCCA 17

RESULT 415
US-09-685-664B-712
; Sequence 712, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 712
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-712

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1054 CCTTATCTTTCCAGTGG 1070
| : : : : ||
Db 1 CUUUAUCUUCCAUGGG 17

RESULT 416
US-09-685-664B-1788
; Sequence 1788, Application US/09685664B

; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1788
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1788

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 881 TAAAGTGTGCCCCACA 897
: ||| : |||||
Db 1 UACAAGCUUGGCCACA 17

RESULT 417
US-09-685-664B-2553/c
; Sequence 2553, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2553
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2553

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 421 CCTTATATTGGAAGAG 437
||| ||| |||||
Db 17 CCTTCTATTATGAAGAG 1

RESULT 418
US-09-685-664B-2594/c
; Sequence 2594, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2594
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2594

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 219 TCATTGCCAAAGAGTC 235
Db 17 TCAATTCCAAAGCGTC 1

RESULT 419
US-09-685-664B-3206/c
; Sequence 3206, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3206
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3206

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 GGTTTTAAATACCTT 580

Db 17 GGTTTTAAATAGCCTT 1
RESULT 420
US-09-685-664B-3797
; Sequence 3797, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3797
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3797

Query Match 1.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 2.3e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 465 AGCACTTTATTCTGATT 481
Db 1 AGCACUUUAUGCUCCUU 17

RESULT 421
PCT-US95-02219-5
; Sequence 5, Application PC/TUS9502219
; .GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880

iss.res

Fri Aug 19 10:59:59 2005

```
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-02219-5

    Query Match      1.1%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 2.3e+02;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      839 AAGGCCGGGTGGATCC 855
      ||||| ||||| |||||
Db      1 AAGGCTGGTGTGGATAC 17

RESULT 422
PCT-US95-02219A-5
; Sequence 5, Application PC/TUS9502219A
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tummuru, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND THE RELATED METHODS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-02219A-5

    Query Match      1.1%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 2.3e+02;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      839 AAGGCCGGGTGGATCC 855
      ||||| ||||| |||||
Db      1 AAGGCTGGTGTGGATAC 17

RESULT 423
US-09-338-907-372

; Sequence 372, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-338-907-372

    Query Match      1.0%; Score 11.6; DB 1; Length 19;
    Best Local Similarity 77.8%; Pred. No. 3e+02;
    Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      850 GGATCCCTCTTTGTGTTG 867
      ||||| ||||| |||||
Db      2 GGCTCCCTTTTGAGTTG 19

RESULT 424
US-09-218-207-372
; Sequence 372, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 372
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer for SEQ 251, SEQ 328
US-09-218-207-372

    Query Match      1.0%; Score 11.6; DB 1; Length 19;
    Best Local Similarity 77.8%; Pred. No. 3e+02;
    Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      850 GGATCCCTCTTTGTGTTG 867
      ||||| ||||| |||||
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Db 2 GGCTCCCTTTTGAGTTG 19

RESULT 425

US-09-422-978-4387

; Sequence 4387, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 4387

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind

; LOCATION: 1..19

; OTHER INFORMATION: upstream amplification primer 99-1481 for SEQ 453,

US-09-422-978-4387

Query Match

Best Local Similarity 1.0%; Score 11.6; DB 1; Length 19;

Mismatches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 850 GGATCCCTCTTTGTGTTG 867

||||| ||||| ||||| |||||

Db 2 GGCTCCCTTTTGAGTTG 19

RESULT 426

US-09-792-594-57/c

; Sequence 57, Application US/09792594

; Patent No. 6436706

; GENERAL INFORMATION:

; APPLICANT: Donna T. Ward

; APPLICANT: Andrew T. Watt

; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL4 EXPRESSION

; FILE REFERENCE: RTS-0209

; CURRENT APPLICATION NUMBER: US/09/792,594

; CURRENT FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 57

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-792-594-57

Query Match

Best Local Similarity 1.0%; Score 11.4; DB 1; Length 20;

Mismatches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GGGCAGGCTGCC 22

||||| ||||| |||||

Db 13 GGGCAGCCTGCC 1

RESULT 427

US-09-866-108A-2565

; Sequence 2565, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 2565

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-2565

Query Match 1.0%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 3.4e+02;

Mismatches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 GAAGCCGGAAGCAGCC 50

||||| ||||| ||||| |||||

Db 1 GAAGCGGCAGCTGCC 16

RESULT 428

US-09-866-108A-2564

; Sequence 2564, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

```
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2564
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2564

Query Match          1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      35 GAAGCCGGAAGCAGCC 50
      |||| |||| |||| ||||
Db      2 GAAGCGGCAGCTGCC 17

RESULT 429
US-09-827-998-515
; Sequence 515, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 515
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-515

Query Match          1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      976 GATGAGATCCAAAGGA 991
      ||| ||| ||| ||| |||
Db      1 GAGGAAATTCAAAGGA 16

RESULT 430
US-09-827-998-514
; Sequence 514, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
```

```
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 514
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-514

Query Match          1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      976 GATGAGATCCAAAGGA 991
      ||| ||| ||| ||| |||
Db      2 GAGGAAATTCAAAGGA 17

RESULT 431
US-09-324-867-24/c
; Sequence 24, Application US/09324867A
; Patent No. 6251632
; GENERAL INFORMATION:
; APPLICANT: Lillcrap, David
; APPLICANT: Cameron, Cherie
; APPLICANT: No. 6251632ley, Colleen
; APPLICANT: Horrocks, L. Suzanne Hoyle
; APPLICANT: Hough, Christine
; TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
; FILE REFERENCE: 1669.0010002/JAG/BJD
; CURRENT APPLICATION NUMBER: US/09/324,867A
; CURRENT FILING DATE: 1999-06-03
; EARLIER APPLICATION NUMBER: 09/035,141
; EARLIER FILING DATE: 1998-03-059
; EARLIER APPLICATION NUMBER: 60/039,953
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Synthetic oligonucleotide
US-09-324-867-24

Query Match          1.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      109 TGGGGCTATTGGGACTG 124
      ||| ||| ||| ||| |||
Db      17 TGGAGCTCTTGGGGCTG 2

RESULT 432
US-09-392-580-12
; Sequence 12, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
```

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; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-580-12

Query Match      1.0%; Score 11; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      586 TCATGTTCACTTTTAAGAAA 604
      ||||| ||||| ||||| |||||
Db      2 TCATCTTCTCTTGAAAAATA 20

RESULT 433
US-09-371-772B-4538
; Sequence 4538, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4538
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4538

Query Match      1.0%; Score 10.8; DB 1; Length 17;
Best Local Similarity 35.7%; Pred. No. 3.9e+02;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      316 TGGATTTCCTGTGA 329
      :|| :|| :|| :|| :||
Db      1 UGGGUUUAUGUUA 14

RESULT 434
US-09-433-699-36
; Sequence 36, Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; FILE REFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433,699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
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US-09-433-699-36

Query Match      1.0%; Score 10.8; DB 1; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      391 AGTCATTTTCCTTA 404
      ||||| ||||| ||||| |||||
Db      7 AGTCATCTTCCTCA 20

RESULT 435
US-09-866-108A-7015
; Sequence 7015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7015
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7015

Query Match      1.0%; Score 10.6; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      736 GTCTTGATGGCAGCTGC 752
      | | | | | | | | | | | | | |
Db      1 GCCATGGTGGCAGCTGC 17

RESULT 436
US-09-422-978-4732
; Sequence 4732, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
```



```
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4732
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1739 for SEQ 798,
US-09-422-978-4732

Query Match      1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      350 ATCAAATGGGGAGCCTG 366
Db      2 ATGAAATGCTGAGGCTG 18

RESULT 437
US-09-422-978-6041/c
; Sequence 6041, Application US/094222978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6041
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8576 for SEQ 2107,
US-09-422-978-6041

Query Match      1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      614 AGTAGGAGATGAGTTT 630
Db      17 AGTGGGGTTGAGATT 1

RESULT 438
US-09-422-978-7460
; Sequence 7460, Application US/094222978
; Patent No. 6537751
```

```
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7460
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-49 for SEQ 3526,
US-09-422-978-7460

Query Match      1.0%; Score 10.6; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      932 AGAAATGCAGAAATCTGA 948
Db      1 AGAAATCCACAGTCAGA 17

RESULT 439
US-09-198-452A-5159/c
; Sequence 5159, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment.
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5159
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5159

Query Match      1.0%; Score 10.6; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      599 AAGAAAGACTTCATAAG 615
Db      18 AACAACTCCAGTCCAGAAG 2

RESULT 440
US-09-198-452A-5166/c
; Sequence 5166, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
```

```
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5166

Query Match          1.0%; Score 10.6; DB 1; Length 20;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      599 AAGAAAGACTTCATAAG 615
Db      18 AACAAAGACTCCAGAAG 2

RESULT 441
US-09-657-472-1733
; Sequence 1733, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1733
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1733

Query Match          1.0%; Score 10.6; DB 1; Length 21;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      9 TGGGACGCGCTGCCCGGCC 27
Db      1 TGGACAGCCTRCCCCAGGC 19

RESULT 442
US-08-373-124A-2437/c
; Sequence 2437, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles

Query Match          1.0%; Score 10.4; DB 1; Length 17;
Best Local Similarity 91.7%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      489 ATTGAATTTCCT 500
Db      12 ATTAATTTCCT 1

RESULT 443
US-08-435-628-2437/c
; Sequence 2437, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
```

```
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-2437

Query Match          0.9%; Score 10.4; DB 1; Length 17;
Best Local Similarity 91.7%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      489 ATTGAATTTCCT 500
Db      12 ATTAATTTCCT 1

RESULT 443
US-08-435-628-2437/c
; Sequence 2437, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-435-628-2437
Query Match 0.9%; Score 10.4; DB 1; Length 17;
Best Local Similarity 91.7%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 489 ATTGAATTCTT 500
Db 12 ATTAATTCTT 1

RESULT 444
US-09-544-398B-310
; Sequence 310, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-544-398B-310
Query Match 0.9%; Score 10.4; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 886 GTGTGGCCCA 897
Db 12 ATTAATTCTT 1

Db 3 GTGTGGGCCACA 14

RESULT 445
US-09-543-771B-310
; Sequence 310, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-543-771B-310
Query Match 0.9%; Score 10.4; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 886 GTGTGGGCCACA 897
Db 3 GTGTGGGCCACA 14

RESULT 446
US-09-422-978-4185
; Sequence 4185, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-13853 for SEQ 251,
;
US-09-422-978-4185
Query Match 0.9%; Score 10.4; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CCTATTAGAA 936


```
RESULT 450
US-09-827-998-516
; Sequence 516, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 516
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-516

Query Match      0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      977 ATGAGATCCAAAGGA 991
      |||||
Db      1 AGGAAATTCAAAGGA 15

RESULT 451
US-09-866-108A-7017
; Sequence 7017, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
```

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; Patent No. 6686188
; SEQ ID NO 7017
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7017

Query Match      0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      738 CTTGTAGGCAGCTGC 752
      |||||
Db      1 CATGGTGGCAGCTGC 15

RESULT 452
US-09-827-998-513
; Sequence 513, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 513
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-513

Query Match      0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      976 GATGAGATCCAAAGG 990
      |||||
Db      3 GAGGAAATTCAAAGG 17

RESULT 453
US-09-866-108A-7016
; Sequence 7016, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
```

Db 16 AGACACAACATTCC 2

RESULT 457

US-08-836-261A-72/c

; Sequence 72, Application US/08836261A

; Patent No. 6221582

; GENERAL INFORMATION:

; APPLICANT: GIESENDORF, BELINDA

; APPLICANT: QUINT, WILHELMUS

; APPLICANT: VAN DOORN, LEENDERT-JAN

; TITLE OF INVENTION: NEW POLYNUCLEIC ACID SEQUENCES FOR USE IN THE

; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF PROKARYOTIC ORGANISMS

; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 6.0 / ASCII text output

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,261A

; FILING DATE: 25 Apr 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP95/04264

; FILING DATE: 30 Oct 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94870171.9

; FILING DATE: 28 Oct 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: KAMMERER, PATRICIA A.

; REGISTRATION NUMBER: 29,775

; REFERENCE/DOCKET NUMBER: INNS:005

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-836-261A-72

Query Match 0.9%; Score 10.2; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 526 TGCACATGCGGCATT 540

Db 20 TGCAGATTCTGCATT 6

RESULT 458

US-09-980-052-219/c

; Sequence 219, Application US/09980052

; Patent No. 6670130

; GENERAL INFORMATION:

; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.

; APPLICANT: KIM, Cheol Min

; APPLICANT: PARK, Hee Kyung

; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria

; FILE REFERENCE: PP05020/PCT

; CURRENT APPLICATION NUMBER: US/09/980,052

; CURRENT FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: KR 10-1999-0019631

; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019632

; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019633

; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019634

; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019635

; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-2000-0018189

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 243

; SOFTWARE: KopatentIn 1.71

; SEQ ID NO 219

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium

; OTHER INFORMATION: diernhoferi

US-09-980-052-219

Query Match 0.9%; Score 10.2; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 668 TACTCAAAATTATGTT 682

Db 20 TTCTCAAAGTTTGTT 6

RESULT 459

US-08-785-750-2

; Sequence 2, Application US/08785750

; Patent No. 5846528

; GENERAL INFORMATION:

; APPLICANT: PODSAKOFF, GREGORY M.

; APPLICANT: KURTZMAN, GARY J.

; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING

; TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ROBINS & ASSOCIATES

; STREET: 90 MIDDLEFIELD ROAD, SUITE 200

; CITY: MENLO PARK

; STATE: CA

; COUNTRY: USA

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/785,750

; FILING DATE: 16-JAN-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/588,355

; FILING DATE: 18-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MCCracken, THOMAS P.

; REGISTRATION NUMBER: 38,548

; REFERENCE/DOCKET NUMBER: 0800-0009.21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 325-7812

; TELEFAX: (415)325-7823

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-785-750-2

```

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7016
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7016

Query Match          0.9%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      738 CTTGTAGGACGTGC 752
      ||| ||||| |||
Db      2 CATGGTGGCAGCTGC 16

RESULT 454
US-09-182-145-131/c
; Sequence 131, Application US/09182145B
; Patent No. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 131
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-18
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6387657
US-09-182-145-131

Query Match          0.9%; Score 10.2; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      109 TGGGGCTATTGGACT 123
```

```

Db      15 TGAGACTCTTGACT 1
      ||| ||| ||||| |||

RESULT 455
US-09-544-398B-588/c
; Sequence 588, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11ql3.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-588

Query Match          0.9%; Score 10.2; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      905 AGCCTCAACATTTC 919
      ||| ||||| |||||
Db      16 AGACACAACATTTC 2

RESULT 456
US-09-543-771B-588/c
; Sequence 588, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11ql3.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-588

Query Match          0.9%; Score 10.2; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      905 AGCCTCAACATTTC 919
      ||| ||||| |||||
```

```

Query Match      0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
Db      1 GGCAGCTGCC 10

RESULT 460
US-08-588-355-1
; Sequence 1, Application US/08588355
; Patent No. 5858351
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,355
; FILING DATE: 18-JAN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-588-355-1

Query Match      0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
Db      1 GGCAGCTGCC 10

RESULT 461
US-09-116-780-5
; Sequence 5, Application US/09116780
; Patent No. 5945335
; GENERAL INFORMATION:
; APPLICANT: Colosi, Peter
; TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
; TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences

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; FILE REFERENCE: 2555.2.2
; CURRENT APPLICATION NUMBER: US/09/116,780
; CURRENT FILING DATE: 1998-07-16
; EARLIER APPLICATION NUMBER: 08/745,957
; EARLIER FILING DATE: 1996-11-07
; EARLIER APPLICATION NUMBER: 60/006,402
; EARLIER FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-116-780-5

Query Match      0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
Db      1 GGCAGCTGCC 10

RESULT 462
US-08-812-102-1
; Sequence 1, Application US/08812102
; Patent No. 5952221
; GENERAL INFORMATION:
; APPLICANT: KURTZMAN, GARY J.
; APPLICANT: COLOSI, PETER C.
; APPLICANT: YOSHIDA, JUN
; APPLICANT: MIZUNO, MASAOKI
; APPLICANT: OKADA, HIDEHO
; TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
; TITLE OF INVENTION: TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,102
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,209
; FILING DATE: 06-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-812-102-1

```



```
Query Match          0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
      |||||
Db      1 GGCAGCTGCC 10

RESULT 463
US-08-784-757-1
; Sequence 1, Application US/08784757
; Patent No. 5962313
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,757
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,355
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-784-757-1

Query Match          0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
      |||||
Db      1 GGCAGCTGCC 10

RESULT 464
US-08-745-957-1
; Sequence 1, Application US/08745957
; Patent No. 6004797
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
```

```
; TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,957
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,402
; FILING DATE: 09-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-745-957-1

Query Match          0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744 GGCAGCTGCC 753
      |||||
Db      1 GGCAGCTGCC 10

RESULT 465
US-09-309-042-1
; Sequence 1, Application US/09309042
; Patent No. 6211163
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,042
; FILING DATE:
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```

; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/588,355
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-09-309-042-1
;
Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 744 GGCAGCTGCC 753
   |||||
Db 1 GGCAGCTGCC 10

RESULT 466
US-09-205-337-2
; Sequence 2, Application US/09205337
; Patent No. 6325998
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
;
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,337
; FILING DATE: 04-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,750
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

```

US-09-205-337-2
;
Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 744 GGCAGCTGCC 753
   |||||
Db 1 GGCAGCTGCC 10

RESULT 467
US-09-406-362-1
; Sequence 1, Application US/09406362
; Patent No. 6335011
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
;
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,362
; FILING DATE: 28-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/784,757
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;
US-09-406-362-1
;
Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 744 GGCAGCTGCC 753
   |||||
Db 1 GGCAGCTGCC 10

RESULT 468
US-09-755-734-1
; Sequence 1, Application US/09755734
; Patent No. 6391858
; GENERAL INFORMATION:

```

APPLICANT: PODSAKOFF, GREGORY M.
KESSLER, PAUL D.
BYRNE, BARRY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/755,734
FILING DATE: 04-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/588,355
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-755-734-1
Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 744 GGCAGCTGCC 753
Db 1 GGCAGCTGCC 10
RESULT 469
US-09-406-363-1
Sequence 1, Application US/09406363
Patent No. 6482633
GENERAL INFORMATION:
APPLICANT: COLOSI, PETER C.
TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
RECOMBINANT AAV VIRION PRODUCTION
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,363
FILING DATE: 28-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,957
FILING DATE: 11-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-406-363-1
Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 744 GGCAGCTGCC 753
Db 1 GGCAGCTGCC 10
RESULT 470
US-09-649-890-1
Sequence 1, Application US/09649890
Patent No. 6531456
GENERAL INFORMATION:
APPLICANT: KURTZMAN, GARY J.
COLOSI, PETER C.
YOSHIDA, JUN
MIZUNO, MASAOKI
OKADA, HIDEHO
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/649,890
FILING DATE: 28-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/812,102
FILING DATE: 05-MAR-1997
APPLICATION NUMBER: US 60/013,209
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812

TELEFAX: (415) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-649-890-1

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGCAGCTGCC 10

RESULT 471
US-09-969-204A-1
Sequence 1, Application US/09969204A
Patent No. 6610290
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
KESSLER, PAUL D.
BYRNE, BARRY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS
VIRIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,204A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/406,362
FILING DATE: 28-Sep-1999
APPLICATION NUMBER: 08/784,757
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-969-204A-1

Query Match 0.9%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCAGCTGCC 10
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Job time : 9 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:52:25 ; Search time 5 Seconds
(without alignments)
2.757 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctggttgccagcgtgc.....gttacctgctcatttggttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 325 seqs, 6187 residues

Total number of hits satisfying chosen parameters: 650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 326 summaries

Database : gedb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| C 3 | 49.4 | 4.4 | 51 | 1 | AX189879 |
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| C 12 | 20 | 1.8 | 20 | 1 | CQ860114 |
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| C 14 | 20 | 1.8 | 20 | 1 | CQ860116 |
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| C 20 | 20 | 1.8 | 20 | 1 | CQ878361 |
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| C 22 | 20 | 1.8 | 21 | 1 | CQ860126 |
| C 23 | 19.8 | 1.8 | 25 | 1 | AX378941 |
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| C 31 | 17 | 1.5 | 17 | 1 | AX738199 |
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Fri Aug 19 10:59:59 2005

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| 209 | 13.8 | 1.2 | 19 | 1 | AX149152 | ACCESSION:AX149152 |
| 210 | 13.8 | 1.2 | 19 | 1 | BD012154 | ACCESSION:BD012154 |
| 211 | 13.4 | 1.2 | 15 | 1 | AX348064 | ACCESSION:AX348064 |
| 212 | 13.4 | 1.2 | 15 | 1 | AX540329 | ACCESSION:AX540329 |
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| 221 | 13.4 | 1.2 | 17 | 1 | CQ617827 | ACCESSION:CQ617827 |
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| 225 | 13.4 | 1.2 | 17 | 1 | I54174 | ACCESSION:I54174 |
| 226 | 13.4 | 1.2 | 17 | 1 | AR327041 | ACCESSION:AR327041 |
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| 228 | 13.4 | 1.2 | 17 | 1 | AR462610 | ACCESSION:AR462610 |
| 229 | 13.4 | 1.2 | 17 | 1 | AR462611 | ACCESSION:AR462611 |
| 230 | 13.4 | 1.2 | 17 | 1 | AR462612 | ACCESSION:AR462612 |
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| 237 | 13.4 | 1.2 | 17 | 1 | AX674640 | ACCESSION:AX674640 |
| 238 | 13.4 | 1.2 | 17 | 1 | AX688034 | ACCESSION:AX688034 |
| 239 | 13.4 | 1.2 | 17 | 1 | AX688035 | ACCESSION:AX688035 |
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| 249 | 13.4 | 1.2 | 17 | 1 | AX754467 | ACCESSION:AX754467 |
| 250 | 13.4 | 1.2 | 17 | 1 | AX759999 | ACCESSION:AX759999 |
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| 252 | 13.4 | 1.2 | 18 | 1 | AR119278 | ACCESSION:AR119278 |

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| ACCESSION:CQ617824 | ACCESSION:CQ617824 |
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| ACCESSION:AX273034 | ACCESSION:AX273034 |
| ACCESSION:AX273719 | ACCESSION:AX273719 |
| ACCESSION:AX502936 | ACCESSION:AX502936 |
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| ACCESSION:BD104790 | ACCESSION:BD104790 |
| ACCESSION:AR071523 | ACCESSION:AR071523 |
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| ACCESSION:AR292997 | ACCESSION:AR292997 |
| ACCESSION:AR294306 | ACCESSION:AR294306 |
| ACCESSION:AR299617 | ACCESSION:AR299617 |
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| ACCESSION:BD012154 | ACCESSION:BD012154 |
| ACCESSION:AX348064 | ACCESSION:AX348064 |
| ACCESSION:AX540329 | ACCESSION:AX540329 |
| ACCESSION:I35386 | ACCESSION:I35386 |
| ACCESSION:AR047122 | ACCESSION:AR047122 |
| ACCESSION:BD232102 | ACCESSION:BD232102 |
| ACCESSION:BD254620 | ACCESSION:BD254620 |
| ACCESSION:BD256417 | ACCESSION:BD256417 |
| ACCESSION:BD256555 | ACCESSION:BD256555 |
| ACCESSION:BD256865 | ACCESSION:BD256865 |
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| ACCESSION:CQ621549 | ACCESSION:CQ621549 |
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| ACCESSION:AX502938 | ACCESSION:AX502938 |
| ACCESSION:AX674640 | ACCESSION:AX674640 |
| ACCESSION:AX688034 | ACCESSION:AX688034 |
| ACCESSION:AX688035 | ACCESSION:AX688035 |
| ACCESSION:AX688036 | ACCESSION:AX688036 |
| ACCESSION:AX723809 | ACCESSION:AX723809 |
| ACCESSION:AX728020 | ACCESSION:AX728020 |
| ACCESSION:AX729829 | ACCESSION:AX729829 |
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| ACCESSION:AX736422 | ACCESSION:AX736422 |
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| ACCESSION:AR119278 | ACCESSION:AR119278 |

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| 259 | 13.4 | 1.2 | 18 | 1 | AR218558 | ACCESSION:AR218558 |
| 260 | 13.4 | 1.2 | 18 | 1 | AR218696 | ACCESSION:AR218696 |
| 261 | 13.4 | 1.2 | 18 | 1 | AR223111 | ACCESSION:AR223111 |
| 262 | 13.4 | 1.2 | 18 | 1 | AR229873 | ACCESSION:AR229873 |
| 263 | 13.4 | 1.2 | 18 | 1 | AR262129 | ACCESSION:AR262129 |
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| 266 | 13.4 | 1.2 | 18 | 1 | AR344567 | ACCESSION:AR344567 |
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| C 279 | 13.4 | 1.2 | 19 | 1 | BD088340 | ACCESSION:BD088340 |
| C 280 | 13.4 | 1.2 | 19 | 1 | AB068097 | ACCESSION:AB068097 |
| C 281 | 13.2 | 1.2 | 18 | 1 | A87858 | ACCESSION:A87858 |
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| C 283 | 13.2 | 1.2 | 18 | 1 | AR018185 | ACCESSION:AR018185 |
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| 294 | 13.2 | 1.2 | 18 | 1 | E54096 | ACCESSION:E54096 |
| 295 | 13.2 | 1.2 | 18 | 1 | AR210385 | ACCESSION:AR210385 |
| 296 | 13.2 | 1.2 | 18 | 1 | AR293973 | ACCESSION:AR293973 |
| 297 | 13.2 | 1.2 | 18 | 1 | AR298224 | ACCESSION:AR298224 |
| C 298 | 13.2 | 1.2 | 18 | 1 | AR351536 | ACCESSION:AR351536 |
| C 299 | 13.2 | 1.2 | 18 | 1 | AR364672 | ACCESSION:AR364672 |
| C 300 | 13.2 | 1.2 | 18 | 1 | AR482570 | ACCESSION:AR482570 |
| C 301 | 13.2 | 1.2 | 18 | 1 | AX035247 | ACCESSION:AX035247 |
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| 303 | 13.2 | 1.2 | 18 | 1 | AX348093 | ACCESSION:AX348093 |
| 304 | 13.2 | 1.2 | 18 | 1 | AX398208 | ACCESSION:AX398208 |
| C 305 | 13.2 | 1.2 | 18 | 1 | AX599791 | ACCESSION:AX599791 |
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| C 308 | 13.2 | 1.2 | 18 | 1 | AX837801 | ACCESSION:AX837801 |
| C 309 | 13.2 | 1.2 | 18 | 1 | BD065371 | ACCESSION:BD065371 |
| C 310 | 13 | 1.2 | 16 | 1 | AR028977 | ACCESSION:AR028977 |
| C 311 | 13 | 1.2 | 16 | 1 | AR156859 | ACCESSION:AR156859 |
| C 312 | 13 | 1.2 | 16 | 1 | AR412057 | ACCESSION:AR412057 |
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| C 316 | 13 | 1.2 | 17 | 1 | AX226887 | ACCESSION:AX226887 |
| C 317 | 13 | 1.2 | 17 | 1 | AX226888 | ACCESSION:AX226888 |
| C 318 | 13 | 1.2 | 17 | 1 | AX227245 | ACCESSION:AX227245 |
| C 319 | 13 | 1.2 | 17 | 1 | AX227246 | ACCESSION:AX227246 |
| C 320 | 13 | 1.2 | 17 | 1 | AX227395 | ACCESSION:AX227395 |
| 321 | 13 | 1.2 | 17 | 1 | AX735823 | ACCESSION:AX735823 |
| C 322 | 13 | 1.2 | 17 | 1 | AX758667 | ACCESSION:AX758667 |
| C 323 | 13 | 1.2 | 17 | 1 | AX760253 | ACCESSION:AX760253 |
| C 324 | 13 | 1.2 | 18 | 1 | AX822240 | ACCESSION:AX822240 |
| C 325 | 13 | 1.2 | 18 | 1 | AX825880 | ACCESSION:AX825880 |

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| C 326 | 12 | 1.1 | 17 | 1 | AX726789 | ACCESSION:AX726789 |
| ALIGNMENTS | | | | | | |
| RESULT 1 | | | | | | |
| AX677227 | AX677227 | | | | 60 bp | DNA |
| LOCUS | Sequence 5 from Patent WO02086122. | | | | | linear |
| DEFINITION | AX677227 | | | | | |
| ACCESSION | AX677227.1 | GI:29334643 | | | | |
| VERSION | | | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | 1 | | | | | |
| AUTHORS | Legrain,P. and Daviet,L. | | | | | |
| TITLE | Protein-protein interactions in adipocytes | | | | | |
| JOURNAL | Patent: WO 02086122-A 5 31-OCT-2002; | | | | | |
| FEATURES | Hybrigenics (FR) | | | | | |
| source | Location/Qualifiers | | | | | |
| | 1. .60 | | | | | |
| | /organism="Homo sapiens" | | | | | |
| | /mol_type="unassigned DNA" | | | | | |
| | /db_xref="taxon:9606" | | | | | |
| Query Match | 5.4%; | Score 60; | DB 1; | Length 60; | | |
| Best Local Similarity | 100.0%; | Pred. No. 1.3e-07; | | | | |
| Matches | 60; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |
| QY | 221 | ATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCTGGGAACCTGGCA | 280 | | | |
| Db | 1 | ATTGCCAAAAGAGTCACCTATGACTCAGATGCAACCACTAGTGCCTGTCTGGGAACCTGGCA | 60 | | | |
| RESULT 2 | | | | | | |
| AX189878/c | AX189878 | | | | 51 bp | DNA |
| LOCUS | Sequence 57 from Patent WO0147942. | | | | | linear |
| DEFINITION | AX189878 | | | | | |
| ACCESSION | AX189878.1 | GI:15143249 | | | | |
| VERSION | | | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | 1 | | | | | |
| AUTHORS | Shimkets,R.A. and Leach,M. | | | | | |
| TITLE | Nucleic acids containing single nucleotide polymorphisms and methods of use thereof | | | | | |
| JOURNAL | Patent: WO 0147942-A 57 05-JUL-2001; | | | | | |
| FEATURES | Curagen Corporation (US) | | | | | |
| source | Location/Qualifiers | | | | | |
| | 1. .51 | | | | | |
| | /organism="Homo sapiens" | | | | | |
| | /mol_type="unassigned DNA" | | | | | |
| | /db_xref="taxon:9606" | | | | | |
| | /note="1 of 2 allelic variants (58 is other entry)-Accession number cg43922807" | | | | | |
| Query Match | 4.6%; | Score 51; | DB 1; | Length 51; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.9e-06; | | | | |
| Matches | 51; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |
| QY | 820 | AGGCCTCTCATGACCCAGGAAGCCGGGGTGGATCCCTCTTTGTGTGTAG | 870 | | | |
| Db | 51 | AGGCCTCTCATGACCCAGGAAGCCGGGGTGGATCCCTCTTTGTGTGTAG | 1 | | | |
| RESULT 3 | | | | | | |
| AX189879/c | | | | | | |

LOCUS AX189879 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 58 from Patent WO0147942.
ACCESSION AX189879
VERSION AX189879.1 GI:15143250
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Shimkets,R.A. and Leach,M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE Methods of use thereof
JOURNAL Patent: WO 0147942-A 58 05-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source
1..51
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="2 of 2 allelic variants (57 is other entry)-Accession number cg43922807"
Query Match 4.4%; Score 49.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 1.4e-05;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 820 AGGCCTCTCATGACCCAGGAGCGGGTGGATCCCTCTTTGTGTGTAG 870
Db 51 AGGCCTCTCATGACCCAGGAGCGGGTGGATCCCTCTTTGTGTGTAG 1
RESULT 4
CQ860120/c
LOCUS CQ860120 22 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 32 from Patent WO2004072293.
ACCESSION CQ860120
VERSION CQ860120.1 GI:51982008
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 Jockers,R., Couturier,C. and Uhlmann,E.
AUTHORS Oligonucleotides which inhibit the expression of the ob-rgrp
TITLE protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 32 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS11"
Query Match 2.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 264 CCTGTCGGGAAGTGGCATATT 285
Db 22 CCTGTCGGGAAGTGGCATATT 1
RESULT 5
CQ878362/c
LOCUS CQ878362 21 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 15 from Patent WO2004080272.
ACCESSION CQ878362

VERSION CQ878362.1 GI:53790915
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 Bailleul,B., Rouille,Y., Seron,K. and Belouzard,S.
AUTHORS Use of the genes leptol1 and ob-rgrp for the screening of active
TITLE compounds for weight gain or loss or diabetes in human or animal subjects
JOURNAL Patent: WO 2004080272-A 15 23-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
source
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/organism="unidentified"
/mol_type="unassigned DNA"
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misc_feature
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/note="Amorce antisens pour PCR en temps r el de OB-RGRP"
Query Match 1.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 353 AAATGGGGAGCCTGCGCCTT 373
Db 21 AAATGGGGAGCCTGCGCCTT 1
RESULT 6
CQ784159/c
LOCUS CQ784159 20 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 4299 from Patent EP1396543.
ACCESSION CQ784159
VERSION CQ784159.1 GI:45538647
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
AUTHORS Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primers for synthesizing full length cDNA clones and their use
JOURNAL Patent: EP 1396543-A 4299 10-MAR-2004;
Research Association for Biotechnology (JP)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Description of Artificial Sequence: an artificially synthesized primer se q uence"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1029 GAGAAAGTAAACATCACACCC 1048
Db 20 GAGAAAGTAAACATCACACCC 1
RESULT 7
CQ860090/c
LOCUS CQ860090 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 2 from Patent WO2004072293.
ACCESSION CQ860090
VERSION CQ860090.1 GI:51981978
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 2 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="AS14"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 521 ACATGTGCACATGCGGCATT 540
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Db 20 ACATGTGCACATGCGGCATT 1
RESULT 8
CQ860110/c
LOCUS CQ860110 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 22 from Patent WO2004072293.
ACCESSION CQ860110
VERSION CQ860110.1 GI:51981998
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 22 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS01"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 CCCGGCCGTGGCAGGAAGC 39
|||||
Db 20 CCCGGCCGTGGCAGGAAGC 1
RESULT 9
CQ860111/c
LOCUS CQ860111 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 23 from Patent WO2004072293.
ACCESSION CQ860111
VERSION CQ860111.1 GI:51981999
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1

AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 23 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS02"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 56 CCCAGTTCGGGAGACATGGC 75
|||||
Db 20 CCCAGTTCGGGAGACATGGC 1
RESULT 10
CQ860112/c
LOCUS CQ860112 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 24 from Patent WO2004072293.
ACCESSION CQ860112
VERSION CQ860112.1 GI:51982000
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 24 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS03"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 63 CGGGAGACATGGCGGCGTT 82
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Db 20 CGGGAGACATGGCGGCGTT 1
RESULT 11
CQ860113/c
LOCUS CQ860113 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 25 from Patent WO2004072293.
ACCESSION CQ860113
VERSION CQ860113.1 GI:51982001
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.

TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 25 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS04"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ATGGCGGGCGTTAAAGCTCT 90
|||||

Db 20 ATGGCGGGCGTTAAAGCTCT 1

RESULT 12
CQ860114/c
LOCUS CQ860114 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 26 from Patent WO2004072293.
ACCESSION CQ860114
VERSION CQ860114.1 GI:51982002
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 26 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS05"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 AAGCTCTCGTGGCATTATCC 103
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Db 20 AAGCTCTCGTGGCATTATCC 1

RESULT 13
CQ860115/c
LOCUS CQ860115 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 27 from Patent WO2004072293.
ACCESSION CQ860115
VERSION CQ860115.1 GI:51982003
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp

protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 27 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS06"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 CTTATGCTGGGATGTCCTT 150
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Db 20 CTTATGCTGGGATGTCCTT 1

RESULT 14
CQ860116/c
LOCUS CQ860116 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 28 from Patent WO2004072293.
ACCESSION CQ860116
VERSION CQ860116.1 GI:51982004
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 28 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS07"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGTGCCTTAGAGGATTATGG 162
|||||

Db 20 TGTGCCTTAGAGGATTATGG 1

RESULT 15
CQ860117/c
LOCUS CQ860117 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 29 from Patent WO2004072293.
ACCESSION CQ860117
VERSION CQ860117.1 GI:51982005
KEYWORDS . synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the

interaction between the proteins of the ob-rgrp family and the leptin receptor
Patent: WO 2004072293-A 29 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

JOURNAL

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS08"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 GAGGATTATGGCGTTTACTG 171
|||||
Db 20 GAGGATTATGGCGTTTACTG 1

RESULT 16
CQ860118/c
LOCUS CQ860118 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 30 from Patent WO2004072293.
ACCESSION CQ860118
VERSION CQ860118.1 GI:51982006
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL
Patent: WO 2004072293-A 30 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS09"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GGCCTTACTGGCCCTTATT 180
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Db 20 GGCCTTACTGGCCCTTATT 1

RESULT 17
CQ860119/c
LOCUS CQ860119 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 31 from Patent WO2004072293.
ACCESSION CQ860119
VERSION CQ860119.1 GI:51982007
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the

leptin receptor
Patent: WO 2004072293-A 31 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

JOURNAL

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS10"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TGCCTGTCTGGGAACCTGGCAT 281
|||||
Db 20 TGCCTGTCTGGGAACCTGGCAT 1

RESULT 18
CQ860121/c
LOCUS CQ860121 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 33 from Patent WO2004072293.
ACCESSION CQ860121
VERSION CQ860121.1 GI:51982009
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL
Patent: WO 2004072293-A 33 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS12"

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 CGGGAACCTGGCATATTCTT 288
|||||
Db 20 CGGGAACCTGGCATATTCTT 1

RESULT 19
CQ860122/c
LOCUS CQ860122 20 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 34 from Patent WO2004072293.
ACCESSION CQ860122
VERSION CQ860122.1 GI:51982010
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor

JOURNAL Patent: WO 2004072293-A 34 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AS13"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 370 CCTTGTGTTGGCAGGCAATG 389
Db 20 CCTTGTGTTGGCAGGCAATG 1
RESULT 20
CQ878361 20 bp DNA linear PAT 04-OCT-2004
LOCUS Sequence 14 from Patent WO2004080272.
DEFINITION CQ878361
ACCESSION CQ878361
VERSION CQ878361.1 GI:53790914
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Bailleur,B., Rouille,Y., Seron,K. and Belouzard,S.
TITLE Use of the genes leptol1 and ob-rgrp for the screening of active
compounds for weight gain or loss or diabetes in human or animal
subjects
JOURNAL Patent: WO 2004080272-A 14 23-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
misc_feature 1..20
/note="Amorce sens pour PCR en temps r el de OB-RGRP"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 AGCAGCCGCGGCCCCAGTTC 63
Db 1 AGCAGCCGCGGCCCCAGTTC 20
RESULT 21
BD128083/c 20 bp DNA linear PAT 18-SEP-2002
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD128083
ACCESSION BD128083
VERSION BD128083.1 GI:23223028
KEYWORDS JP 2002017375-A/3514.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 3514 22-JAN-2002;
HELIIX RESEARCH INSTITUTE
COMMENT OS Unidentified
PN JP 2002017375-A/3514

PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10, C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Description of Artificial Sequence: an artificially
synthesized primer
CC sequence Location/Qualifiers
FH Key 1..20
FT source /organism='Unidentified'.
FT Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1029 GAGAAGTAAACATCACACCC 1048
Db 20 GAGAAGTAAACATCACACCC 1
RESULT 22
CQ860126/c 21 bp DNA linear PAT 10-SEP-2004
LOCUS Sequence 38 from Patent WO2004072293.
DEFINITION CQ860126
ACCESSION CQ860126
VERSION CQ860126.1 GI:51982014
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp
protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL Patent: WO 2004072293-A 38 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificiel"
Query Match 1.8%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 260 AGTGCCTGTCTGGGAAGTGGC 279
Db 20 AGTGCCTGTCTGGGAAGTGGC 1
RESULT 23
AX378941/c 25 bp DNA linear PAT 18-MAR-2002
LOCUS AX378941
DEFINITION Sequence 59 from Patent WO0210347.
ACCESSION AX378941

VERSION AX378941.1 GI:19574784
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Benvenisty,N.
TITLE Directed differentiation of embryonic cells
JOURNAL Patent: WO 0210347-A 59 07-FEB-2002; Yisum Research and Dev. Company of the Hebrew Univ. of Jerusalem (IL)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="3' primer of Parathyroid Hormone"
Query Match 1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 7.6;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 794 CTTGGAGAGGCAGATAACGCTGA 816
|||||
Db 23 CTTGGAGAGGCAGACAAAGCTGA 1
RESULT 24
CQ860125
LOCUS CQ860125 21 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 37 from Patent WO2004072293.
ACCESSION CQ860125
VERSION CQ860125.1 GI:51982013
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 37 26-AUG-2004; Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificiel"
Query Match 1.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 261 GTGCTGTGCGGAACCTGGCAT 281
|||||
Db 1 GTGCTGTGCGGAACCTGGCTT 21
RESULT 25
AR166701
LOCUS AR166701 19 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 51 from patent US 6281346.
ACCESSION AR166701
VERSION AR166701.1 GI:16242129
KEYWORDS Unknown.
SOURCE Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sean.
TITLE Rat ob-receptors and nucleotides encoding them
JOURNAL Patent: US 6281346-A 51 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 TCGTGGCATTATCCTTCAG 108
|||||
Db 1 TCGTGGCATTATCCTTCAG 19
RESULT 26
AR166700
LOCUS AR166700 18 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 50 from patent US 6281346.
ACCESSION AR166700
VERSION AR166700.1 GI:16242127
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sean.
TITLE Rat ob-receptors and nucleotides encoding them
JOURNAL Patent: US 6281346-A 50 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 CTTATGCTGGGATGTGCC 148
|||||
Db 1 CTTATGCTGGGATGTGCC 18
RESULT 27
AR302819/c
LOCUS AR302819 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 30 from patent US 6541604.
ACCESSION AR302819
VERSION AR302819.1 GI:31691306
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,B. and Matthews,W.
TITLE Leptin receptor having a WSX motif
JOURNAL Patent: US 6541604-A 30 01-APR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 136 GCTGGGATGTGCCCTTAGA 153
|||||
Db 18 GCTGGGATGTGCCCTTAGA 1

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RESULT 28
AR302820
LOCUS          AR302820          18 bp    DNA          linear          PAT 12-JUN-2003
DEFINITION     Sequence 31 from patent US 6541604.
ACCESSION      AR302820
VERSION        AR302820.1  GI:31691307
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
                Unclassified.
REFERENCE
AUTHORS        Bennett,B. and Matthews,W.
TITLE          Leptin receptor having a WSX motif
JOURNAL        Patent: US 6541604-A 31 01-APR-2003;
FEATURES
source
1. .18
/organism="unknown"
/mol_type="genomic DNA"

Query Match          1.6%;  Score 18;  DB 1;  Length 18;
Best Local Similarity 100.0%;  Pred. No. 19;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      136  GCTGGGATGTGCCTTAGA 153
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Db       1   GCTGGGATGTGCCTTAGA 18

RESULT 29
AX412234/c
LOCUS          AX412234          24 bp    DNA          linear          PAT 14-JUN-2002
DEFINITION     Sequence 60 from Patent WO0222879.
ACCESSION      AX412234
VERSION        AX412234.1  GI:21444692
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        Bacher,J.W., Flanagan,L. and Nassif,N.
TITLE          Detection of microsatellite instability and its use in diagnosis of
                tumors
JOURNAL        Patent: WO 0222879-A 60 21-MAR-2002;
                PROMEGA CORPORATION (US)
FEATURES
source
1. .24
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="BAT-25 primer"

Query Match          1.6%;  Score 17.6;  DB 1;  Length 24;
Best Local Similarity 83.3%;  Pred. No. 20;
Matches 20;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

QY      921  AGAGCCTTATTAGAAATGCAGAAT 944
          |||||
Db       24  AGAGCCATAGTTAAATGCAGAAT 1

RESULT 30
AX548339
LOCUS          AX548339          24 bp    DNA          linear          PAT 26-NOV-2002
DEFINITION     Sequence 263 from Patent WO0240716.
ACCESSION      AX548339
VERSION        AX548339.1  GI:25813373
KEYWORDS
SOURCE          synthetic construct
ORGANISM        synthetic construct
                other sequences; artificial sequences.
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REFERENCE
AUTHORS        Palm,K.
TITLE          Profiling tumor specific markers for the diagnosis and treatment of
                neoplastic disease
JOURNAL        Patent: WO 0240716-A 263 23-MAY-2002;
                Cemines, LLC (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

Query Match          1.6%;  Score 17.6;  DB 1;  Length 24;
Best Local Similarity 83.3%;  Pred. No. 20;
Matches 20;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

QY      834  CCAGGAAGCCGGGTGGATCCCT 857
          |||||
Db       1   CCAGTATGCCGGGATGGATACCT 24

RESULT 31
AX738199
LOCUS          AX738199          17 bp    DNA          linear          PAT 08-MAY-2003
DEFINITION     Sequence 3789 from Patent WO03025177.
ACCESSION      AX738199
VERSION        AX738199.1  GI:30517487
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        Telerman,A., Anson,R. and Tuijnder,M.
TITLE          Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL        Patent: WO 03025177-A 3789 27-MAR-2003;
                Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match          1.5%;  Score 17;  DB 1;  Length 17;
Best Local Similarity 100.0%;  Pred. No. 30;
Matches 17;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      981  GATCCAAAGGAGTTGTA 997
          |||||
Db       1   GATCCAAAGGAGTTGTA 17

RESULT 32
BD223822/c
LOCUS          BD223822          21 bp    DNA          linear          PAT 17-JUL-2003
DEFINITION     Novel method of regulating seed development in plants and genetic
                sequences therefor.
ACCESSION      BD223822
VERSION        BD223822.1  GI:33033592
KEYWORDS        JP 2002526052-A/15.
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE
AUTHORS        Bilodeau,P., Chaudhury,A.M., Dennis,E.S., Koltunow,A.M.G., Luo,M.
                and Peacock,W.J.
TITLE          Novel method of regulating seed development in plants and genetic
                sequences therefor
JOURNAL        Patent: JP 2002526052-A 15 20-AUG-2002;
                COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
```

| | | | |
|------------|---|--|--|
| | OS | Artificial Sequence | |
| | PN | JP 2002526052-A/15 | |
| | PD | 20-AUG-2002 | |
| | Pf | 21-SEP-1999 JP 2000573582 | |
| | PR | 21-SEP-1998 US 60/101184,22-SEP-1998 AU PP 6061 PR | |
| | 22-SEP-1998 AU | PP 6062,22-SEP-1998 AU PP 6063 PR | |
| | 01-JUL-1999 AU | . PQ 1345,01-JUL-1999 AU PQ 1346 PI PIERRE | |
| | BILODEAU,ABDUL MUTAKABBIR CHAUDHURY,ELIZABETH SALISBURY | | |
| | PI DENNIS, | | |
| | PI ANNA MARIA GRAZYNA KOLTUNOW,MING LUO,WILLIAM JAMES PEACOCK PC | | |
| | C12N15/09,A01H5/00,C07K14/415,C12N5/10,C12N15/00,C12N5/00 CC | | |
| | Description of Artificial Sequence:primer | | |
| | FH Key Location/Qualifiers | | |
| | FT source 1..21 /organism='Artificial Sequence'. | | |
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| | /organism="synthetic construct" | | |
| | /mol_type="genomic DNA" | | |
| | /db_xref="taxon:32630" | | |
| | Query Match 1.5%; Score 16.8; DB 1; Length 21; | | |
| | Best Local Similarity 90.0%; Pred. No. 30; | | |
| | Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | | |
| QY | 606 ACTTCATAAGTAGGATGA 625 | | |
| Dd | | | |
| | 20 AC TTCATAAGGAAGATGA 1 | | |
| RESULT 33 | E13776 | | |
| LOCUS | PCR primer for discriminating genotype 1a of HCV (Hepatitis C virus). | 24 bp DNA linear PAT 27-APR-1998 | |
| DEFINITION | E13776 | | |
| ACCESSION | E13776.1 GI:3252544 | | |
| VERSION | JP 1997234072-A/28. | | |
| KEYWORDS | unidentified | | |
| SOURCE | unidentified | | |
| ORGANISM | unclassified. | | |
| REFERENCE | 1 (bases 1 to 24) | | |
| AUTHORS | Ono,T., Mukaide,M., Hikichi,K. and Mizogami,M. | | |
| TITLE | NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER Patent: JP 1997234072-A 28 09-SEP-1997; | | |
| JOURNAL | S R L:KK | | |
| COMMENT | OC None | | |
| | OC Artificial sequences. | | |
| | PN JP 1997234072-A/28 | | |
| | PD 09-SEP-1997 | | |
| | PF 01-FEB-1996 JP 1996038875 | | |
| | PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI MIZOGAMI MASAFUMI | | |
| | PC C12N15/09,C07H21/04,C12Q1/68,C12Q1/70,(C12N15/09,C12R1:92); CC strandedness: Single; | | |
| | CC topology: Linear; | | |
| | CC hypothetical: No; | | |
| | CC anti-sense: No; | | |
| | FH Key Location/Qualifiers | | |
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| | FT source 1..24 /organism='Artificial sequences' FT | | |
| | misc_feature 1..24 /note='Primer,MNS54'. | | |
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| source | Location/Qualifiers | | |
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| | /organism="unidentified" | | |
| | /mol_type="genomic DNA" | | |
| | /db_xref="taxon:32644" | | |

Fri Aug 19 10:59:59 2005

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AR067252
LOCUS AR067252 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 600 from patent US 5851760.
ACCESSION AR067252
VERSION AR067252.1 GI:5998474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Evans,G.A. and Smith,M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 600 22-DEC-1998;
FEATURES
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1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 37
LOCUS I31384 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 296 from patent US 5582979.
ACCESSION I31384
VERSION I31384.1 GI:1822175
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 296 10-DEC-1996;
FEATURES
source
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 38
LOCUS AX665946/c 23 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 23 from Patent WO0242458.
ACCESSION AX665946
VERSION AX665946.1 GI:29290816
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Tian,H., Zhao,J., Chen,J.L., Cutler,G., An,S., Dai,K. and
AUTHORS Gupte,J.S.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0242458-A 23 30-MAY-2002;
Tularik Inc. (US)
FEATURES
Location/Qualifiers
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source
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TGR342Right PCR expression profiling primer"

Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 117 TTGGACTGACTTTTCTTATGC 137
Db 22 TTGGAATGCCTTTTCTTATTC 2

RESULT 39
LOCUS CQ860133 16 bp DNA linear PAT 10-SEP-2004
DEFINITION Sequence 45 from Patent WO2004072293.
ACCESSION CQ860133
VERSION CQ860133.1 GI:51982021
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Jockers,R., Couturier,C. and Uhlmann,E.
AUTHORS Oligonucleotides which inhibit the expression of the ob-rgrp
TITLE protein and method for detection of compounds modifying the
interaction between the proteins of the ob-rgrp family and the
leptin receptor
JOURNAL Patent: WO 2004072293-A 45 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche
Scientifique (CNRS) (FR)
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificiel"

Query Match 1.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 CTTGCTCGTGTGGCTG 347
Db 16 CTTGCTCGTGTGGCTG 1

RESULT 40
LOCUS AX738983 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4573 from Patent WO03025177.
ACCESSION AX738983
VERSION AX738983.1 GI:30518273
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4573 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1048 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 958 CTGGACCCAGGACATTT 974
Db 1 CTGGACTCAGGACATTT 17
RESULT 50
AX732552/c
LOCUS AX732552 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4186 from Patent WO03025175.
ACCESSION AX732552
VERSION AX732552.1 GI:30511895
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4186 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 838 GAAGCGCGGGTGGATC 854
Db 17 GAAGGCCTGGGTGGATC 1
RESULT 51
AX759882/c
LOCUS AX759882 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3203 from Patent WO03040369.
ACCESSION AX759882
VERSION AX759882.1 GI:32254498
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3203 15-MAY-2003;
Molecular Engines Laboratories (FR)
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source 1. .17
Location/Qualifiers

/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 838 GAAGCGCGGGTGGATC 854
Db 17 GAAGGCCTGGGTGGATC 1
RESULT 52
AR299925
LOCUS AR299925 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 11660 from patent US 6537751.
ACCESSION AR299925
VERSION AR299925.1 GI:31687209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11660 25-MAR-2003;
FEATURES
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 104 TTCAGTGGGGCTATTGG 120
Db 2 TTCAATGGGGCTATTGG 18
RESULT 53
AX713192/c
LOCUS AX713192 18 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 78 from Patent WO03018837.
ACCESSION AX713192
VERSION AX713192.1 GI:29823781
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Waschuetza,S., Schnakenberg,E. and Lustig,M.
TITLE Method and diagnostic kit for the molecular diagnosis of
pharmacologically relevant genes
JOURNAL Patent: WO 03018837-A 78 06-MAR-2003;
Adnagen AG (DE)
FEATURES
source 1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 19 GCCCGGGCGGTGGCAGG 35
Db 17 GCCCGGGCAGTGGCAGG 1
Location/Qualifiers

Fri Aug 19 10:59:59 2005

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RESULT 54
AX132091/c
LOCUS          AX132091          19 bp    DNA          linear          PAT 15-MAY-2001
DEFINITION     Sequence 3309 from Patent WO0130362.
ACCESSION      AX132091
VERSION        AX132091.1  GI:14138396
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Robbins,J.M. and Tritz,R.
TITLE          Ribozyme therapy for the treatment of proliferative skin and eye
               diseases
JOURNAL        Patent: WO 0130362-A 3309 03-MAY-2001;
               IMMUSOL, INC. (US)
FEATURES       source
               1..19
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
               /note="Cyclin B1 ribozyme binding site"
Query Match    1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 790 TGTGCTTGGAGAGGCAG 806
Db 18 TGGGCTTGGAGAGGCAG 2

RESULT 55
I88036/c
LOCUS          I88036          20 bp    DNA          linear          PAT 10-AUG-1998
DEFINITION     Sequence 14 from patent US 5716846.
ACCESSION      I88036
VERSION        I88036.1  GI:3407976
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Brown,S.Joel., Dattagupta,N. and Naidu,Y.M.
TITLE          Method for inhibiting cellular proliferation using antisense
               oligonucleotides to interleukin-6 receptor mRNA
JOURNAL        Patent: US 5716846-A 14 10-FEB-1998;
FEATURES       source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match    1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 54;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CAGGAAGCCGGAAGCAG 48
Db 18 CAGGAAGCCGGAAGCAG 2

RESULT 56
AR136416/c
LOCUS          AR136416          20 bp    DNA          linear          PAT 16-JUN-2001
DEFINITION     Sequence 11 from patent US 6136604.
ACCESSION      AR136416
VERSION        AR136416.1  GI:14477088
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.

REFERENCE      1 (bases 1 to 20)
AUTHORS        Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
               Sankaran,B. and Fletcher,L.D.
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 6064 06-MAY-2003;
FEATURES       source
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               /organism="unknown"
               /mol_type="genomic DNA"
Query Match    1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

REFERENCE      1 (bases 1 to 20)
AUTHORS        Monia,B.P. and Wyatt,J.
TITLE          Antisense inhibition of methionine aminopeptidase 2 expression
JOURNAL        Patent: US 6136604-A 11 24-OCT-2000;
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match    1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 TCGGGAGACATGGCGGCGT 81
Db 20 TCGGGCAACATGGCGGCGT 1

RESULT 57
CQ767202
LOCUS          CQ767202          20 bp    DNA          linear          PAT 03-MAR-2004
DEFINITION     Sequence 30 from Patent WO2004005513.
ACCESSION      CQ767202
VERSION        CQ767202.1  GI:44909292
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Besterman,J.M., Li,Z., Delorme,D. and Bonfils,C.
TITLE          Methods for specifically inhibiting histone deacetylase-7 and 8
JOURNAL        Patent: WO 2004005513-A 30 15-JAN-2004;
               Methylgene, Inc. (CA)
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Description of Combined DNA/RNA Molecule: Synthetic
               oligonucleotide-Description of Artificial Sequence:
               Synthetic oligonucleotide"
Query Match    1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 58
AR315527/c
LOCUS          AR315527          20 bp    DNA          linear          PAT 12-JUN-2003
DEFINITION     Sequence 6064 from patent US 6559294.
ACCESSION      AR315527
VERSION        AR315527.1  GI:31708953
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
               Sankaran,B. and Fletcher,L.D.
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 6064 06-MAY-2003;
FEATURES       source
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               /organism="unknown"
               /mol_type="genomic DNA"
Query Match    1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 459 AGTGGTAGCACATTATTCTG 478
Db 20 AGCGGTAGCAGTTTCTTCTG 1

RESULT 59
AR442611
LOCUS AR442611 20 bp DNA PAT 20-FEB-2004
DEFINITION Sequence 219 from patent US 6670130.
ACCESSION AR442611
VERSION AR442611.1 GI:42669868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Kim,C.M., Park,H.K. and Jang,H.J.
JOURNAL Oligonucleotide for detection and identification of Mycobacteria
FEATURES Patent: US 6670130-A 219 30-DEC-2003;
source Location/Qualifiers
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 998 TGCACATGAAAGTTTGAGAA 1017
Db 1 TGCACACAAAACTTTGAGAA 20

RESULT 60
AX293011/c
LOCUS AX293011 20 bp DNA PAT 21-NOV-2001
DEFINITION Sequence 4773 from Patent WO0179548.
ACCESSION AX293011
VERSION AX293011.1 GI:17054694
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1
TITLE Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
JOURNAL Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
Patent: WO 0179548-A 4773 25-OCT-2001;
FEATURES CORNELL RESEARCH FOUNDATION, INC. (US)
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 767 CATCGAAACCTTTGCTTGG 786
Db 20 CATCGACACCGTTGCTTCG 1

RESULT 61
AX456087
LOCUS AX456087 20 bp DNA PAT 06-JUL-2002
DEFINITION Sequence 17 from Patent WO0170675.
ACCESSION AX456087
VERSION AX456087.1 GI:21715042

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Delorme,D., Woo,S.H. and Vaisburg,A.
TITLE Inhibitors of histone deacetylase
JOURNAL Patent: WO 0170675-A 17 27-SEP-2001;
FEATURES Methylgene, Inc. (CA)
source Location/Qualifiers
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 743 AGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 62
AX589807/c
LOCUS AX589807 20 bp DNA PAT 24-JAN-2003
DEFINITION Sequence 9 from Patent WO02079249.
ACCESSION AX589807
VERSION AX589807.1 GI:27901058
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Escary,J.L.
TITLE New polynucleotides and polypeptides of the ifn_g(a)-21 gene
JOURNAL Patent: WO 02079249-A 9 10-OCT-2002;
FEATURES GenOdysee (FR)
source Location/Qualifiers
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 608 TTCATAAGTAGGAGATGAGT 627
Db 20 TTCCCAAGTAGCAGATGAGT 1

RESULT 63
AX703629
LOCUS AX703629 20 bp DNA PAT 03-APR-2003
DEFINITION Sequence 33 from Patent WO03006652.
ACCESSION AX703629
VERSION AX703629.1 GI:29538528
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Li,Z., Bonfils,C. and Besterman,J.
TITLE Inhibition of specific histone deacetylase isoforms
JOURNAL Patent: WO 03006652-A 33 23-JAN-2003;
FEATURES Methylgene, Inc. (CA)
source Location/Qualifiers

Fri Aug 19 10:59:59 2005

source 1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
||| ||||| ||||| |||||
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 64
AX962777/c
LOCUS
DEFINITION
Sequence 33 from Patent WO03104458.
ACCESSION
AX962777
VERSION
AX962777.1 GI:40881890
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
TITLE
Baker,B.F., Freier,S.M. and Dobie,K.W.
Antisense modulation of il-1 receptor-associated kinase-1
expression
JOURNAL
Patent: WO 03104458-A 33 18-DEC-2003;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCCTCTCATGACCCA 836
||| ||||| ||||| |||||
Db 20 AGGAGGCCTCCTATGACCCA 1

RESULT 65
AX962848
LOCUS
DEFINITION
Sequence 104 from Patent WO03104458.
ACCESSION
AX962848
VERSION
AX962848.1 GI:40881971
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
Baker,B.F., Freier,S.M. and Dobie,K.W.
Antisense modulation of il-1 receptor-associated kinase-1
expression
JOURNAL
Patent: WO 03104458-A 104 18-DEC-2003;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 817 AGCAGGCCTCTCATGACCCA 836
||| ||||| ||||| |||||
Db 1 AGGAGGCCTCCTATGACCCA 20

RESULT 66
BD012571
LOCUS
DEFINITION
Human cytochrome P450-transgenic mouse.
ACCESSION
BD012571
VERSION
BD012571.1 GI:22092760
KEYWORDS
WO 0111951-A/10.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS
TITLE
Ishida,I., Tomizuka,K., Kuroiwa,Y., Oshima,T., Suzuk,M. and Ito,K.
Human cytochrome P450-transgenic mouse
JOURNAL
Patent: WO 0111951-A 10 22-FEB-2001;
KIRIN BEER KK,ISAO ISHIDA,KAZUMA TOMIZUKA,YOSHIMI KUROIWA, AKESHI
OSHIMA, MUTSUMI SUZUKI,KUNIO ITO
COMMENT
OS Artificial Sequence
PN WO 0111951-A/10
PD 22-FEB-2001
PF 11-AUG-2000 WO 2000JP005424
PR 13-AUG-1999 JP 99P 229094
PI ISAO ISHIDA,KAZUMA TOMIZUKA,YOSHIMI KUROIWA,TAKESHI OSHIMA, PI
MUTSUMI SUZUKI,
PI KUNIO ITO
PC A01K67/027,C12N15/00,C12Q1/68,C12N15/85,C12N5/10,G01N33/50, PC
G01N33/15
CC Description of Artificial Sequence:primer
for detecting CYP3A4 CDNA
CC G01N33/15
FH Key Location/Qualifiers.
source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 105 TCAGTGGGCTATTGGACTG 124
||||| ||||| ||||| |||||
Db 1 TCAGTGAGGCTGTTGGATTG 20

RESULT 67
BD143015
LOCUS
DEFINITION
Method of assaying human ABC transporter and probe and kit therefor.
ACCESSION
BD143015
VERSION
BD143015.1 GI:27848773
KEYWORDS
JP 2002112775-A/86.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 21)
AUTHORS
TITLE
Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
Method of assaying human ABC transporter and probe and kit therefor
JOURNAL
Patent: JP 2002112775-A 86 16-APR-2002;
OTSUKA PHARMACEUTICAL FACTORY INC
COMMENT
OS human ABCB4 gene
PN JP 2002112775-A/86
PD 16-APR-2002
PF 03-OCT-2000 JP 2000303404
PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAOKA
PC C12N15/09,C12Q1/68,C12N15/00
CC Method of assaying human ABC transporter and probe and kit CC

therefor

 FH Key Location/Qualifiers
 FT source 1. .21
 FT /organism='human ABCB4 gene'.

FEATURES
 source
 Location/Qualifiers
 1. .21
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

 Query Match 1.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 58;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 295 TGGAAATGTTGTTTCTGCCT 314
 ||||| ||||| ||||| |||||

Db 1 TGGAGTTCTTGTGCTGCCT 20

RESULT 68

E12685

LOCUS 21 bp DNA linear PAT 27-APR-1998

DEFINITION Primer.

ACCESSION E12685

VERSION E12685.1 GI:3251517

KEYWORDS JP 1997056380-A/2.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 21)

AUTHORS Tanida,E., Que,C., Yagi,S., Hasegawa,A., Kiyozawa,K. and Yano,A.

TITLE ASIALOGLYCOPROTEIN RECEPTOR DERIVATIVE AND ITS USE

JOURNAL Patent: JP 1997056380-A 2 04-MAR-1997;

COMMENT TONEN CORP, INTERNATL REAGENTS CORP, KIYOZAWA KENDOU

OS None

OC Artificial sequences.

PN JP 1997056380-A/2

PD 04-MAR-1997

PF 21-AUG-1995 JP 1995212118

PI TANIDA EMIKO, OUE CHI HARU, YAGI SHINTARO, HASEGAWA AKIRA, PI KIYOZAWA KENDOU,

PI YANO AKIHIKO

PC C12N15/09,C07H21/04,C07K14/705,C12N1/21,C12N5/10,C12P21/02, PC G01N33/53.

PC G01N33/566,G01N33/576,(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), PC (C12P21/02,

PC C12R1:19),(C12P21/02,C12R1:91);

CC strandedness: Single;

CC topology: Linear;

CC hypothetical: No;

FH Key Location/Qualifiers

FT source 1. .21

FT /organism='Artificial sequences'.

FT Location/Qualifiers

 1. .21
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

FEATURES
 source

 Query Match 1.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 58;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 820 AGGCCTCTCATGACCCAGGA 839
 || ||| ||||| ||||| |||||

Db 1 AGCCCTATCATGACCAAGGA 20

RESULT 69

AR529487/c

LOCUS 21 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 690 from patent US 6727063.

ACCESSION AR529487

VERSION AR529487.1 GI:53917924

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 21)

AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.

TITLE Single nucleotide polymorphisms in genes

JOURNAL Patent: US 6727063-A 690 27-APR-2004;

FEATURES
 Location/Qualifiers
 source 1. .21
 /organism="unknown"
 /mol_type="genomic DNA"

 Query Match 1.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 58;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 733 GCAGTCTTGTAGGCAGCTGC 752
 ||||| | ||||| |||||

Db 20 GCAGTCATTRAGGCAGCTGC 1

RESULT 70

AX095512/c

LOCUS AX095512 21 bp DNA linear PAT 30-MAR-2001

DEFINITION Sequence 690 from Patent WO0118250.

ACCESSION AX095512

VERSION AX095512.1 GI:13511715

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.

TITLE Single nucleotide polymorphisms in genes

JOURNAL Patent: WO 0118250-A 690 15-MAR-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)

FEATURES
 Location/Qualifiers
 source 1. .21
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

 Query Match 1.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 58;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 733 GCAGTCTTGTAGGCAGCTGC 752
 ||||| | ||||| |||||

Db 20 GCAGTCATTRAGGCAGCTGC 1

RESULT 71

AX956467

LOCUS AX956467 21 bp DNA linear PAT 08-JAN-2004

DEFINITION Sequence 17 from Patent WO03097869.

ACCESSION AX956467

VERSION AX956467.1 GI:40784976

KEYWORDS

SOURCE Rosa sp.

ORGANISM Rosa sp.

REFERENCE 1

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

TITLE Sues, K.H. Microsatellite markers for genetic analyses and the differentiation

[illegible]

AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: WO 02072815-A 69 19-SEP-2002;
EIIICHI SOEDA,TAKESHI KUKITA
COMMENT OS Artificial Sequence
PN WO 02072815-A/69
PD 19-SEP-2002
PF 17-MAY-2001 WO 2001JP004139
PR 12-MAR-2001 JP O1P 68285
PI EIIICHI SOEDA
PC Cl2N15/09,C12Q1/68
CC Description of Artificial Sequence: Synthetic DNA FH Key
FT source 1. .20
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1010 TTGAGAAGCATCATCAT 1027
Db 1 TTGAAAAGCATCAGCAT 18
RESULT 77
BD247804
LOCUS BD247804 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of interleukin-5 signal transduction.
ACCESSION BD247804
VERSION BD247804.1 GI:33057574
KEYWORDS JP 2002539846-A/152.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Karras,J.G. and Mckay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: JP 2002539846-A 152 26-NOV-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002539846-A/152
PD 26-NOV-2002
PF 17-MAR-2000 JP 2000608790
PR 26-MAR-1999 US 09/280799
PI NICHOLAS M DEAN,JAMES G KARRAS,ROBERT MCKAY
PC Cl2N15/09,A61K31/711,A61K48/00,A61P11/06,A61P29/00,A61P35/00,
A61P43/00,
PC A61P43/00,C12N5/02,C12N15/00
CC Description of Artificial Sequence:Synthetic
FH Key Location/Qualifiers
FT source 1. .20
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 78
E43993/c
LOCUS E43993 ACE-analogous gene. 20 bp DNA linear PAT 31-JAN-2002
DEFINITION ACE-analogous gene.
ACCESSION E43993
VERSION E43993.1 GI:18629196
KEYWORDS JP 2001046072-A/7.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sugano,S. and Komatsu,T.
TITLE ACE-analogous gene
JOURNAL Patent: JP 2001046072-A 7 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001046072-A/7
PD 20-FEB-2001
PF 06-AUG-1999 JP 1999223892
PR
PI SUMIO SUGANO,TAKAMI KOMATSU
PC
Cl2N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K39/395, PC
A61K39/395,
PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
C12N1/19,
PC Cl2N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC
A61K37/64,
PC C12N5/00
CC
FH Key Location/Qualifiers
FT source 1. .20
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 182 GTCCTGATTTTCCACGCC 199
Db 18 GTTCTGATTTTCCAGCC 1
RESULT 79
AR183974/c
LOCUS AR183974 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6342392.
ACCESSION AR183974
VERSION AR183974.1 GI:20227943
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.
TITLE Nucleotide and deduced amino acid sequences of tumor gene Int6
JOURNAL Patent: US 6342392-A 9 29-JAN-2002;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 926 CTTATTAGAAATGCAGAA 943

Db 20 CTAATTAAAAATGCAGAA 3

RESULT 80

AR540678/c

LOCUS AR540678 linear PAT 08-OCT-2004

DEFINITION Sequence 9 from patent US 6737251.

ACCESSION AR540678

VERSION AR540678.1 GI:53931994

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Marchetti,A., Buttitta,F., Smith,G.H. and Callahan,R.

TITLE Nucleotide and deduced amino acid sequences of tumor gene Int6

JOURNAL Patent: US 6737251-A 9 18-MAY-2004;

FEATURES

source

1. .20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 70;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 CTTATTAGAAATGCAGAA 943

|||||

Db 20 CTAATTAAAAATGCAGAA 3

RESULT 81

AX417273/c

LOCUS AX417273 linear PAT 18-JUN-2002

DEFINITION Sequence 2 from Patent EP1197553.

ACCESSION AX417273

VERSION AX417273.1 GI:21522583

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Kronenwett,R., Graef,T., Haas,R. and Nedbal,W.

TITLE Antisense nucleic acid against alphav integrin

JOURNAL Patent: EP 1197553-A 2 17-APR-2002;

JOURNAL A3D GmbH, Antisense Design & Drug Development (DE)

FEATURES

source

1. .20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Antisense ODN directed against alphav integrin chain"

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 70;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 417 TTTTCCTTATATTTGGAA 434

|||||

Db 18 TTTTCCTTATATTTCCAA 1

RESULT 82

AX467276/c

LOCUS AX467276 linear PAT 16-JUL-2002

DEFINITION Sequence 2 from Patent WO0231142.

ACCESSION AX467276

VERSION AX467276.1 GI:21900554

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Kronenwett,R., Graef,T., Haas,R. and Nedbal,W.

TITLE Antisense nucleic acid against alphav integrin

JOURNAL Patent: WO 0231142-A 2 18-APR-2002;

JOURNAL A3D GmbH, Antisense Design & Drug Development (DE)

FEATURES

source

1. .20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Antisense ODN directed against alphav integrin chain"

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 70;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 417 TTTTCCTTATATTTGGAA 434

|||||

Db 18 TTTTCCTTATATTTCCAA 1

RESULT 83

AX544228/c

LOCUS AX544228 linear PAT 23-NOV-2002

DEFINITION Sequence 52 from Patent WO0244426.

ACCESSION AX544228

VERSION AX544228.1 GI:25277780

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Nunez,G., Inohara,N., Ogura,Y., Cho,J., Nicolae,D.L. and Bonen,D.

TITLE Nod2 nucleic acids and proteins

JOURNAL Patent: WO 0244426-A 52 06-JUN-2002;

JOURNAL THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US) ; The University of Chicago (US)

FEATURES

source

1. .20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Synthetic"

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 70;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 784 TGGGGATGTGCTTGAGA 801

|||||

Db 18 TGGGGATGTGTTGAAGA 1

RESULT 84

BD090191

LOCUS BD090191 linear PAT 27-AUG-2002

DEFINITION A method of arraying genome clone.

ACCESSION BD090191

VERSION BD090191.1 GI:22635801

KEYWORDS JP 2001321190-A/2435.

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 20)

AUTHORS Soeda,E.

TITLE A method of arraying genome clone

JOURNAL Patent: JP 2001321190-A 2435 20-NOV-2001;

JOURNAL THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA

COMMENT

OS Artificial Sequence

PN JP 2001321190-A/2435

PD 20-NOV-2001

PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1. .20
FT /organism='Artificial Sequence'.
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1010 TTTGAGAAGCATCATCAT 1027
||||| ||||| ||||| |||||
Db 1 TTTGAAAAGCATCAGCAT 18

RESULT 85
AR530530/c
LOCUS AR530530 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1733 from patent US 6727063.
ACCESSION AR530530
VERSION AR530530.1 GI:53918967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 1733 27-APR-2004;
FEATURES
source 1. .21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTGGCTGGGCAGGCTGCC 22
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Db 21 CTGCCTGGGGYAGGCTGTCC 2

RESULT 86
AX096555/c
LOCUS AX096555 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1733 from Patent WO0118250.
ACCESSION AX096555
VERSION AX096555.1 GI:13512809
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1733 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1. .21
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTGGCTGGGCAGGCTGCC 22
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Db 21 CTGCCTGGGGYAGGCTGTCC 2

RESULT 87
AX539512
LOCUS AX539512 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 299 from Patent WO02059142.
ACCESSION AX539512
VERSION AX539512.1 GI:25273003
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug resistance-associated protein 1 (mrp-1) and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02059142-A 299 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
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source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
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Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
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Db 4 AATCACTCAACCTCTCTG 21

RESULT 88
AX539513/c
LOCUS AX539513 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 300 from Patent WO02059142.
ACCESSION AX539513
VERSION AX539513.1 GI:25273004
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug resistance-associated protein 1 (mrp-1) and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02059142-A 300 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
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Db 4 AATCACTCAACCTCTCTG 21

Fri Aug 19 10:59:59 2005

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Db      18 AATCACTCAACCTCTCTG 1
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RESULT 89
AX539514
LOCUS      AX539514                21 bp      DNA          linear      PAT 23-NOV-2002
DEFINITION Sequence 301 from Patent WO02059142.
ACCESSION  AX539514
VERSION    AX539514.1  GI:25273006
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE      Polymorphisms in the human gene for the multidrug
           resistance-associated protein 1 (mrp-1) and their use in diagnostic
           and therapeutic applications
JOURNAL    Patent: WO 02059142-A 301 01-AUG-2002;
           Epidauros Biotechnologie AG (DE)
FEATURES   Location/Qualifiers
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               /db_xref="taxon:32630"
               /note="m=a or c"
Query Match      1.3%;   Score 14.8;   DB 1;   Length 21;
Best Local Similarity 88.9%;   Pred. No. 68;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      1074 AACCACTTAACCTCTCTG 1091
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Db      4 AATCACTMAACCTCTCTG 21

RESULT 90
AX539515/c
LOCUS      AX539515                21 bp      DNA          linear      PAT 23-NOV-2002
DEFINITION Sequence 302 from Patent WO02059142.
ACCESSION  AX539515
VERSION    AX539515.1  GI:25273008
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE      Polymorphisms in the human gene for the multidrug
           resistance-associated protein 1 (mrp-1) and their use in diagnostic
           and therapeutic applications
JOURNAL    Patent: WO 02059142-A 302 01-AUG-2002;
           Epidauros Biotechnologie AG (DE)
FEATURES   Location/Qualifiers
           source
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="k=g or t"
Query Match      1.3%;   Score 14.8;   DB 1;   Length 21;
Best Local Similarity 88.9%;   Pred. No. 68;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      1074 AACCACTTAACCTCTCTG 1091
          || |||| | |||| |||| ||||
Db      18 AATCACTMAACCTCTCTG 1

RESULT 91
AX539516
LOCUS      AX539516                21 bp      DNA          linear      PAT 23-NOV-2002
DEFINITION Sequence 303 from Patent WO02059142.
ACCESSION  AX539516
VERSION    AX539516.1  GI:25273010
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE      Polymorphisms in the human gene for the multidrug
           resistance-associated protein 1 (mrp-1) and their use in diagnostic
           and therapeutic applications
JOURNAL    Patent: WO 02059142-A 303 01-AUG-2002;
           Epidauros Biotechnologie AG (DE)
FEATURES   Location/Qualifiers
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               /db_xref="taxon:32630"
Query Match      1.3%;   Score 14.8;   DB 1;   Length 21;
Best Local Similarity 88.9%;   Pred. No. 68;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      1074 AACCACTTAACCTCTCTG 1091
          || |||| | |||| |||| ||||
Db      18 AATCACTAAACCTCTCTG 1

RESULT 93
AX706596
LOCUS      AX706596                21 bp      DNA          linear      PAT 04-APR-2003
DEFINITION Sequence 293 from Patent WO03013534.
ACCESSION  AX706596
VERSION    AX706596.1  GI:29563019
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
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AUTHORS Heinrich, G. and Kerb, R.
TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5
JOURNAL Patent: WO 03013534-A 293 20-FEB-2003;
Epidauros Biotechnologie AG (DE)
FEATURES Location/Qualifiers

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
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Db 4 AATCACTAAACCTCTCTG 21

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| RESULT 94 | | | | | | PAT 04-APR-2003 |
| AX706597/c | | | | | | |
| LOCUS | AX706597 | 21 bp | DNA | linear | | |
| DEFINITION | Sequence 294 from Patent WO03013534. | | | | | |
| ACCESSION | AX706597 | | | | | |
| VERSION | AX706597.1 | GI:29563020 | | | | |
| KEYWORDS | . | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | | |

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Qy | 1074 | AACCACTTAACCTCTCTG | 1091 |
| | | | |
| D _b | 18 | AATCACTAAACCTCTCTG | 1 |

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|------------|---|-------------|-----|--------|-----------------|
| RESULT | 95 | | | | |
| AX706598 | | | | | |
| LOCUS | AX706598 | | | | |
| DEFINITION | Sequence 295 from Patent WO03013534. | 21 bp | DNA | linear | PAT 04-APR-2003 |
| ACCESSION | AX706598 | | | | |
| VERSION | AX706598.1 | GI:29563021 | | | |
| KEYWORDS | | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |

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misc_feature 11 /note="m=a or c"
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Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
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Db 4 AATCACTMAACCTCTCTG 21

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| RESULT 96 | | | |
| AX706599/c | | | |
| LOCUS | AX706599 | 21 bp | DNA |
| DEFINITION | Sequence 296 from Patent WO03013534. | linear | PAT 04-APR-2003 |

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misc_feature
11
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Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
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Db 18 AATCACTMAAACCTCTCTG 1

| | |
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| RESULT | 97 |
| AX707526 | |
| LOCUS | 21 bp DNA |
| DEFINITION | Sequence 293 from Patent WO03013536. |
| ACCESSION | AX707526 |
| VERSION | AX707526.1 GI:29563699 |
| | linear PAT 04-APR-2003 |

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Query Match      1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1074 AACCACTTAACCTCTCTG 1091
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pb 4 AATCACTAAACCTCTCTG 21

TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 1797 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/1797
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PJ JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1023 ATCATAGAGAAGTAAA 1038
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Db 2 ATCATATAGAAGTAAA 17
RESULT 103
CQ617825/c
LOCUS CQ617825 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2565 from Patent WO0192524.
ACCESSION CQ617825
VERSION CQ617825.1 GI:41668043
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2565 06-DEC-2001;
Aeomica, Inc. (US)
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source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
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Db 17 AGGCAGCTGCCGCCTT 2
RESULT 104
CQ617826/c
LOCUS CQ617826 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2566 from Patent WO0192524.

ACCESSION CQ617826
VERSION CQ617826.1 GI:41668044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2566 06-DEC-2001;
Aeomica, Inc. (US)
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source Location/Qualifiers
1. .17
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Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
||||| ||||||| |||||
Db 16 AGGCAGCTGCCGCCTT 1
RESULT 105
AR458888/c
LOCUS AR458888 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2565 from patent US 6686188.
ACCESSION AR458888
VERSION AR458888.1 GI:42693945
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2565 03-FEB-2004;
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source Location/Qualifiers
1. .17
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Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
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Db 17 AGGCAGCTGCCGCCTT 2
RESULT 106
AR458889/c
LOCUS AR458889 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2566 from patent US 6686188.
ACCESSION AR458889
VERSION AR458889.1 GI:42693946
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle

Fri Aug 19 10:59:59 2005

JOURNAL Patent: US 686188-A 2566 03-FEB-2004;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTT 758
Db 16 AGGCAGCTGCCGCCTT 1

RESULT 107
AX421988
LOCUS AX421988 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 324 from Patent WO0188124.
ACCESSION AX421988
VERSION AX421988.1 GI:21525370
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 324 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 958 CTGGACCCAGGACATT 973
Db 2 CTGGACTCAGGACATT 17

RESULT 108
AX423718
LOCUS AX423718 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2054 from Patent WO0188124.
ACCESSION AX423718
VERSION AX423718.1 GI:21527100
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 2054 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 959 TGGACCCAGGACATT 974
Db 1 TGGACTCAGGACATT 16

RESULT 109
AX674053/c
LOCUS AX674053 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2498 from Patent WO03004526.
ACCESSION AX674053
VERSION AX674053.1 GI:29332401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
JOURNAL Patent: WO 03004526-A 2498 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 969 ACATTTTGATGAGATC 984
Db 16 ACATTCGTGATGAGATC 1

RESULT 110
AX726789
LOCUS AX726789 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4476 from Patent WO03025176.
ACCESSION AX726789
VERSION AX726789.1 GI:30506132
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 4476 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 519 ATACATGTGCACATGC 534
Db 2 ATCCATGTGCACATGC 17

RESULT 111

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AX736977/c
LOCUS      AX736977              17 bp      DNA          linear      PAT 08-MAY-2003
DEFINITION Sequence 2567 from Patent WO03025177.
ACCESSION  AX736977
VERSION     AX736977.1  GI:30516265
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL     Patent: WO 03025177-A 2567 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      839 AAGCCCGGGTGGATC 854
Db      16 AAGCCCTGGTGGATC 1

RESULT 112
AX762887/c
LOCUS      AX762887              17 bp      DNA          linear      PAT 25-JUN-2003
DEFINITION Sequence 6208 from Patent WO03040369.
ACCESSION  AX762887
VERSION     AX762887.1  GI:32257503
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 6208 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      839 AAGCCCGGGTGGATC 854
Db      16 AAGCCTGGGTGGATC 1

RESULT 113
AX132090/c
LOCUS      AX132090              19 bp      DNA          linear      PAT 15-MAY-2001
DEFINITION Sequence 3308 from Patent WO0130362.
ACCESSION  AX132090
VERSION     AX132090.1  GI:14138395
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
```

```
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
JOURNAL     Patent: WO 0130362-A 3308 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="Cyclin B1 ribozyme binding site"

Query Match      1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      791 GTGCTTGGAGAGGCAG 806
Db      19 GGGCTTGGAGAGGCAG 4

RESULT 114
BD266785
LOCUS      BD266785              20 bp      DNA          linear      PAT 17-JUL-2003
DEFINITION Methods for treating cancer and for mediating chemotaxis of
            dendritic cells.
ACCESSION  BD266785
VERSION     BD266785.1  GI:33076553
KEYWORDS    JP 2002533402-A/5.
SOURCE      synthetic construct
            ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Keting,C., Xin,H., Chan,V.W.F., Kothakota,S., Williams,L.T. and
            Winter,J.A.
TITLE       Methods for treating cancer and for mediating chemotaxis of
            dendritic cells
JOURNAL     Patent: JP 2002533402-A 5 08-OCT-2002;
            CHIRON CORP
COMMENT     OS Artificial Sequence
            PN JP 2002533402-A/5
            PD 08-OCT-2002
            PF 28-DEC-1999 JP 2000590657
            PR 31-DEC-1998 US 60/114498
            PI CHU KETING,HONG XIN,VIVIEN W F CHAN,SRINIVAS
            KOTHAKOTA,LEWIS T
            PI WILLIAMS,
            PI JILL A WINTER
            PC
            AG1K38/00,AG1K31/711,AG1K39/395,AG1K39/395,AG1K45/00,AG1K48/00, PC
            AG1P35/00,
            PC AG1P37/00,AG1P43/00,C07K14/47//C12N15/02,AG1K37/02,C12N15/00
            CC PCR Primer
            FH Key
            FT source
            FT
            Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      781 GCTTGGGGATGTGCTT 796
Db      2 GCTTGGTGATGTGCTT 17
```

```
RESULT 115
AR295060      AR295060      20 bp      DNA      linear      PAT 12-JUN-2003
LOCUS
DEFINITION    Sequence 6795 from patent US 6537751.
ACCESSION    AR295060
VERSION      AR295060.1  GI:31682344
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL      Patent: US 6537751-A 6795 25-MAR-2003;
FEATURES     Location/Qualifiers
            1. .20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      218 TTCATTGCCAAAGAG 233
Db      5 TTCTTTGCCAAAGAG 20

RESULT 116
AR311266/c    AR311266      20 bp      DNA      linear      PAT 12-JUN-2003
LOCUS
DEFINITION    Sequence 1803 from patent US 6559294.
ACCESSION    AR311266
VERSION      AR311266.1  GI:31704692
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE       Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 1803 06-MAY-2003;
FEATURES     Location/Qualifiers
            1. .20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      287 TTCACTACTGGGATTG 302
Db      19 TTCACTACGGGATTG 4

RESULT 117
AR489914      AR489914      20 bp      DNA      linear      PAT 15-MAY-2004
LOCUS
DEFINITION    Sequence 37 from patent US 6710174.
ACCESSION    AR489914
VERSION      AR489914.1  GI:47257027
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Bennett,C.F. and Watt,A.T.
TITLE       Antisense inhibition of vascular endothelial growth factor
```

```
receptor-1 expression
JOURNAL      Patent: US 6710174-A 37 23-MAR-2004;
FEATURES     Location/Qualifiers
            1. .20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      626 GTTTTATTCTCAGCAA 641
Db      4 GTTTTATGCTCAGCAA 19

RESULT 118
AR565745/c    AR565745      20 bp      DNA      linear      PAT 08-OCT-2004
LOCUS
DEFINITION    Sequence 91 from patent US 6767739.
ACCESSION    AR565745
VERSION      AR565745.1  GI:53981799
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Crooke,R.M. and Graham,M.J.
TITLE       Antisense modulation of microsomal triglyceride transfer protein
            expression
JOURNAL      Patent: US 6767739-A 91 27-JUL-2004;
FEATURES     Location/Qualifiers
            1. .20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      130 TCATTATGCTGGGATGT 145
Db      18 TCATTATGCTGGCATGT 3

RESULT 119
BD185951      BD185951      19 bp      DNA      linear      PAT 17-JUN-2003
LOCUS
DEFINITION    A stabilization method and a preservation method for a reagent for
            nucleic acid amplification or detection reaction.
ACCESSION    BD185951
VERSION      BD185951.1  GI:31878151
KEYWORDS     WO 02101042-A/147.
SOURCE       synthetic construct
ORGANISM     synthetic construct
            other sequences; artificial sequences.
            1 (bases 1 to 19)
REFERENCE    Sagawa,H., Uemori,T., Mukai,H., Yamamoto,J., Tomono,J.,
            Kobayashi,E., Enoki,T., Asada,K. and Kato,I.
AUTHORS     A stabilization method and a preservation method for a reagent for
            nucleic acid amplification or detection reaction
            Patent: WO 02101042-A 147 19-DEC-2002;
            TAKARA BIO INC,HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO
            YAMAMOTO, JUN TOMONO,EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO
            ASADA,IKUNOSHIN KATO
COMMENT      OS Artificial Sequence
            PN WO 02101042-A/147
            PD 19-DEC-2002
            PF 12-JUN-2002 WO 2002JP005832
            PR 12-JUN-2001 JP 01P 177737,20-AUG-2001 JP 01P 249689 PI
            HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO YAMAMOTO, PI
            JUN TOMONO,
            PI EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO ASADA,IKUNOSHIN KATO PC
```

C12N15/09,C12Q1/68
CC Designed oligonucleotide probe as Mycol70-probe to detect a
CC DNA fragment
CC amplifying a portion of ATPase operon from Mycoplasma CC
pneumoniae.
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1064 CCAGTGGCTAAACCACTTA 1082
Db 1 CCAGAGGCTGAACCACTTA 19
|||||
RESULT 120
BD004746
LOCUS
BD004746 19 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting specific nucleic acid sequence.
ACCESSION BD004746
VERSION BD004746.1 GI:18632707
KEYWORDS JP 2001013147-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ishiguro,T., Otsuka,M., Inoue,T., Yahata,H. and Sugiyur,Y.
TITLE Method for detecting specific nucleic acid sequence
JOURNAL Patent: JP 2001013147-A 4 19-JAN-2001;
TOSOH CORP
COMMENT
OS Artificial Sequence
PN JP 2001013147-A/4
PD 19-JAN-2001
PF 22-MAY-2000 JP 2000154431
PR TAKAHIKO ISHIGURO,MASAMI OTSUKA,TERUHIKO INOUE,HIDEO YAHATA,
PI YUKIO SUGIURA
PC G01N33/566,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/536,
PC C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 189 TTTTCACGCGCATCTCCCC 207
Db 1 TTTTCCTCTCCCTCTCCCC 19
|||||
RESULT 121
A36286/c
LOCUS
A36286 20 bp DNA linear PAT 04-MAR-1997
DEFINITION Sequence 9 from Patent EP0574345.
ACCESSION A36286
VERSION A36286.1 GI:2293718
KEYWORDS

unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bardosa,N.N., De,B.B., Borja,T.M., Pons,A.F. and Torres,P.V.
TITLE Procedure for the detection and identification of viral and
subviral pathogens
JOURNAL Patent: EP 0574345-A 9 15-DEC-1993;
INST NACIONAL DE INVESTIGACION (ES)
COMMENT Other publication JP 6062900 940308
Other publication AU 4120093 931223
Other publication CA 2098270 931213
Other publication ES 2044784 940101.
FEATURES
source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 857 TCTTTGTGTTGTAGTCCAT 875
Db 19 TCTTTGTTCGTCGTCAT 1
|||||
RESULT 122
AR011463
LOCUS
AR011463 20 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 336 from patent US 5762938.
ACCESSION AR011463
VERSION AR011463.1 GI:3969453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Paolletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,W.I., Audonnet,J.-C.Francis. and Gettig,R.Robert.
TITLE Modified recombinant vaccinia virus and expression vectors thereof
JOURNAL Patent: US 5762938-A 336 09-JUN-1998;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 394 CATTTTCCTTACAATCAA 412
Db 1 CATGTTCTCTTCAAGTCAA 19
|||||
RESULT 123
AR071524/c
LOCUS
AR071524 20 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 24 from patent US 5911982.
ACCESSION AR071524
VERSION AR071524.1 GI:7222412
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chao,Y.-C.
TITLE Hz-1 virus persistence-associated-gene 1 (PAG1) promoter uses
therefor, and compositions containing same or products therefrom
JOURNAL Patent: US 5911982-A 24 15-JUN-1999;

| | | | | | |
|-----------------------|--------|---|--|-----------------|--|
| FEATURES | | Location/Qualifiers | | | |
| source | | 1. .20 | | | |
| | | /organism="synthetic construct" | | | |
| | | /mol_type="genomic DNA" | | | |
| | | /db_xref="taxon:32630" | | | |
| Query Match | | 1.3%; Score 14.2; DB 1; Length 20; | | | |
| Best Local Similarity | | 84.2%; Pred. No. 89; | | | |
| Matches | | 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | |
| QY | 952 | CCCACTCTGGACCCAGGAC 970 | | | |
| | | | | | |
| Db | 2 | CCACACGACCCAGGAC 20 | | | |
| | | | | | |
| RESULT 128 | | | | | |
| BD176347/c | | | | | |
| LOCUS | | BD176347 | | 20 bp DNA | |
| DEFINITION | | A method of arraying genome clone. | | linear | |
| ACCESSION | | BD176347 | | PAT 18-MAR-2003 | |
| VERSION | | BD176347.1 | | | |
| KEYWORDS | | WO 02072815-A/147. | | | |
| SOURCE | | synthetic construct | | | |
| ORGANISM | | synthetic construct | | | |
| REFERENCE | | 1 (bases 1 to 20) | | | |
| AUTHORS | | Soeda,E. | | | |
| TITLE | | A method of arraying genome clone | | | |
| JOURNAL | | Patent: WO 02072815-A 147 19-SEP-2002; | | | |
| | | EIICHI SOEDA,TAKESHI KUKITA | | | |
| COMMENT | | OS Artificial Sequence | | | |
| | | PN WO 02072815-A/147 | | | |
| | | PD 19-SEP-2002 | | | |
| | | PF 17-MAY-2001 WO 2001JP004139 | | | |
| | | PR 12-MAR-2001 JP 01P 68285 | | | |
| | | PI EIICHI SOEDA | | | |
| | | PC C12N15/09,C12Q1/68 | | | |
| | | CC Description of Artificial Sequence: Synthetic DNA FH Key | | | |
| | | Location/Qualifiers | | | |
| FT | source | 1. .20 | | | |
| FT | | /organism='Artificial Sequence'. | | | |
| FEATURES | | Location/Qualifiers | | | |
| source | | 1. .20 | | | |
| | | /organism="synthetic construct" | | | |
| | | /mol_type="genomic DNA" | | | |
| | | /db_xref="taxon:32630" | | | |
| Query Match | | 1.3%; Score 14.2; DB 1; Length 20; | | | |
| Best Local Similarity | | 84.2%; Pred. No. 89; | | | |
| Matches | | 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | |
| QY | 96 | CATTATCCTTCAGTGGGC 114 | | | |
| | | | | | |
| Db | 20 | CATGACCTACAGTTGGC 2 | | | |
| | | | | | |
| RESULT 129 | | | | | |
| CQ763898 | | | | | |
| LOCUS | | CQ763898 | | 20 bp DNA | |
| DEFINITION | | Sequence 2516 from Patent WO2004003201. | | linear | |
| ACCESSION | | CQ763898 | | PAT 03-MAR-2004 | |
| VERSION | | CQ763898.1 | | | |
| KEYWORDS | | GI:44907134 | | | |
| SOURCE | | synthetic construct | | | |
| ORGANISM | | synthetic construct | | | |
| REFERENCE | | 1 | | | |
| AUTHORS | | Kane,C.D. | | | |
| TITLE | | Antisense modulation of lrlh1 expression | | | |
| JOURNAL | | Patent: WO 2004003201-A 2516 08-JAN-2004; | | | |
| | | Pharmacia Corporation (US) | | | |
| FEATURES | | Location/Qualifiers | | | |
| source | | 1. .20 | | | |
| | | /organism="synthetic construct" | | | |
| | | /mol_type="unassigned DNA" | | | |
| | | /db_xref="taxon:32630" | | | |
| Query Match | | 1.3%; Score 14.2; DB 1; Length 20; | | | |
| Best Local Similarity | | 84.2%; Pred. No. 89; | | | |
| Matches | | 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | |
| QY | 391 | AGTCATTTTCCCTTACAATT 409 | | | |
| | | | | | |
| Db | 2 | AGTCATTTCCCTTAATATT 20 | | | |
| | | | | | |
| RESULT 130 | | | | | |
| CQ764016 | | | | | |
| LOCUS | | CQ764016 | | 20 bp DNA | |
| DEFINITION | | Sequence 2634 from Patent WO2004003201. | | linear | |
| ACCESSION | | CQ764016 | | PAT 03-MAR-2004 | |
| VERSION | | CQ764016.1 | | | |
| KEYWORDS | | GI:44907252 | | | |
| SOURCE | | synthetic construct | | | |
| ORGANISM | | synthetic construct | | | |
| REFERENCE | | 1 | | | |
| AUTHORS | | Kane,C.D. | | | |
| TITLE | | Antisense modulation of lrlh1 expression | | | |
| JOURNAL | | Patent: WO 2004003201-A 2634 08-JAN-2004; | | | |
| | | Pharmacia Corporation (US) | | | |
| FEATURES | | Location/Qualifiers | | | |
| source | | 1. .20 | | | |
| | | /organism="synthetic construct" | | | |
| | | /mol_type="unassigned DNA" | | | |
| | | /db_xref="taxon:32630" | | | |
| Query Match | | 1.3%; Score 14.2; DB 1; Length 20; | | | |
| Best Local Similarity | | 84.2%; Pred. No. 89; | | | |
| Matches | | 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | |
| QY | 391 | AGTCATTTTCCCTTACAATT 409 | | | |
| | | | | | |
| Db | 2 | AGTCATTTCCCTTAATATT 20 | | | |
| | | | | | |
| RESULT 131 | | | | | |
| CQ764195 | | | | | |
| LOCUS | | CQ764195 | | 20 bp DNA | |
| DEFINITION | | Sequence 2813 from Patent WO2004003201. | | linear | |
| ACCESSION | | CQ764195 | | PAT 03-MAR-2004 | |
| VERSION | | CQ764195.1 | | | |
| KEYWORDS | | GI:44907431 | | | |
| SOURCE | | synthetic construct | | | |
| ORGANISM | | synthetic construct | | | |
| REFERENCE | | 1 | | | |
| AUTHORS | | Kane,C.D. | | | |
| TITLE | | Antisense modulation of lrlh1 expression | | | |
| JOURNAL | | Patent: WO 2004003201-A 2813 08-JAN-2004; | | | |
| | | Pharmacia Corporation (US) | | | |
| FEATURES | | Location/Qualifiers | | | |
| source | | 1. .20 | | | |
| | | /organism="synthetic construct" | | | |
| | | /mol_type="unassigned DNA" | | | |
| | | /db_xref="taxon:32630" | | | |
| Query Match | | 1.3%; Score 14.2; DB 1; Length 20; | | | |
| Best Local Similarity | | 84.2%; Pred. No. 89; | | | |
| Matches | | 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | |
| QY | 433 | AAGAGGAGATGATTTTAGC 451 | | | |
| | | | | | |

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 822 GCCTCTCATGACCCAGGAA 840
Db 1 GCCACTCCAGACCCAGGAA 19

RESULT 137
AR272138/c
LOCUS AR272138 20 bp DNA PAT 10-APR-2003
DEFINITION Sequence 208 from patent US 6503756.
ACCESSION AR272138
VERSION AR272138.1 GI:29703706
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Freier,S.M. and Wyatt,J.
TITLE Antisense modulation of syntaxin 4 interacting protein expression
JOURNAL Patent: US 6503756-A 208 07-JAN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 932 AGAATGCAGAATCTGAAG 950
Db 19 AGAACTCCAGAATGTGAAG 1

RESULT 138
AR297674/c
LOCUS AR297674 20 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 9409 from patent US 6537751.
ACCESSION AR297674
VERSION AR297674.1 GI:31684958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 9409 25-MAR-2003;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 427 ATTTGGAAGAGGAGATGAT 445
Db 19 AGTTGGAGGGGAGATGAT 1

RESULT 139
AR300858/c
LOCUS AR300858 20 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 86 from patent US 6537973.
ACCESSION AR300858
VERSION AR300858.1 GI:31688425
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 20)
Bennett,C.F., Dean,N.M., Holmlund,J.T. and Dorr,F.A.
TITLE Oligonucleotide inhibition of protein kinase C
JOURNAL Patent: US 6537973-A 86 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTAGCT 452
Db 19 AGAGAAGAGGATTTTGGCT 1

RESULT 140
AR311588
LOCUS AR311588 20 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 2125 from patent US 6559294.
ACCESSION AR311588
VERSION AR311588.1 GI:31705014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2125 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 940 AGAATCTGAAGCCCACTC 958
Db 1 AGAATCGGAACCCCAACGC 19

RESULT 141
AR313584
LOCUS AR313584 20 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 4121 from patent US 6559294.
ACCESSION AR313584
VERSION AR313584.1 GI:31707010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4121 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 771 GAAACCTTTTGCTGGGGA 789


```
RESULT 147
AX101073/c
LOCUS          AX101073          20 bp      DNA          linear          PAT 10-APR-2001
DEFINITION     Sequence 47 from Patent WO0121822.
ACCESSION      AX101073
VERSION        AX101073.1  GI:13619929
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Dean,C. and Levy,Y.Y.
TITLE          Methods and means for modification of plant flowering
               characteristics
JOURNAL        Patent: WO 0121822-A 47 29-MAR-2001;
               Plant Bioscience Limited (GB)
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide"

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      448 TAGCTGGGAGCAGTGGTAG 466
Db      19 TAGGTGGGAACGTGGTAG 1

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

RESULT 148
AX259829/c
LOCUS          AX259829          20 bp      DNA          linear          PAT 26-OCT-2001
DEFINITION     Sequence 56 from Patent WO0172822.
ACCESSION      AX259829
VERSION        AX259829.1  GI:16508903
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Hugot,J.P., Thomas,G., Zouali,M., Lesage,S. and Chamaillard,M.
TITLE          Genes involved in intestinal inflammatory diseases and use thereof
JOURNAL        Patent: WO 0172822-A 56 04-OCT-2001;
               Fondation Jean Dausset-Ceph (FR)
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      776 CTTTGTGCTGGGATGTC 794
Db      20 CTTGTGCTGGTGATGCC 2

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

RESULT 149
AX590749/c
LOCUS          AX590749          20 bp      DNA          linear          PAT 27-JAN-2003
DEFINITION     Sequence 189 from Patent WO02086113.
ACCESSION      AX590749
VERSION        AX590749.1  GI:27949298
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
```

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other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Cookson,W.O., Moffat,M.F., Allen,M. and Lench,N.
TITLE          Enzyme and snp marker for disease
JOURNAL        Patent: WO 02086113-A 189 31-OCT-2002;
               Isis Innovation Limited (GB)
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Primer"

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      472 TATTTCTGATTACAGTGCGAT 490
Db      19 TGTCTCTGGTTACAATGCGAT 1

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

RESULT 150
AX601142/c
LOCUS          AX601142          20 bp      DNA          linear          PAT 17-FEB-2003
DEFINITION     Sequence 237 from Patent WO02092851.
ACCESSION      AX601142
VERSION        AX601142.1  GI:28401215
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Binns,M.M. and Swinburne,J.E.
TITLE          Genetic typing
JOURNAL        Patent: WO 02092851-A 237 21-NOV-2002;
               ANIMAL HEALTH TRUST (GB) ; The British Horseracing Board (GB)
FEATURES       Location/Qualifiers
               source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Primer"

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      317 GGATTTCTCTGTTATTCCTG 335
Db      19 GGATTTCTTGTGTTGCTTG 1

               Query Match          1.3%;   Score 14.2;   DB 1;   Length 20;
               Best Local Similarity 84.2%;   Pred. No. 89;
               Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

RESULT 151
AX804893
LOCUS          AX804893          20 bp      DNA          linear          PAT 25-NOV-2003
DEFINITION     Sequence 1061 from Patent WO03060160.
ACCESSION      AX804893
VERSION        AX804893.1  GI:38522034
KEYWORDS       .
SOURCE         Oreochromis niloticus (Nile tilapia)
ORGANISM       Oreochromis niloticus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; percomorpha; Perciformes;
               Labroidae; Cichlidae; Oreochromis.
REFERENCE      1
AUTHORS        Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE          Verification of food origin based on nucleic acid pattern
               recognition
JOURNAL        Patent: WO 03060160-A 1061 24-JUL-2003;
               Genomar ASA (NO)
FEATURES       Location/Qualifiers
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Fri Aug 19 10:59:59 2005

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source      1. .20
            /organism="Oreochromis niloticus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:8128"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      782 CTTGGGGATGCTTGGAG 800
        ||||| ||||| ||||| |||||
Db      2 CTTGGGTTTGAGCTTGGAG 20

RESULT 152
AX815889/c
LOCUS      AX815889      20 bp      DNA      linear      PAT 09-DEC-2003
DEFINITION      Sequence 144 from Patent WO03066891.
ACCESSION      AX815889
VERSION      AX815889.1 GI:39646569
KEYWORDS
SOURCE      Sus scrofa (pig)
ORGANISM      Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE      1
AUTHORS      Harge,T., Schellander,K. and Wimmers,K.
TITLE      Genetic markers for the diagnosis of the expression of inverted
            nipples in pets, breeding animals and domestic cattle
JOURNAL      Patent: WO 03066891-A 144 14-AUG-2003;
            Foerderverein Biotechnologieforschung der deutschen
            Schweineproduktion e.V. (DE)
FEATURES
source      1. .20
            /organism="Sus scrofa"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9823"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      406 AATTCAGGGTTCCTT 424
        ||||| ||||| ||||| |||||
Db      19 AACTCAGGGTTCCTT 1

RESULT 153
BD016085/c
LOCUS      BD016085      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Oligonucleotide modulation of protein kinase C-epsilon.
ACCESSION      BD016085
VERSION      BD016085.1 GI:22557223
KEYWORDS      JP 2001224386-A/94.
SOURCE      synthetic construct
ORGANISM      other sequences; artificial sequences.

REFERENCE      1 (bases 1 to 20)
AUTHORS      Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE      Oligonucleotide modulation of protein kinase C-epsilon
JOURNAL      Patent: JP 2001224386-A 94 21-AUG-2001;
            ISIS PHARMACEUTICALS INC
COMMENT      OS Artificial Sequence
            PN JP 2001224386-A/94
            PD 21-AUG-2001
            PF 13-DEC-2000 JP 2000379218
            PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
            FRANK C BENNETT,RUSSELL T BOGGS,NICHOLAS M DEAN PC
            C12N15/09,A61K48/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,PC
            G01N33/53,
            PC G01N33/566,G01N33/573//A61K31/711,A61K31/712,A61K31/7125,PC
            A61P35/00,
            PC A61P43/00,A61P43/00,C12N5/10,C12N5/00,C12N5/00 CC synthetic

source      1. .20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      434 AGAGGAGATGATTTTAGCT 452
        ||||| ||||| ||||| |||||
Db      19 AGAGAAGAGGATTTGGCT 1

RESULT 155
BD017356/c
LOCUS      BD017356      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Oligonucleotide modulation of protein kinase C-eta.
ACCESSION      BD017356
VERSION      BD017356.1 GI:22558532
KEYWORDS      JP 2001231579-A/94.
SOURCE      synthetic construct
ORGANISM      other sequences; artificial sequences.
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FH Key      Location/Qualifiers
FT source      1. .20
FT          /organism='Artificial Sequence'.

FEATURES
source      1. .20
            Location/Qualifiers
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      434 AGAGGAGATGATTTTAGCT 452
        ||||| ||||| ||||| |||||
Db      19 AGAGAAGAGGATTTGGCT 1

RESULT 154
BD016204/c
LOCUS      BD016204      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Oligonucleotide modulation of protein kinase C-zeta.
ACCESSION      BD016204
VERSION      BD016204.1 GI:23557342
KEYWORDS      JP 2001224387-A/94.
SOURCE      synthetic construct
ORGANISM      synthetic construct
            other sequences; artificial sequences.

REFERENCE      1 (bases 1 to 20)
AUTHORS      Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE      Oligonucleotide modulation of protein kinase C-zeta
JOURNAL      Patent: JP 2001224387-A 94 21-AUG-2001;
            ISIS PHARMACEUTICALS INC
COMMENT      OS Artificial Sequence
            PN JP 2001224387-A/94
            PD 21-AUG-2001
            PF 13-DEC-2000 JP 2000379249
            PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
            FRANK C BENNETT,RUSSELL T BOGGS,NICHOLAS M DEAN PC
            C12N15/09,A61K31/7088,A61K48/00,A61P29/00,A61P35/00,A61P43/00,PC
            C07H21/00,
            PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
            G01N33/573//
            PC C12N5/10,C12N15/00,C12N5/00
            CC synthetic
            FH Key      Location/Qualifiers
            FT source      1. .20
            FT          /organism='Artificial Sequence'.

FEATURES
source      1. .20
            Location/Qualifiers
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      434 AGAGGAGATGATTTTAGCT 452
        ||||| ||||| ||||| |||||
Db      19 AGAGAAGAGGATTTTGCT 1

RESULT 155
BD017356/c
LOCUS      BD017356      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Oligonucleotide modulation of protein kinase C-eta.
ACCESSION      BD017356
VERSION      BD017356.1 GI:22558532
KEYWORDS      JP 2001231579-A/94.
SOURCE      synthetic construct
ORGANISM      other sequences; artificial sequences.
```

REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-eta
JOURNAL Patent: JP 2001231579-A 94 28-AUG-2001;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001231579-A/94
PD 28-AUG-2001
PF 13-DEC-2000 JP 2000379234
PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
FRANK C BENNETT,RUSSELL T BOGGS,NICHOLAS M DEAN PC
C12N15/09,A61K31/711,A61K31/712,A61K31/7125,A61K48/00,A61P29/ PC
00,A61P35/00,
PC A61P43/00,C07H21/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
G01N33/50,
PC G01N33/53,G01N33/566//C12N5/10,G01N33/68,C12N15/00,C12N5/00 CC
synthetic
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 434 AGAGGAGATGATTTTAGCT 452
Db ||||| ||| ||||| ||||| |||||
19 AGAGAAGAGGATTTTGGCT 1
RESULT 156
BD089267/c
LOCUS A method of arraying genome clone. 20 bp DNA linear PAT 27-AUG-2002
DEFINITION BD089267
ACCESSION BD089267
VERSION BD089267.1 GI:22634877
KEYWORDS JP 2001321190-A/1511.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1511 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1511
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 385 CAATGCAGTCATTTTCCTT 403
Db ||||| ||| ||||| ||||| |||||
20 CGATGCATTCATTTTCCTT 2
RESULT 157
BD090269/c
LOCUS A method of arraying genome clone. 20 bp DNA linear PAT 27-AUG-2002
DEFINITION BD090269
ACCESSION BD090269
VERSION BD090269.1 GI:22635879
KEYWORDS JP 2001321190-A/2513.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 2513 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/2513
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 96 CATTATCCTTCAGTGGGC 114
Db ||||| ||| ||||| ||||| |||||
20 CATTAGCCTACAGTTGGC 2
RESULT 158
CQ860131
LOCUS Sequence 43 from Patent WO2004072293. 14 bp DNA linear PAT 10-SEP-2004
DEFINITION CQ860131
ACCESSION CQ860131
VERSION CQ860131.1 GI:51982019
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jockers,R., Couturier,C. and Uhlmann,E.
TITLE Oligonucleotides which inhibit the expression of the ob-rgrp protein and method for detection of compounds modifying the interaction between the proteins of the ob-rgrp family and the leptin receptor
JOURNAL Patent: WO 2004072293-A 43 26-AUG-2004;
Aventis Pharma S.A. (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR); Centre National de la Recherche Scientifique (CNRS) (FR)
FEATURES
source Location/Qualifiers
1..14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="Artificial"

 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 26 CCGTGGCAGGAAGC 39
 Db 1 CCGTGGCAGGAAGC 14

 RESULT 159
 BD208449 15 bp RNA linear PAT 17-JUL-2003
 LOCUS BD208449
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
 ACCESSION BD208449
 VERSION BD208449.1 GI:33018219
 KEYWORDS JP 2002512791-A/2039.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
 JOURNAL Patent: JP 2002512791-A 2039 08-MAY-2002;
 COMMENT OS Hepatitis virus (hepatitis C virus)
 PN JP 2002512791-A/2039
 PD 08-MAY-2002
 PF 26-APR-1999 JP 2000545991
 PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
 LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
 PAVCO,
 PI DENNIS MACEJAK
 PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
 PC A61K37/66,
 PC C12N15/00
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC hepatitis C virus infection.
 FH Key Location/Qualifiers
 FT source 1..15
 FT /organism='Hepatitis virus (hepatitis C FT
 virus)',
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unidentified"
 /mol_type="genomic RNA"
 /db_xref="taxon:32644"

 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 346 TGTGATCAAATGGG 359
 Db 2 TGTGATCAAATGGG 15

 RESULT 160
 I39422 15 bp DNA linear PAT 13-MAY-1997
 LOCUS I39422
 DEFINITION Sequence 460 from patent US 5616488.
 ACCESSION I39422
 VERSION I39422.1 GI:2083902
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 15)

Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
 IL-5 targeted ribozymes
 Patent: US 5616488-A 460 01-APR-1997;
 Location/Qualifiers
 source 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 123 TGACTTTTCTTATG 136
 Db 1 TGACTTTTCTTATG 14

 RESULT 161
 AX635727 15 bp RNA linear PAT 21-FEB-2003
 LOCUS AX635727
 DEFINITION Sequence 2866 from Patent EP1260586.
 ACCESSION AX635727
 VERSION AX635727.1 GI:28471341
 KEYWORDS .
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1
 AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
 TITLE Method and reagent for inhibiting the expression of disease related genes
 JOURNAL Patent: EP 1260586-A 2866 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

 Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 123 TGACTTTTCTTATG 136
 Db 1 TGACTTTTCTTATG 14

 RESULT 162
 AX733784/C 17 bp DNA linear PAT 08-MAY-2003
 LOCUS AX733784
 DEFINITION Sequence 5418 from Patent WO03025175.
 ACCESSION AX733784
 VERSION AX733784.1 GI:30513127
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
 JOURNAL Patent: WO 03025175-A 5418 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

971 ATTTTGATGAGTC 984
|||||

Db

14 ATTTTGATGAGTC 1

RESULT 163

AR293818

LOCUS AR293818 18 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 5553 from patent US 6537751.

ACCESSION AR293818

VERSION AR293818.1 GI:31681102

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.

TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome

JOURNAL Patent: US 6537751-A 5553 25-MAR-2003;

FEATURES Location/Qualifiers

source 1..18

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

200 ATCTCCCCCATCCC 213
|||||

Db

5 ATCTCCCCCATCCC 18

RESULT 164

AR292450/c

LOCUS AR292450 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 4185 from patent US 6537751.

ACCESSION AR292450

VERSION AR292450.1 GI:31679734

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.

TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome

JOURNAL Patent: US 6537751-A 4185 25-MAR-2003;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 100.0%; Pred. No. 96;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

562 TGGGTTTTTAATA 575
|||||

Db

19 TGGGTTTTTAATA 6

RESULT 165

AR293889

LOCUS AR293889 20 bp DNA linear PAT 12-JUN-2003

Definition

Accession

Version

Keywords

Source

Organism

Sequence 5624 from patent US 6537751.

AR293889

AR293889.1 GI:31681173

Unknown.

Unknown.

Unclassified.

Reference

Authors

Title

Journal

Features

1 (bases 1 to 20)

Cohen,D., Chumakov,I. and Blumenfeld,M.

Biallelic markers for use in constructing a high density disequilibrium map of the human genome

Patent: US 6537751-A 5624 25-MAR-2003;

Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 100.0%; Pred. No. 96;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

324 CTGTATTCTTGCT 337
|||||

Db

4 CTGTATTCTTGCT 17

RESULT 166

AR432356/c

LOCUS AR432356 20 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 156 from patent US 6653133.

ACCESSION AR432356

VERSION AR432356.1 GI:40194629

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dean,N.M., Marcussen,E.G. and Wyatt,J.

TITLE Antisense modulation of Fas mediated signaling

JOURNAL Patent: US 6653133-A 156 25-NOV-2003;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 100.0%; Pred. No. 96;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

620 AGATGAGTATTATT 633
|||||

Db

18 AGATGAGTATTATT 5

RESULT 167

AR542543

LOCUS AR542543 20 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 55 from patent US 6743909.

ACCESSION AR542543

VERSION AR542543.1 GI:53935031

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Cowser,L.M. and Dobie,K.W.

TITLE Antisense modulation of PTPN12 expression

JOURNAL Patent: US 6743909-A 55 01-JUN-2004;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Definition

Accession

Version

Keywords

Source

Organism

Sequence 5624 from patent US 6537751.

AR293889

AR293889.1 GI:31681173

Unknown.

Unknown.

Unclassified.

Reference

Authors

Title

Journal

Features

1 (bases 1 to 20)

Cohen,D., Chumakov,I. and Blumenfeld,M.

Biallelic markers for use in constructing a high density disequilibrium map of the human genome

Patent: US 6537751-A 5624 25-MAR-2003;

Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 100.0%; Pred. No. 96;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

324 CTGTATTCTTGCT 337
|||||

Db

4 CTGTATTCTTGCT 17

RESULT 166

AR432356/c

LOCUS AR432356 20 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 156 from patent US 6653133.

ACCESSION AR432356

VERSION AR432356.1 GI:40194629

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dean,N.M., Marcussen,E.G. and Wyatt,J.

TITLE Antisense modulation of Fas mediated signaling

JOURNAL Patent: US 6653133-A 156 25-NOV-2003;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 100.0%; Pred. No. 96;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

620 AGATGAGTATTATT 633
|||||

Db

18 AGATGAGTATTATT 5

RESULT 167

AR542543

LOCUS AR542543 20 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 55 from patent US 6743909.

ACCESSION AR542543

VERSION AR542543.1 GI:53935031

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Cowser,L.M. and Dobie,K.W.

TITLE Antisense modulation of PTPN12 expression

JOURNAL Patent: US 6743909-A 55 01-JUN-2004;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

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|--|------------|--|---------------|------------|------------|--------|----|-----------------|----|
| Query Match 1.3%; Score 14; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 96; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 345 | CTGTGATCAAAATGG | 358 | | | | | | |
| Db | 1 | CTGTGATCAAAATGG | 14 | | | | | | |
| RESULT 168 | | | | | | | | | |
| AX417278/c | AX417278 | Sequence 7 from Patent EP1197553. | 20 bp | DNA | linear | | | PAT 18-JUN-2002 | |
| DEFINITION | AX417278 | Antisense nucleic acid against alphav integrin | | | | | | | |
| ACCESSION | AX417278 | Patent: EP 1197553-A 7 17-APR-2002; | | | | | | | |
| VERSION | AX417278.1 | A3D GmbH, Antisense Design & Drug Development (DE) | | | | | | | |
| KEYWORDS | | Location/Qualifiers | | | | | | | |
| SOURCE | | 1. .20 | | | | | | | |
| ORGANISM | | /organism="synthetic construct" | | | | | | | |
| REFERENCE | | /mol_type="unassigned DNA" | | | | | | | |
| AUTHORS | | /db_xref="taxon:32630" | | | | | | | |
| TITLE | | /note="Antisense ODN directed against alphav integrin chain" | | | | | | | |
| JOURNAL | | | | | | | | | |
| FEATURES | | | | | | | | | |
| source | | 1. .20 | | | | | | | |
| Query Match | | 1.3%; | Score 14; | DB 1; | Length 20; | | | | |
| Best Local Similarity | | 100.0%; | Pred. No. 96; | | | | | | |
| Matches | 14; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| QY | 417 | TTTTTCCTTATATTT | 430 | | | | | | |
| Db | 17 | TTTTTCCTTATATTT | 4 | | | | | | |
| RESULT 169 | | | | | | | | | |
| AX467281/c | AX467281 | Sequence 7 from Patent WO0231142. | 20 bp | DNA | linear | | | PAT 16-JUL-2002 | |
| DEFINITION | AX467281 | Antisense nucleic acid against alphav integrin | | | | | | | |
| ACCESSION | AX467281 | Patent: WO 0231142-A 7 18-APR-2002; | | | | | | | |
| VERSION | AX467281.1 | A3D GmbH, Antisense Design & Drug Development (DE) | | | | | | | |
| KEYWORDS | | Location/Qualifiers | | | | | | | |
| SOURCE | | 1. .20 | | | | | | | |
| ORGANISM | | /organism="synthetic construct" | | | | | | | |
| REFERENCE | | /mol_type="unassigned DNA" | | | | | | | |
| AUTHORS | | /db_xref="taxon:32630" | | | | | | | |
| TITLE | | /note="Antisense ODN directed against alphav integrin chain" | | | | | | | |
| JOURNAL | | | | | | | | | |
| FEATURES | | | | | | | | | |
| source | | 1. .20 | | | | | | | |
| Query Match | | 1.3%; | Score 14; | DB 1; | Length 20; | | | | |
| Best Local Similarity | | 100.0%; | Pred. No. 96; | | | | | | |
| Matches | 14; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| QY | 417 | TTTTTCCTTATATTT | 430 | | | | | | |
| Db | 17 | TTTTTCCTTATATTT | 4 | | | | | | |
| RESULT 170 | | | | | | | | | |
| AX467285/c | AX467285 | Sequence 11 from Patent WO0231142. | 20 bp | DNA | linear | | | PAT 16-JUL-2002 | |
| DEFINITION | AX467285 | Antisense nucleic acid against alphav integrin | | | | | | | |
| ACCESSION | AX467285 | Patent: WO 0231142-A 11 18-APR-2002; | | | | | | | |
| VERSION | AX467285.1 | A3D GmbH, Antisense Design & Drug Development (DE) | | | | | | | |
| KEYWORDS | | Location/Qualifiers | | | | | | | |
| SOURCE | | 1. .20 | | | | | | | |
| ORGANISM | | /organism="synthetic construct" | | | | | | | |
| REFERENCE | | /mol_type="unassigned DNA" | | | | | | | |
| AUTHORS | | /db_xref="taxon:32630" | | | | | | | |
| TITLE | | /note="Antisense ODN directed against alphav integrin chain" | | | | | | | |
| JOURNAL | | | | | | | | | |
| FEATURES | | | | | | | | | |
| source | | 1. .20 | | | | | | | |
| Query Match | | 1.3%; | Score 14; | DB 1; | Length 20; | | | | |
| Best Local Similarity | | 100.0%; | Pred. No. 96; | | | | | | |
| Matches | 14; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| QY | 417 | TTTTTCCTTATATTT | 430 | | | | | | |
| Db | 17 | TTTTTCCTTATATTT | 4 | | | | | | |
| RESULT 171 | | | | | | | | | |
| AX815827 | AX815827 | Sequence 82 from Patent WO03066891. | 20 bp | DNA | linear | | | PAT 09-DEC-2003 | |
| DEFINITION | AX815827 | Antisense nucleic acid against alphav integrin | | | | | | | |
| ACCESSION | AX815827 | Patent: WO 03066891-A 82 14-AUG-2003; | | | | | | | |
| VERSION | AX815827.1 | Foerderverein Biotechnologieforschung der deutschen Schweineproduktion e.V. (DE) | | | | | | | |
| KEYWORDS | | Location/Qualifiers | | | | | | | |
| SOURCE | | 1. .20 | | | | | | | |
| ORGANISM | | /organism="Sus scrofa (pig)" | | | | | | | |
| REFERENCE | | /mol_type="unassigned DNA" | | | | | | | |
| AUTHORS | | /db_xref="taxon:9823" | | | | | | | |
| TITLE | | | | | | | | | |
| JOURNAL | | | | | | | | | |
| FEATURES | | | | | | | | | |
| source | | 1. .20 | | | | | | | |
| Query Match | | 1.3%; | Score 14; | DB 1; | Length 20; | | | | |
| Best Local Similarity | | 100.0%; | Pred. No. 96; | | | | | | |
| Matches | 14; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| QY | 894 | CACAGACCAAGAGC | 907 | | | | | | |
| Db | 2 | CACAGACCAAGAGC | 15 | | | | | | |
| RESULT 172 | | | | | | | | | |
| AR083038/c | AR083038 | Sequence 64 from patent US 5976798. | 17 bp | DNA | linear | | | PAT 01-SEP-2000 | |
| DEFINITION | AR083038 | Antisense nucleic acid against alphav integrin | | | | | | | |
| ACCESSION | AR083038 | Patent: US 5,976,798 A 1 18-APR-2000; | | | | | | | |
| VERSION | AR083038.1 | Antisense Design & Drug Development (DE) | | | | | | | |
| KEYWORDS | | Location/Qualifiers | | | | | | | |
| SOURCE | | 1. .20 | | | | | | | |
| ORGANISM | | /organism="Sus scrofa" | | | | | | | |
| REFERENCE | | /mol_type="unassigned DNA" | | | | | | | |
| AUTHORS | | /db_xref="taxon:9823" | | | | | | | |
| TITLE | | | | | | | | | |
| JOURNAL | | | | | | | | | |
| FEATURES | | | | | | | | | |
| source | | 1. .20 | | | | | | | |
| Query Match | | 1.3%; | Score 14; | DB 1; | Length 20; | | | | |
| Best Local Similarity | | 100.0%; | Pred. No. 96; | | | | | | |
| Matches | 14; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| QY | 417 | TTTTTCCTTATATTT | 430 | | | | | | |
| Db | 17 | TTTTTCCTTATATTT | 4 | | | | | | |

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Parker,W.Davis., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
TITLE Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid
JOURNAL Patent: US 5976798-A 64 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 173
AR124365/c
LOCUS AR124365 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 140 from patent US 6171859.
ACCESSION AR124365
VERSION AR124365.1 GI:14109726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrnstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 140 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 174
AR124376/c
LOCUS AR124376 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 151 from patent US 6171859.
ACCESSION AR124376
VERSION AR124376.1 GI:14109737
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrnstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 151 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 175
AR124410/c
LOCUS AR124410 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 185 from patent US 6171859.
ACCESSION AR124410
VERSION AR124410.1 GI:14109771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrnstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 185 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 176
AR124411/c
LOCUS AR124411 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 186 from patent US 6171859.
ACCESSION AR124411
VERSION AR124411.1 GI:14109772
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrnstadt,C. and Parker,W.Davis.
TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 186 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 563 GGGTTTTTTAATACCTT 579
Db 17 GGTTTTTTCTAATACCTT 1

RESULT 177
AR124413/c
LOCUS AR124413 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 188 from patent US 6171859.
ACCESSION AR124413
VERSION AR124413.1 GI:14109774
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrnstadt,C. and Parker,W.Davis.

TITLE Method of targeting conjugate molecules to mitochondria
JOURNAL Patent: US 6171859-A 188 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 563 GGGTTTTTTTAATACCTT 579
Db 17 GGTTCCTTAATACCTT 1
RESULT 178
BD198972 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning
DEFINITION molecule participating in vasculogenic response.
ACCESSION BD198972
VERSION BD198972.1 GI:33008742
KEYWORDS JP 2002509721-A/1998.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 1998 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/1998
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES source
1..17 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 939 CAGAATCTGAAGCCCCA 955
Db 1 CAGAATCTCAAGCACCA 17
RESULT 179
BD256418 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor genes using nucleic acid molecules.
DEFINITION
ACCESSION BD256418
VERSION BD256418.1 GI:33066188

KEYWORDS JP 2002541795-A/4211.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4211 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/4211
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
FEATURES source
1..17 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 396 TTTTCCTTACAATTCAA 412
Db 1 TTTTCCTTACAACCTCCA 17
RESULT 180
BD256866 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor genes using nucleic acid molecules.
DEFINITION
ACCESSION BD256866
VERSION BD256866.1 GI:33066636
KEYWORDS JP 2002541795-A/4659.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4659 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/4659
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers

FT source 1. .17
FT /organism='Eukaryote'.
Location/Qualifiers
1. .17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 396 TTTTCCTTACAATTCAA 412
Db 1 TTTTCCTTACAACCTCCA 17

RESULT 181
CQ617823/c
LOCUS CQ617823 2563 from Patent WO0192524. 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2563 from Patent WO0192524.
ACCESSION CQ617823
VERSION CQ617823.1 GI:41668041
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2563 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 745 GCAGCTGCCACCTTATG 761
Db 17 GCAGCTGCCGCCTTCTG 1

RESULT 182
CQ617824/c
LOCUS CQ617824 2564 from Patent WO0192524. 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2564 from Patent WO0192524.
ACCESSION CQ617824
VERSION CQ617824.1 GI:41668042
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2564 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 744 GCAGCTGCCACCTTAT 760
Db 17 GCAGCTGCCGCCTTCT 1

RESULT 183
CQ622009
LOCUS CQ622009 6749 from Patent WO0192524. 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 6749 from Patent WO0192524.
ACCESSION CQ622009
VERSION CQ622009.1 GI:41672227
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6749 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 836 AGGAAGGCCGGGTGGA 852
Db 1 AGGAAGGCCGTGGAGGA 17

RESULT 184
I27376/c
LOCUS I27376 12 from patent US 5565323. 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5565323.
ACCESSION I27376
VERSION I27376.1 GI:1818152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Parker,W.Davis. and Herrnstadt,C.
TITLE Cytochrome oxidase mutations aiding diagnosis of sporadic alzheimer's disease
JOURNAL Patent: US 5565323-A 12 15-OCT-1996;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 185
AR458886/c
LOCUS AR458886
DEFINITION Sequence 2563 from patent US 6686188. 17 bp DNA linear PAT 20-FEB-2004

ACCESSION AR458886
VERSION AR458886.1 GI:42693943
SOURCE .
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2563 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 745 GCAGCTGCCACCTTATG 761
|||||
Db 17 GCAGCTGCCGCTTCTG 1

RESULT 186
AR458887/c
LOCUS AR458887 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2564 from patent US 6686188.
ACCESSION AR458887
VERSION AR458887.1 GI:42693944
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2564 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 744 GGCAGCTGCCACCTTAT 760
|||||
Db 17 GGCAGCTGCCGCTTCT 1

RESULT 187
AR463072
LOCUS AR463072 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6749 from patent US 6686188.
ACCESSION AR463072
VERSION AR463072.1 GI:42698129
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6749 03-FEB-2004;
FEATURES Location/Qualifiers

source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 836 AGGAAGCCGGGTGGA 852
|||||
Db 1 AGGAAGCCGTGAGGA 17

RESULT 188
AX217125/c
LOCUS AX217125 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2567 from Patent WO0159103.
ACCESSION AX217125
VERSION AX217125.1 GI:15527186
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2567 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 413 GGGTTTTCCTTATTT 429
|||||
Db 17 GAGTTTTCCTTATTTT 1

RESULT 189
AX259837
LOCUS AX259837 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 64 from Patent WO0172822.
ACCESSION AX259837
VERSION AX259837.1 GI:16508911
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hugot,J.P., Thomas,G., Zouali,M., Lesage,S. and Chamaillard,M.
TITLE Genes involved in intestinal inflammatory diseases and use thereof
JOURNAL Patent: WO 0172822-A 64 04-OCT-2001;
Fondation Jean Dausset-Ceph (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 GCCATCTCCCCCATCCC 213

Db 1 ||||| 1 GCCATCTCCCAAGCCC 17

RESULT 190
AX273034 LOCUS AX273034 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 603 from Patent WO0162911.
ACCESSION AX273034
VERSION AX273034.1 GI:16545771
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 603 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 105 TCAGTGGGGCTATTGGA 121
|||||
Db 1 TCAGTGGGGCTGTGGGA 17

RESULT 191
AX423719 LOCUS AX423719 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2055 from Patent WO0188124.
ACCESSION AX423719
VERSION AX423719.1 GI:21527101
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 2055 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 960 GGACCCAGGACATTTTG 976
|||||
Db 1 GGACTCAGGACATTTGG 17

RESULT 192
AX502936 LOCUS AX502936 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 4243 from Patent EP1229046.
ACCESSION AX502936

VERSION AX502936.1 GI:23385229
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 4243 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 673 AAATTATGTTACTTGT 689
|||||
Db 1 AGATTATGTTTCTTGT 17

RESULT 193
BD070507/c LOCUS BD070507 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid.
ACCESSION BD070507
VERSION BD070507.1 GI:22616110
KEYWORDS JP 2001514500-A/64.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Parker,W.D., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
TITLE Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid
JOURNAL Patent: JP 2001514500-A 64 11-SEP-2001;
MITOKOR
COMMENT OS Unidentified
PN JP 2001514500-A/64
PD 11-SEP-2001
PF 27-FEB-1998 JP 1998537738
PR 28-FEB-1997 US 08/810599
PI WILLIAM DAVIS PARKER,CORINNA HERRNSTADT,SOUMITRA GHOSH,BOIN D FAHY
PC C12Q1/68,C07H21/04
CC Strandedness: Double;
CC Topology: Linear;
CC Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of CC mitochondrial nucleic acid
CC acid
FH Key Location/Qualifiers
FT source 1. .17
FT Location/Qualifiers
1. .17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Fri Aug 19 10:59:59 2005

Qy 562 TGGGTTTTTTAATACCT 578
||| ||||| ||||| |||||
Db 17 TGGTTTTTCTAATACCT 1

RESULT 194
BD104790 17 bp DNA linear PAT 27-AUG-2002
LOCUS Kit and method for determining HLA type.
DEFINITION BD104790
ACCESSION BD104790
VERSION BD104790.1 GI:22650364
KEYWORDS WO 0192572-A/894.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichiهارa,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 894 06-DEC-2001;
NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/894
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI MATSUMURA,
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 404 ACAATTCAAGGTTTTT 420
||| ||||| ||||| |||||
Db 1 ACAATTACAGGTTTTT 17

RESULT 195
AR071523/c 18 bp DNA linear PAT 18-FEB-2000
LOCUS Sequence 23 from patent US 5911982.
DEFINITION AR071523
ACCESSION AR071523
VERSION AR071523.1 GI:7222411
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chao,Y.-C.
TITLE H2-1 virus persistence-associated-gene 1 (PAG1) promoter uses therefor, and compositions containing same or products therefrom
JOURNAL Patent: US 5911982-A 23 15-JUN-1999;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 566 TTTTAAATACCTTTAT 582
|| ||||| ||||| |||||
Db 17 TTGTTAATACCTTTGT 1

RESULT 196
CQ799849/c 18 bp DNA linear PAT 28-APR-2004
LOCUS Sequence 499 from Patent WO2004031413.
DEFINITION CQ799849
ACCESSION CQ799849
VERSION CQ799849.1 GI:46848796
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,Y., Daigo,Y. and Nakatsuru,S.
TITLE Method for diagnosing non-small cell lung cancers
JOURNAL Patent: WO 2004031413-A 499 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the president of the university of Tokyo (JP)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized S-oligonucleotide sequence for antisense method"

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 432 GAAGAGGAGATGATTTT 448
||| ||||| ||||| |||||
Db 18 GAGGAGGAATGATTTT 2

RESULT 197
CQ807685 18 bp DNA linear PAT 10-MAY-2004
LOCUS Sequence 1135 from Patent WO2004035803.
DEFINITION CQ807685
ACCESSION CQ807685
VERSION CQ807685.1 GI:47113079
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.
TITLE Method and nucleic acids for the improved treatment of breast cell proliferative disorders
JOURNAL Patent: WO 2004035803-A 1135 29-APR-2004;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for CDH1"

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 152 GAGGATTATGGCGTTTA 168
||||| ||||| ||||| |||||
Db 1 GAGGTTATCGCGTTTA 17

RESULT 198
I27387/c
LOCUS I27387 18 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 23 from patent US 5565323.
ACCESSION I27387
VERSION I27387.1 GI:1818163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Parker,W.Davis. and Herrnstadt,C.
TITLE Cytochrome oxidase mutations aiding diagnosis of sporadic alzheimer's disease
JOURNAL Patent: US 5565323-A 23 15-OCT-1996;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 562 TGGGTTTTTTAATACCT 578
Db 18 TGGTTTTTCTAATACCT 2
RESULT 199
AR292997/c
LOCUS AR292997 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4732 from patent US 6537751.
ACCESSION AR292997
VERSION AR292997.1 GI:31680281
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4732 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 905 AGCCTCAACATTTCCTA 921
Db 17 AGCCTCAGCATTTCTA 1
RESULT 200
AR294306
LOCUS AR294306 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6041 from patent US 6537751.
ACCESSION AR294306
VERSION AR294306.1 GI:31681590
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome

JOURNAL Patent: US 6537751-A 6041 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 942 AATCTGAAGCCCCACTC 958
Db 2 AATCTCAACCCCCACTC 18
RESULT 201
AR299617/c
LOCUS AR299617 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 11352 from patent US 6537751.
ACCESSION AR299617
VERSION AR299617.1 GI:31686901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11352 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 CCCCCATCCCCCATTC 220
Db 18 CCTCCATCCCCCATCTC 2
RESULT 202
AX181724
LOCUS AX181724 18 bp DNA linear PAT 07-AUG-2001
DEFINITION Sequence 6 from Patent WO0146696.
ACCESSION AX181724
VERSION AX181724.1 GI:15133047
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and Mushahwar,I.K.
TITLE Methods and compositions for detecting hepatitis e virus
JOURNAL Patent: WO 0146696-A 6 28-JUN-2001;
FEATURES ABBOTT LABORATORIES (US)
Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer C375"
Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1035 TAAACATCACCCCAAC 1051
| | | | | | | | | | | | | | | |

Fri Aug 19 10:59:59 2005

Db2 TGAACATCAGCCCAAC 18

RESULT 203

AX705606

LOCUS

DEFINITION

AX705606

ACCESSION

AX705606

VERSION

AX705606.1

GI:29562271

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1

Distler,J., Model,F. and Taubert,H.

Method and nucleic acids for the analysis of colon cancer

Patent: WO 03014388-A 275 20-FEB-2003;

Epigenomics AG (DE)

Location/Qualifiers

1. .18

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Detection oligonucleotide for PCR"

Query Match

1.2%;

Score 13.8;

DB 1;

Length 18;

Best Local Similarity

88.2%;

Pred. No. 1.1e+02;

Matches

15;

Conservative

0;

Mismatches

2;

Indels

0;

Gaps

0;

Qy

616

TAGGAGATGAGTTTAT

632

Db

2

TAGGAGATGAGATTTT

18

RESULT 204

AX705608/c

LOCUS

DEFINITION

AX705608

ACCESSION

AX705608

VERSION

AX705608.1

GI:29562273

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1

Distler,J., Model,F. and Taubert,H.

Method and nucleic acids for the analysis of colon cancer

Patent: WO 03014388-A 277 20-FEB-2003;

Epigenomics AG (DE)

Location/Qualifiers

1. .18

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Detection oligonucleotide for PCR"

Query Match

1.2%;

Score 13.8;

DB 1;

Length 18;

Best Local Similarity

88.2%;

Pred. No. 1.1e+02;

Matches

15;

Conservative

0;

Mismatches

2;

Indels

0;

Gaps

0;

Qy

616

TAGGAGATGAGTTTAT

632

Db

17

TAGGAGATGAGATTTT

1

RESULT 205

AX837940/c

LOCUS

DEFINITION

AX837940

ACCESSION

AX837940

VERSION

AX837940.1

GI:39921632

KEYWORDS

SOURCE

unidentified

ORGANISM

unidentified

unclassified.

1

Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.

Full-length cDNA sequences

Patent: EP 1347046-A 5064 24-SEP-2003;

Research Association for Biotechnology (JP)

Location/Qualifiers

1. .18

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

/note="Description of Artificial Sequence: an artificially synthesized primer se q"

Query Match

1.2%;

Score 13.8;

DB 1;

Length 18;

Best Local Similarity

88.2%;

Pred. No. 1.1e+02;

Matches

15;

Conservative

0;

Mismatches

2;

Indels

0;

Gaps

0;

Qy

295

TGGAATTGTTTCTG

311

Db

18

TGGTATTGTGTCTG

2

RESULT 206

BD077127

LOCUS

DEFINITION

BD077127

ACCESSION

BD077127

VERSION

BD077127.1

GI:22622730

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS

Artificial Sequence

PN

JP

2001520384-A/6

PD

30-OCT-2001

PF

15-OCT-1998

JP

2000516232

PR

15-OCT-1997

US

60/061199

PI

GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J DAWSON,

ISA

K MASHAWER

PI

G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,

PC

C07K14/08,

PC

C07K16/10,C12N15/09,C12Q1/69,G01N33/577

CC

Primer C375

FH

Key

FT

source

1. .18

Location/Qualifiers

/organism='Artificial Sequence'

Query Match

1.2%;

Score 13.8;

DB 1;

Length 18;

Best Local Similarity

88.2%;

Pred. No. 1.1e+02;

Matches

15;

Conservative

0;

Mismatches

2;

Indels

0;

Gaps

0;

Qy

1035

TAAACATCACCCCAAC

1051

Db

2

TGAACATCACGCCCAAC

18

RESULT 207
AX129431/c
LOCUS AX129431 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 649 from Patent WO0130362.
ACCESSION AX129431
VERSION AX129431.1 GI:14135736
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 649 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk6 ribozyme binding site"
Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 603 AAGACTTCATAAGTAGG 619
Db 19 AACACTTCAGAAGTAGG 3
RESULT 208
AX129821/c
LOCUS AX129821 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1039 from Patent WO0130362.
ACCESSION AX129821
VERSION AX129821.1 GI:14136126
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1039 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk8 ribozyme binding site"
Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 415 GTTTTTCCTTATATTG 431
Db 19 GTTTTTCATATACTTG 3
RESULT 209
AX149152/c
LOCUS AX149152 19 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 354 from Patent WO0136625.
ACCESSION AX149152
VERSION AX149152.1 GI:14347676
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wright,J.A., Young,A.H. and Dugourd,D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A 354 25-MAY-2001;
GeneSense Technologies Inc. (CA)
FEATURES
source Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"
Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 567 TTTTAAATACCTTTATA 583
Db 18 TTTTAAACCTTTAGA 2
RESULT 210
BD012154
LOCUS BD012154 19 bp DNA linear PAT 02-AUG-2002
DEFINITION Polypeptide.
ACCESSION BD012154
VERSION BD012154.1 GI:22092343
KEYWORDS WO 0109348-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Koyama,N., Okui,T., Takakura,H., Asada,K. and Kato,I.
TITLE Polypeptide
JOURNAL Patent: WO 0109348-A 7 08-FEB-2001;
TAKARA SHUZO CO LTD,NOBUTO KOYAMA,TOSHITAKE OKUI,HIKARU TAKAKURA,
KIYOZO ASADA,IKUNOSHIN KATO
COMMENT OS Artificial Sequence
PN WO 0109348-A/7
PD 08-FEB-2001
PF 26-JUL-2000 WO 2000JP004956
PR 02-AUG-1999 JP 99P 218778
PI NOBUTO KOYAMA,TOSHITAKE OKUI,HIKARU TAKAKURA,KIYOZO ASADA, PI
IKUNOSHIN KATO
PC C12N15/56,C12N9/26,C12P19/14,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/00
CC PCR primer R4.
FH Key Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 857 TCTTTGTGTTGTAGTCC 873
Db 3 TCCATGTGTTGTAGTCC 19
RESULT 211
AX348064/c
LOCUS AX348064 15 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 2 from Patent EP1172445.
ACCESSION AX348064
VERSION AX348064.1 GI:18614174


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KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Wiebusch,H., Schmitt-John,T. and Weidner,J.
TITLE       A method for direct genetic analysis of target cells by using
            fluorescence probes
JOURNAL     Patent: EP 1172445-A 2 16-JAN-2002;
            Praenadia GmbH (DE)
FEATURES
source      Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR primer for beta-actin, upstream"
Query Match      1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      42 GAAGCAGCGCGGCC 56
        |||||
Db      15 GAAGCAGCGGTGGCC 1

RESULT 212
AX540329/c      15 bp      DNA      linear      PAT 23-NOV-2002
LOCUS
DEFINITION      Sequence 3 from Patent WO0206524.
ACCESSION      AX540329
VERSION        AX540329.1 GI:25273335
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Wiebusch,H., Schmitt-John,T. and Weidner,J.
TITLE       A method for direct genetic analysis of target cells by using
            fluorescence probes
JOURNAL     Patent: WO 0206524-A 3 24-JAN-2002;
            Praenadia GmbH (DE)
FEATURES
source      Location/Qualifiers
            1..15
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      42 GAAGCAGCGCGGCC 56
        |||||
Db      15 GAAGCAGCGGTGGCC 1

RESULT 213
I35386/c      16 bp      DNA      linear      PAT 13-MAY-1997
LOCUS
DEFINITION      Sequence 354 from patent US 5599706.
ACCESSION      I35386
VERSION        I35386.1 GI:2088354
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
            Stichcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Stichcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE       Ribozymes targeted to apo(a) mRNA
JOURNAL     Patent: US 5599706-A 354 04-FEB-1997;
FEATURES
source      Location/Qualifiers

KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Wiebusch,H., Schmitt-John,T. and Weidner,J.
TITLE       A method for direct genetic analysis of target cells by using
            fluorescence probes
JOURNAL     Patent: EP 1172445-A 2 16-JAN-2002;
            Praenadia GmbH (DE)
FEATURES
source      Location/Qualifiers
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR primer for beta-actin, upstream"
Query Match      1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      42 GAAGCAGCGCGGCC 56
        |||||
Db      15 GAAGCAGCGGTGGCC 1

RESULT 212
AX540329/c      15 bp      DNA      linear      PAT 23-NOV-2002
LOCUS
DEFINITION      Sequence 3 from Patent WO0206524.
ACCESSION      AX540329
VERSION        AX540329.1 GI:25273335
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Wiebusch,H., Schmitt-John,T. and Weidner,J.
TITLE       A method for direct genetic analysis of target cells by using
            fluorescence probes
JOURNAL     Patent: WO 0206524-A 3 24-JAN-2002;
            Praenadia GmbH (DE)
FEATURES
source      Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      42 GAAGCAGCGCGGCC 56
        |||||
Db      15 GAAGCAGCGGTGGCC 1

RESULT 213
I35386/c      16 bp      DNA      linear      PAT 13-MAY-1997
LOCUS
DEFINITION      Sequence 354 from patent US 5599706.
ACCESSION      I35386
VERSION        I35386.1 GI:2088354
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
            Stichcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Stichcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE       Ribozymes targeted to apo(a) mRNA
JOURNAL     Patent: US 5599706-A 354 04-FEB-1997;
FEATURES
source      Location/Qualifiers
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source      1..16
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      448 TAGCTGGGAGCAGTG 462
        |||||
Db      16 TAGCTGGGACAGTG 2

RESULT 214
AR047122/c      17 bp      DNA      linear      PAT 29-SEP-1999
LOCUS
DEFINITION      Sequence 1915 from patent US 5817796.
ACCESSION      AR047122
VERSION        AR047122.1 GI:5968587
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
            Stichcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stichcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL     Patent: US 5817796-A 1915 06-OCT-1998;
FEATURES
source      Location/Qualifiers
            1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      274 ACTGGCATATTCTT 288
        |||||
Db      16 ACTGGGATATTCTT 2

RESULT 215
BD232102        17 bp      DNA      linear      PAT 17-JUL-2003
LOCUS
DEFINITION      Complex formed of major histocompatibility antigen gene complex
            product on the phage surface and peptide.
ACCESSION      BD232102
VERSION        BD232102.1 GI:33041872
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
            Gorochov,G., Piqueras,B., Doussal,J.M.L. and Debre,P.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Gorochov,G., Piqueras,B., Doussal,J.M.L. and Debre,P.
TITLE       Complex formed of major histocompatibility antigen gene complex
            product on the phage surface and peptide
JOURNAL     Patent: JP 2002514431-A 20 21-MAY-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE CNRS
COMMENT      OS Unidentified
            PN JP 2002514431-A/20
            PD 21-MAY-2002
            PF 12-MAY-1999 JP 2000548484
            PR 14-MAY-1998 FR 98/06213
            PI GUY GOROCHOV,BERNARD PIQUERAS,JEAN MARC LE DOUSSAL,PATRICE PI
            DEBRE
            PC C12N15/09,A61K38/00,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10,
            PC G01N33/68,C12N15/00,A61K37/02,C12N5/00
            CC Sequence Figure 1A
            FH Key Location/Qualifiers
            FT misc feature (1)..(17).
            source      Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 GAGACATGGCGGCG 80
|||||
Db 2 GAGACATGGCGGCCG 16

RESULT 216
BD254620
LOCUS BD254620 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254620
VERSION BD254620.1 GI:33064390
KEYWORDS JP 2002541795-A/2413.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2413 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2413
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1.17
FT Location/Qualifiers
/organism='Eukaryote'.
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1.17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 TTTTCCTTACAATTC 410
|||||
Db 2 TTTTCCTTACAAC TC 16

RESULT 218
BD256555
LOCUS BD256555 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256555
VERSION BD256555.1 GI:33066325
KEYWORDS JP 2002541795-A/4348.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4348 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/4348
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1.17
FT Location/Qualifiers
/organism='Eukaryote'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTGTTT 308
|||||
Db 2 CTGTAATTGTTGTTT 16

RESULT 217
BD256417
LOCUS BD256417 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256417
VERSION BD256417.1 GI:33066187
KEYWORDS JP 2002541795-A/4210.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4210 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/4210
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1.17
FT Location/Qualifiers
/organism='Eukaryote'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 TTTTCCTTACAATTC 410
|||||
Db 2 TTTTCCTTACAAC TC 16

RESULT 218
BD256555
LOCUS BD256555 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256555
VERSION BD256555.1 GI:33066325
KEYWORDS JP 2002541795-A/4348.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4348 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/4348
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1.17
FT Location/Qualifiers
/organism='Eukaryote'.
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/organism="unidentified"
/mol_type="genomic DNA"

[illegible]

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrrhini; Hominidae; Homo.
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6287 06-DEC-2001;
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 CCGGGCCGTGGCAGG 35
||||| |||||||
Db 3 CCGGGCTGTGGCAGG 17
RESULT 223
CQ621548
LOCUS CQ621548 6288 from Patent WO0192524. linear PAT 02-FEB-2004
DEFINITION Sequence 6288 from Patent WO0192524.
ACCESSION CQ621548
VERSION CQ621548.1 GI:41671766
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrrhini; Hominidae; Homo.
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6288 06-DEC-2001;
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 CCGGGCCGTGGCAGG 35
||||| |||||||
Db 2 CCGGGCTGTGGCAGG 16
RESULT 224
CQ621549
LOCUS CQ621549 6289 from Patent WO0192524. linear PAT 02-FEB-2004
DEFINITION Sequence 6289 from Patent WO0192524.
ACCESSION CQ621549
VERSION CQ621549.1 GI:41671767
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrrhini; Hominidae; Homo.
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6289 06-DEC-2001;

FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 CCGGGCCGTGGCAGG 35
||||| |||||||
Db 1 CCGGGCTGTGGCAGG 15
RESULT 225
I54174/c
LOCUS I54174 1915 from patent US 5646042. linear PAT 07-OCT-1997
DEFINITION Sequence 1915 from patent US 5646042.
ACCESSION I54174
VERSION I54174.1 GI:2475377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1915 08-JUL-1997;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 274 ACTGGCATATTTCTT 288
||||| |||||||
Db 16 ACTGGGATATTTCTT 2
RESULT 226
AR327041/c
LOCUS AR327041 4443 from patent US 6566127. linear PAT 17-AUG-2003
DEFINITION Sequence 4443 from patent US 6566127.
ACCESSION AR327041
VERSION AR327041.1 GI:33712849
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4443 20-MAY-2003;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 626 GTTTTATTTCTCAGCA 640
||||| |||||||
Db 15 GTTTTATGCTCAGCA 1

RESULT 227
AR458890/c
LOCUS AR458890 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2567 from patent US 6686188.
ACCESSION AR458890
VERSION AR458890.1 GI:42693947
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2567 03-FEB-2004;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCGCCT 1
|||||

RESULT 228
AR462610
LOCUS AR462610 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6287 from patent US 6686188.
ACCESSION AR462610
VERSION AR462610.1 GI:42697667
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6287 03-FEB-2004;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 743 AGGCAGCTGCCACCT 757
Db 15 AGGCAGCTGCCGCCT 1
|||||

RESULT 229
AR462611
LOCUS AR462611 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6288 from patent US 6686188.
ACCESSION AR462611
VERSION AR462611.1 GI:42697668
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.

TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6288 03-FEB-2004;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGGCCGTGGCAGG 35
Db 2 CCGGGCTGTGGCAGG 16
|||||

RESULT 230
AR462612
LOCUS AR462612 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6289 from patent US 6686188.
ACCESSION AR462612
VERSION AR462612.1 GI:42697669
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6289 03-FEB-2004;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CCGGGCCGTGGCAGG 35
Db 1 CCGGGCTGTGGCAGG 15
|||||

RESULT 231
AX215376
LOCUS AX215376 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 818 from Patent WO0159103.
ACCESSION AX215376
VERSION AX215376.1 GI:15525419
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 818 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCCAGTTC 63
| | | | | | | | | | |
Db 2 CCGCGGCCCCCAGTGC 16

RESULT 232
AX215377
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCCAGTTC 63
| | | | | | | | | | |
Db 1 CCGCGGCCCCCAGTGC 15

RESULT 233
AX217124/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCCAGTTC 63
| | | | | | | | | | |
Db 1 CCGCGGCCCCCAGTGC 15

RESULT 233
AX217124/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GTTTTCCTTATTT 429
| | | | | | | | | | |
Db 16 GTTTTCCTTATTT 2

RESULT 234
AX422711
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 958 CTGGACCCAGGACAT 972
| | | | | | | | | | |
Db 3 CTGGACTCAGGACAT 17

RESULT 235
AX502937
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 675 ATTATGTTACTTGT 689
| | | | | | | | | | |
Db 2 ATTATGTTTCTTGT 16

RESULT 236
AX502938
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 415 GTTTTCCTTATTT 429
| | | | | | | | | | |
Db 16 GTTTTCCTTATTT 2

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]

Db 1 ||||| ||||| ||||| ||||| |||||

1 CCCAGAGACCAAGAG 15

RESULT 241

AX723809

LOCUS AX723809 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 1496 from Patent WO03025176.

ACCESSION AX723809

VERSION AX723809.1 GI:30503152

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025176-A 1496 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 621 GATGAGTTTATTCT 635

Db 1 ||||| ||||| ||||| ||||| |||||

1 GATCAGTTTATTCT 15

RESULT 242

AX728020/c

LOCUS AX728020 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 5707 from Patent WO03025176.

ACCESSION AX728020

VERSION AX728020.1 GI:30507363

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025176-A 5707 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 606 ACTTCATAAGTAGGA 620

Db 17 ACTTCATCAGTAGGA 3

RESULT 243

AX729829

LOCUS AX729829 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 1463 from Patent WO03025175.

ACCESSION AX729829

VERSION AX729829.1 GI:30509172

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025175-A 1463 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 513 ATCTGTATACATGTG 527

Db 2 ATCTGTATACATATG 16

RESULT 244

AX733736/c

LOCUS AX733736 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 5370 from Patent WO03025175.

ACCESSION AX733736

VERSION AX733736.1 GI:30513079

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025175-A 5370 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 588 ATGTTCACTTTAAGA 602

Db 17 ATGTTCACTTGAAGA 3

RESULT 245

AX736422

LOCUS AX736422 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 2012 from Patent WO03025177.

ACCESSION AX736422

VERSION AX736422.1 GI:30515710

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Db 15 TCATTTTCCTTTCAA 1

RESULT 250
AX759999/c

LOCUS AX759999 17 bp DNA linear PAT 25-JUN-2003

DEFINITION Sequence 3320 from Patent WO03040369.

ACCESSION AX759999

VERSION AX759999.1 GI:32254615

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines

JOURNAL Patent: WO 03040369-A 3320 15-MAY-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 588 ATGTTCACTTTAAGA 602

Db 17 ATGTTCACTTGAAGA 3

RESULT 251
AX762004

LOCUS AX762004 17 bp DNA linear PAT 25-JUN-2003

DEFINITION Sequence 5325 from Patent WO03040369.

ACCESSION AX762004

VERSION AX762004.1 GI:32256620

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines

JOURNAL Patent: WO 03040369-A 5325 15-MAY-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 851 GATCCCTCTTGTTGT 865

Db 1 GATCCCTCTTGTTGT 15

RESULT 252
AR119278

LOCUS AR119278 18 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 41 from patent US 6150104.

ACCESSION AR119278

VERSION AR119278.1 GI:14101188

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 Unclassified.

AUTHORS 1 (bases 1 to 18)

TITLE Splawski,I. and Keating,M.T.

Homozygous mutation in KVLQT1 which causes Jervell and Lange Nielsen syndrome

JOURNAL Patent: US 6150104-A 41 21-NOV-2000;

FEATURES Location/Qualifiers

source 1. .18

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCCAGTT 62

Db 2 GCCGCGGCCCCAGTT 16

RESULT 253
AR164732

LOCUS AR164732 18 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 43 from patent US 6274332.

ACCESSION AR164732

VERSION AR164732.1 GI:16237874

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 Unclassified.

AUTHORS 1 (bases 1 to 18)

TITLE Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Mutations in the KCNE1 gene encoding human minK which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene

JOURNAL Patent: US 6274332-A 43 14-AUG-2001;

FEATURES Location/Qualifiers

source 1. .18

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGGCCCCAGTT 62

Db 2 GCCGCGGCCCCAGTT 16

RESULT 254
BD222843

LOCUS BD222843 18 bp DNA linear PAT 17-JUL-2003

DEFINITION KVLQT1-QT extension syndrome.

ACCESSION BD222843

VERSION BD222843.1 GI:33032613

KEYWORDS JP 2002521045-A/41.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 18)

Keating,M.T., Sanguinetti,M.C., Karan,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.

TITLE KVLQT1-QT extension syndrome

JOURNAL Patent: JP 2002521045-A 41 16-JUL-2002;

COMMENT UNIVERSITY OF UTAH RESEARCH FOUNDATION,GENZYME CORP

OS Homo sapiens (human)

PN JP 2002521045-A/41

PD 16-JUL-2002
PF 12-MAY-1999 JP 2000562052
PR 29-JUL-1998 US 60/094477,17-AUG-1998 US 09/135010 PI
MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KARAN,GREGORY M PI
LANDES,
PI TIMOTHY D CONNORS,TIMOTHY C BURN,IGOR SPLAWSKI PC
C12N15/09,A01K67/027,C07K14/46,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC
C12N1/21,C12N5/10,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/ PC
50,
PC G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68,
PC C12N15/00,
PC C12N5/00
CC KVLQT1-Qr extension syndrome
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 48 GCCGGCGCCCCCAGTT 62
Db 2 GCCGGCGCCCCCAGTT 16
RESULT 255
BD230253/c
LOCUS
DEFINITION
18 bp DNA linear PAT 17-JUL-2003
Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
BD230253
BD230253.1 GI:33040023
BD230253.1 GI:33040023
JP 2002530091-A/122.
Canis familiaris (dog)
Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 18)
Galibert,F. and Andre,C.
Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes
Patent: JP 2002530091-A 122 17-SEP-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/122
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT,CATHERINE ANDRE
PC C12N15/09,C12Q1/68,C12N15/00
CC A0076
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Canis familiaris (dog)'.
FT Location/Qualifiers
1..18
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
FEATURES
source
1..18
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 523 ATGTGCACATGCGGC 537

Db 17 ATGTGCACTTGCGGC 3
RESULT 256
CQ774947/c
LOCUS
DEFINITION
18 bp DNA linear PAT 06-MAR-2004
Sequence 16 from Patent WO2004012817.
CQ774947
ACCESSION
CQ774947.1 GI:45238085
KEYWORDS
synthetic construct
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 van Lohuizen,M.M., Berns,A.J., Martins,C.P., Mikkers,H.M.,
AUTHORS Lenz,J.R., Lund,A.H. and de Koning,J.P.
TITLE Use of genes identified to be involved in tumor development for the
development of anti-cancer drugs
JOURNAL development of anti-cancer drugs
Patent: WO 2004012817-A 16 12-FEB-2004;
Kylrix B.V. (NL)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide PSK RV"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 896 CAGACCAAGAGCCTC 910
Db 15 CAGCCCAAGAGCCTC 1
RESULT 257
CQ799841/c
LOCUS
DEFINITION
18 bp DNA linear PAT 28-APR-2004
Sequence 491 from Patent WO2004031413.
CQ799841
ACCESSION
CQ799841.1 GI:46848788
KEYWORDS
synthetic construct
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Nakamura,Y., Daigo,Y. and Nakatsuru,S.
AUTHORS Method for diagnosing non-small cell lung cancers
TITLE Patent: WO 2004031413-A 491 15-APR-2004;
JOURNAL Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized S-oligonucleotide sequence
for antisense method"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 196 CGCCATCTCCCCCAT 210
Db 16 CGCCATCTCCACCAT 2
RESULT 258
CQ807850
LOCUS
CQ807850
18 bp DNA linear PAT 10-MAY-2004

DEFINITION Sequence 1300 from Patent WO2004035803.
ACCESSION CQ807850
VERSION CQ807850.1 GI:47113244
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.
TITLE Method and nucleic acids for the improved treatment of breast cell proliferative disorders
JOURNAL Patent: WO 2004035803-A 1300 29-APR-2004;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for X51730 PGR"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 616 TAGGAGATGAGTTT 630
|||||
Db 3 TAGGAGATGAGATTT 17
RESULT 259
AR218558
LOCUS AR218558 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 6 from patent US 6420117.
ACCESSION AR218558
VERSION AR218558.1 GI:23319338
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wesler,S.R. and Casa,A.M.
TITLE Miniature inverted repeat transposable elements and methods of use
JOURNAL Patent: US 6420117-A 6 16-JUL-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 909 TCAACATTCCTAGA 923
|||||
Db 1 TCAACGTTTCCTAGA 15
RESULT 260
AR218696
LOCUS AR218696 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 43 from patent US 6420124.
ACCESSION AR218696
VERSION AR218696.1 GI:23319591
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long qt syndrome gene

JOURNAL Patent: US 6420124-A 43 16-JUL-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCAGTT 62
|||||
Db 2 GCCGCGGCCCCAGTT 16
RESULT 261
AR223111
LOCUS AR223111 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 43 from patent US 6432644.
ACCESSION AR223111
VERSION AR223111.1 GI:23330964
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human minK which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6432644-A 43 13-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCAGTT 62
|||||
Db 2 GCCGCGGCCCCAGTT 16
RESULT 262
AR229873
LOCUS AR229873 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 43 from patent US 6451534.
ACCESSION AR229873
VERSION AR229873.1 GI:27269751
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6451534-A 43 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCAGTT 62
|||||
Db 2 GCCGCGGCCCCAGTT 16
RESULT 263
AR229873
LOCUS AR229873 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 43 from patent US 6451534.
ACCESSION AR229873
VERSION AR229873.1 GI:27269751
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6451534-A 43 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCAGTT 62
|||||
Db 2 GCCGCGGCCCCAGTT 16

RESULT 263
AR262129 LOCUS AR262129 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 43 from patent US 6323026.
ACCESSION AR262129
VERSION AR262129.1 GI:28073490
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human mink which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6323026-A 43 27-NOV-2001;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCCAGTT 62
Db 2 GCCGCGGCCCCCAGTT 16
RESULT 264
AR293760/c LOCUS AR293760 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5495 from patent US 6537751.
ACCESSION AR293760
VERSION AR293760.1 GI:31681044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 5495 25-MAR-2003;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1060 CTTTCCAGTGGCTAA 1074
Db 18 CTTACCAGTGGCTAA 4
RESULT 265
AR294009 LOCUS AR294009 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5744 from patent US 6537751.
ACCESSION AR294009
VERSION AR294009.1 GI:31681293
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 5744 25-MAR-2003;

FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 612 TAAGTAGGAGATGAG 626
Db 3 TAAGTAAGAGATGAG 17
RESULT 266
AR344567 LOCUS AR344567 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 43 from patent US 6582913.
ACCESSION AR344567
VERSION AR344567.1 GI:33740636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 43 24-JUN-2003;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCCAGTT 62
Db 2 GCCGCGGCCCCCAGTT 16
RESULT 267
AX119482/c LOCUS AX119482 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 139 from Patent WO0129251.
ACCESSION AX119482
VERSION AX119482.1 GI:14036401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nf1 gene
JOURNAL Patent: WO 0129251-A 139 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 416 TTTTTCCTTATATT 430
Db 18 TTTTTCCTTATAGTT 4

RESULT 268
AX119538/c
LOCUS AX119538 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 195 from Patent WO0129251.
ACCESSION AX119538
VERSION AX119538.1 GI:14036457
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nf1 gene
JOURNAL Patent: WO 0129251-A 195 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 416 TTTTTCCTTATATT 430
Db 18 TTTTTCCTTAGTT 4
RESULT 269
BD196757/c
LOCUS BD196757 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Prostatic cancer gene.
ACCESSION BD196757
VERSION BD196757.1 GI:33006527
KEYWORDS JP 2002516657-A/346.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
Prostatic cancer gene
PATENT: JP 2002516657-A 346 11-JUN-2002;
COMMENT GENSET
OS Homo sapiens (human)
PN JP 2002516657-A/346
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
C12N15/00,C12N5/00,
PC C12N5/00,C12N15/00
CC upstream amplification primer for SEQ 251, SEQ 328 FH Key
location amplification
FT primer_bind 1. .19.
location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 351 TCAAATGGGAGCCT 365

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15 TCAAAAGGGGAGCCT 1
Db
RESULT 270
CQ801939
LOCUS CQ801939 19 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 256 from Patent WO2004033720.
ACCESSION CQ801939
VERSION CQ801939.1 GI:47058520
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Schrenzel,J., Francois,P., Charbonnier,Y., Jacquet,J.G.,
Uttinger,D., Kresbach,G.M., Abel,A. and Ehrat,M.
TITLE Analytical chip for the detection of 16s-rRNA from clinically
relevant bacteria and analytical method based thereon
JOURNAL Patent: WO 2004033720-A 256 22-APR-2004;
Hopitaux Universitaires de Geneve (CH)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe for Bacteroides fragili"
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 466 GCACTTTATTCTGAT 480
Db 3 GCACTTTATTCTTAT 17
RESULT 271
E08864/c
LOCUS E08864 19 bp DNA linear PAT 29-SEP-1997
DEFINITION linker.
ACCESSION E08864
VERSION E08864.1 GI:2176968
KEYWORDS JP 1995067667-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Akiyoshi,M., Yabusaki,Y., Sakaki,T., Murakami,H. and Okawa,H.
TITLE BOVINE ADRENAL ADRENODOXIN PRODUCING STRAIN
JOURNAL Patent: JP 1995067667-A 4 14-MAR-1995;
SUMITOMO CHEM CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1995067667-A/4
PD 14-MAR-1995
PF 24-MAY-1990 JP 1994193294
PI AKIYOSHI MEGUMI, YABUSAKI YOSHIYASU, SAKAKI TOSHIYUKI, PI
MURAKAMI HIROKO,
PI OKAWA HIDEO
PC C12N15/09,C12N1/19,C12N9/02,(C12N1/19,C12R1:865),(C12N9/02, PC
C12R1:865);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1. .19
/organism='Artificial sequences'.
FEATURES
source
1. .19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1100 CTGCTCATTTGTTTA 1114
Db 19 CTGCTCATTTTTTTA 5

RESULT 272
AR211777 AR211777 19 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 23 from patent US 6399370.
ACCESSION AR211777
VERSION AR211777.1 GI:21515190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Wilson,J.M., Goldman,M., Bals,R., Stolzenberg,E.D., Anderson,M.,
Zaslhoff,M. and Kari,P.
TITLE Compositions and methods for use of defensin
JOURNAL Patent: US 6399370-A 23 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 954 CACTCTGGACCCAGG 968
Db 3 CACTCTGGACCCTGG 17

RESULT 273
AR292652/c AR292652 19 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 4387 from patent US 6537751.
ACCESSION AR292652
VERSION AR292652.1 GI:31679936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 4387 25-MAR-2003;
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAAATGGGGAGCCT 365
Db 15 TCAAAAGGGGAGCCT 1

RESULT 274
AR299591 AR299591 19 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 11326 from patent US 6537751.
ACCESSION AR299591

VERSION AR299591.1 GI:31686875
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 11326 25-MAR-2003;
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 CATTTCCTTACAAT 408
Db 4 CATTGCGCTTACAAT 18

RESULT 275
AR452230/c AR452230 19 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 80 from patent US 6677146.
ACCESSION AR452230
VERSION AR452230.1 GI:42683776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Janjic,N., Bullard,J.M., McHenry,C.S. and Kery,V.
TITLE Thermophilic polymerase III holoenzyme
JOURNAL Patent: US 6677146-A 80 13-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAAGCGCGGGT 849
Db 15 CTGGAAGCGCGGGT 1

RESULT 276
AX132453 AX132453 19 bp DNA linear PAT 15-MAY-2001
LOCUS
DEFINITION Sequence 3671 from Patent WO0130362.
ACCESSION AX132453
VERSION AX132453.1 GI:14138758
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
JOURNAL diseases
FEATURES Patent: WO 0130362-A 3671 03-MAY-2001;
source IMMUSOL, INC. (US)
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"

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/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 238 CTATGACTCAGATGC 252
Db 2 CTATCACTCAGATGC 16

RESULT 277
AX262324/c
LOCUS AX262324 19 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 80 from Patent WO0173052.
ACCESSION AX262324
VERSION AX262324.1 GI:16511266
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mchenry,C.S.
TITLE Thermophilic polymerase III holoenzyme
JOURNAL Patent: WO 0173052-A 80 04-OCT-2001;
McHenry, Charles S. (US)
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse/antisense ATG primer #P133-A1237"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 835 CAGGAAGGCCGGGT 849
Db 15 CTGGAAGGCCGGGT 1

RESULT 278
BD009904
LOCUS BD009904 19 bp DNA linear PAT 31-JAN-2002
DEFINITION Compositions and methods for use of defensin.
ACCESSION BD009904
VERSION BD009904.1 GI:18638277
KEYWORDS JP 2001502891-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Wilson,J.M., Goldman,M., Bals,R., Stolzenberg,E.D., Anderson,M.,
Zaslhoff,M. and Kari,P.
TITLE Compositions and methods for use of defensin
JOURNAL Patent: JP 2001502891-A 13 06-MAR-2001;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA, AGAININ
PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001502891-A/13
PD 06-MAR-2001
PF 20-AUG-1997 JP 1998510921
PR 22-AUG-1996 US 60/023424,01-OCT-1996 US 60/027334 PR
18-FEB-1997 US 60/038685
PI JAMES M WILSON,MITCHELL GOLDMAN,ROBERT BALS,
PI ETHAN D STOLZENBERG,
PI MARK ANDERSON,MICHAEL ZASLOFF,PRASAD KARI
PC C12N5/00,C12N15/00,C07H21/04,A61K38/00,A61K48/00,C07K2/00, PC
A01N37/18
CC
FH Key Location/Qualifiers
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FT source 1..19
FT /organism='Artificial Sequence'.

FEATURES
source 1..19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 954 CACTCTGGACCCAGG 968
Db 3 CACTCTGGACCCCTGG 17

RESULT 279
BD088340/c
LOCUS BD088340 19 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088340
VERSION BD088340.1 GI:22633950
KEYWORDS JP 2001321190-A/584.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 584 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/584
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source 1..19
FT /organism='Artificial Sequence'.

FEATURES
source 1..19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 406 AATTC AAGGGTTT 420
Db 16 AATTC AAGGGTTATT 2

RESULT 280
AB068097/c
LOCUS AB068097 19 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-stSG4211
at 1p36.
ACCESSION AB068097
VERSION AB068097.1 GI:15128901
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
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Fri Aug 19 10:59:59 2005

Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H., Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A. and Soeda,E.
A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
21269192
11374902
2 (bases 1 to 19)
Horii,A.
Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1. .19
/note="reverse primer for human STS sts-stSG4211 at 1p36 sts-stSG4211 obtained from clones B293A18, B226F22, B122E3, B372C15, B271G7, Human BAC library RPCI-11"
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 406 AATTCAAGGGTTT 420
Db 16 AATTCAAGGGTTATT 2
RESULT 281
A87858/c
LOCUS A87858 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 6 from Patent WO9833904.
ACCESSION A87858
VERSION A87858.1 GI:6736428
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 6 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
1. .18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 196 CGCCATCTCCCCCATCCC 213
Db 18 CGCGCCTCCCCCATGCC 1
RESULT 282
A89825/c
LOCUS A89825 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 6 from Patent EP0856579.
ACCESSION A89825
VERSION A89825.1 GI:6738339
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified

unclassified.
1 (bases 1 to 18)
Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 6 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
1. .18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 196 CGCCATCTCCCCCATCCC 213
Db 18 CGCGCCTCCCCCATGCC 1
RESULT 283
AR018185/c
LOCUS AR018185 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5780611.
ACCESSION AR018185
VERSION AR018185.1 GI:3973788
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 12 14-JUL-1998;
Location/Qualifiers
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 202 CTCCTCCCCATCCCCCATTT 219
Db 18 CTCCTCCCCCTCTCTCCCTTT 1
RESULT 284
AR031775
LOCUS AR031775 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5866411.
ACCESSION AR031775
VERSION AR031775.1 GI:5946064
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pedersen,F.Skou., Lund,A.Henrik., Lovmand,J., J.O slashed.rgensen,P. and Duch,M.
TITLE Retroviral vector, a replication system for said vector or mammalian cells transfected with said vector
JOURNAL Patent: US 5866411-A 3 02-FEB-1999;
Location/Qualifiers
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 192 TCACGCCCATCTCCCCCA 209
Db 1 TCCCGGCGCATCTCCACCA 18

RESULT 285
AR039068/c

LOCUS AR039068 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 34 from patent US 5807730.
ACCESSION AR039068
VERSION AR039068.1 GI:5958431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
TITLE Nitrile hydratase
JOURNAL Patent: US 5807730-A 34 15-SEP-1998;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 17 CTGCCCGGGCCGTGGCAG 34
Db 18 CTGCTCGTGCCGGGGCAG 1

RESULT 286
AR071248/c

LOCUS AR071248 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5910432.
ACCESSION AR071248
VERSION AR071248.1 GI:7222136
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
TITLE Nitrile hydratase
JOURNAL Patent: US 5910432-A 34 08-JUN-1999;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 17 CTGCCCGGGCCGTGGCAG 34
Db 18 CTGCTCGTGCCGGGGCAG 1

RESULT 287
AR076370/c

LOCUS AR076370 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 37 from patent US 5958772.
ACCESSION AR076370
VERSION AR076370.1 GI:10003116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)

AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.
TITLE Antisense inhibition of cellular inhibitor of apoptosis-1
expression
JOURNAL Patent: US 5958772-A 37 28-SEP-1999;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 974 TTGATGAGATCCAAAGGA 991
Db 18 TTGATGAGATTCAAGGTA 1

RESULT 288
AR107284

LOCUS AR107284 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107478.
ACCESSION AR107284
VERSION AR107284.1 GI:12821814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pedersen,F.Skou., Lund,A.Henrik., Lovmand,J., J.O
slashed.rgensen,P. and Duch,M.
TITLE Retroviral vector, a replication system for said vector and avian
or mammalian cells transfected with said vector
JOURNAL Patent: US 6107478-A 3 22-AUG-2000;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 192 TCCACGCCCATCTCCCCCA 209
Db 1 TCCCGGCGCATCTCCACCA 18

RESULT 289
AR111390/c

LOCUS AR111390 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6127133.
ACCESSION AR111390
VERSION AR111390.1 GI:12828238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Akong,M.Anthony., Harpold,M.Miller., Velicelebi,G. and Brust,P.
TITLE Automated analysis equipment and assay method for detecting cell
surface protein function using same
JOURNAL Patent: US 6127133-A 2 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 695 GTTCATGTAGTCACGGTG 712

SOURCE ORGANISM
unidentified
unclassified.
1 (bases 1 to 18)
Ito,K., Yamaki,T., Arii,T., Tsuruoka,M. and Nakamura,T.
AUTHORS
NEW NITRILE-HYDRATASE
TITLE
JOURNAL
Patent: JP 1997275978-A 32 28-OCT-1997;
MITSUI TOATSU CHEM INC
COMMENT
OS None
OC Artificial sequences.
PN JP 1997275978-A/32
PD 28-OCT-1997
PF 29-JAN-1997 JP 1997015295
PR 14-FEB-1996 JP 96P 27004
PI ITO KIYOSHI, YAMAKI TOSHIBUMI, ARII TERUO, TSURUOKA MIYUKI, PI
NAKAMURA TAKESHI
PC C12N9/88,C12N1/21,C12N15/09,(C12N9/88,C12R1:19),(C12N1/21,PC
C12R1:19),
PC (C12N15/09,C12R1:01);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Key
FH Key
FT source 1..18
FT Location/Qualifiers
FT /organism='Artificial sequences'.
OC 1..18
OC /organism="unidentified"
OC /mol_type="genomic DNA"
OC /db_xref="taxon:32644"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 17 CTGCCCCGGCCGTGGCAG 34
Db 18 CTGCTCGTCCCGGGCAG 1
RESULT 294
E54096
LOCUS 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel gene regulated and decreased in metastatic human melanoma cell and protein thereof, process for producing the same and utilization of the same.
ACCESSION E54096
VERSION E54096.1 GI:18629688
KEYWORDS JP 2000217585-A/5.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Myuien,H.N.P.F. and Zendoman,A.I.W.
TITLE Novel gene regulated and decreased in metastatic human melanoma cell and protein thereof, process for producing the same and utilization of the same
JOURNAL Patent: JP 2000217585-A 5 08-AUG-2000;
F HOFFMANN LA ROCHE AG
COMMENT
OS Artificial Sequence
PN JP 2000217585-A/5
PD 08-AUG-2000
PF 31-JAN-2000 JP 2000021873
PR 29-JAN-1999 EP 99101925:8
PI HOSEN N P FAN MYUIEN,ALBERT IE W ZENDOMAN
PC C12N15/09,C07K14/82,C07K16/32,C12P21/02,C12Q1/68,G01N33/566,
PC G01N33/574,
PC G01N33/577,C12N15/00
CC
FH Key
FT source Location/Qualifiers
1..18

FT /organism='Artificial Sequence'.
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 349 GATCAAAATGGGGAGCCTG 366
Db 1 GAGCTGATGGGGAGCCTG 18
RESULT 295
AR210385 18 bp DNA linear PAT 20-JUN-2002
LOCUS AR210385
DEFINITION Sequence 131 from patent US 6387657.
ACCESSION AR210385
VERSION AR210385.1 GI:21512603
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Botstein,D.A., Cohen,R.L., Goddard,A.D., Gurney,A.L., Hillan,K.J., Lawrence,D.A., Levine,A.J., Pennica,D., Roy,M.Ann. and Wood,W.I.
TITLE WISP polypeptides and nucleic acids encoding same
JOURNAL Patent: US 6387657-A 131 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 897 AGACCAAGAGCCTCAACA 914
Db 1 AGTCCAAGAGTCTCAGCA 18
RESULT 296
AR293973 18 bp DNA linear PAT 12-JUN-2003
LOCUS AR293973
DEFINITION Sequence 5708 from patent US 6537751.
ACCESSION AR293973
VERSION AR293973.1 GI:31681257
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 5708 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 871 TCCATGCTATTAAAGTG 888
Db 1 TCCATGCTCTTACCAGTG 18


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RESULT 297
AR298224
LOCUS AR298224 linear PAT 12-JUN-2003
DEFINITION Sequence 9959 from patent US 6537751.
ACCESSION AR298224
VERSION AR298224.1 GI:31685508
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 9959 25-MAR-2003;
source Location/Qualifiers
1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 209 ATCCCCCATTTTCATTGCC 226
Db 1 ATCCCCCTCTTTCATTTC 18

RESULT 298
AR351536/c
LOCUS AR351536 linear PAT 17-AUG-2003
DEFINITION Sequence 29 from patent US 6586581.
ACCESSION AR351536
VERSION AR351536.1 GI:33753313
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bancroft,F.C., Fliss,M. and Clelland,C.L.
TITLE prolactin regulatory element binding protein and uses thereof
JOURNAL Patent: US 6586581-A 29 01-JUL-2003;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 209 ATCCCCCATTTTCATTGCC 226
Db 1 ATCCCCCTCTTTCATTTC 18

RESULT 299
AR364672/c
LOCUS AR364672 linear PAT 03-SEP-2003
DEFINITION Sequence 3 from patent US 5401629.
ACCESSION AR364672
VERSION AR364672.1 GI:34427596
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Harpold,M.M. and Brust,P.
TITLE Assay methods and compositions useful for measuring the
JOURNAL transduction of an intracellular signal
Patent: US 5401629-A 3 28-MAR-1995;
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FEATURES
source Location/Qualifiers
1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 695 GTTCATGTAGTCACGGTG 712
Db 18 GTTCATGAATTC AAGGTG 1

RESULT 300
AR482570/c
LOCUS AR482570 linear PAT 14-MAY-2004
DEFINITION Sequence 16 from patent US 6703228.
ACCESSION AR482570
VERSION AR482570.1 GI:47245093
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Landers,J., Jordan,B., Housman,D.E. and Charest,A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: US 6703228-A 16 09-MAR-2004;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 568 TTTTAATACCTTTATATA 585
Db 18 TTTTATACCTTCATAAA 1

RESULT 301
AX035247
LOCUS AX035247 linear PAT 15-NOV-2000
DEFINITION Sequence 4 from Patent WO055365.
ACCESSION AX035247
VERSION AX035247.1 GI:11190994
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Mulrooney,C. and Oultram,J.D.
TITLE Enzymatically catalysed signal amplification
JOURNAL Patent: WO 0055365-A 4 21-SEP-2000;
MULROONEY CONOR (GB) ; OULTRAM JOHN DOUGLAS (GB) ; TEPNEL MEDICAL LTD (GB)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:
Endonuclease protected sequence-Detection oligonucleotide"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1056 TTATCTTTCAGTGGCTA 1073
Db 1 TTCTCTTCCAGTTGCTA 18
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RESULT 302
AX078863/c
LOCUS AX078863 18 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 37 from Patent WO0105963.
ACCESSION AX078863
VERSION AX078863.1 GI:13158480
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
TITLE Antisense oligonucleotides for metabotropic glutamate receptor type 1 (mglur1)
JOURNAL Patent: WO 0105963-A 37 25-JAN-2001;
McGill University (CA)
FEATURES
source Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 901 CAAGAGCCTCAACATTTC 918
Db 18 CAAGAGCCTGACCTTTTC 1
RESULT 303
AX348093
LOCUS AX348093 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 10 from Patent WO0202630.
ACCESSION AX348093
VERSION AX348093.1 GI:18614197
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Strijbos,P.J., Bates,S.G., Gloger,I.G. and Davies,C.G.
TITLE New use
JOURNAL Patent: WO 0202630-A 10 10-JAN-2002;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
source Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 144 GTGCCTTAGAGGATTATG 161
Db 1 GTGCCTTCGCGGATGATG 18
RESULT 304
AX398208
LOCUS AX398208 18 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 13 from Patent WO0220790.
ACCESSION AX398208
VERSION AX398208.1 GI:21261023
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Geraci,D., Colombo,P., Duro,G., Izso,V. and Costa,M.A.
AUTHORS Parietaria judaica ns-ltp antigen variants, uses thereof and
TITLE compositions comprising them
JOURNAL Patent: WO 0220790-A 13 14-MAR-2002;
CONSIGLIO NAZIONALE DELLE RICERCHE (IT)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
4
misc_feature /note="Residue mutated with respect to the corresponding
position in Par j1.0102"
6
misc_feature /note="Residue mutated with respect to the corresponding
position in Par j1.0102"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 41 GGAAGCAGCGCGGCCCC 58
Db 1 GGGAGCAGCAGCGCGGCC 18
RESULT 305
AX599791/c
LOCUS AX599791 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1131 from Patent WO02077272.
ACCESSION AX599791
VERSION AX599791.1 GI:28399939
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
AUTHORS Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pelet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 1131 03-OCT-2002;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for Me491/TD63"
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1071 CTAACCACTTAACCTCT 1088
Db 18 CAAACACACGTAACCCCT 1
RESULT 306
AX599792/c
LOCUS AX599792 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1132 from Patent WO02077272.
ACCESSION AX599792
VERSION AX599792.1 GI:28399940
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J., Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E., Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T., Pelet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
JOURNAL Patent: WO 02077272-A 1132 03-OCT-2002;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for Me491/TD63"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1071 CTAACCACTTAACCTCT 1088
Db 18 CAAACCAACATAACCCCT 1

RESULT 307
AX815835
LOCUS AX815835 18 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 90 from Patent WO03066891.
ACCESSION AX815835
VERSION AX815835.1 GI:39646515
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1
REFERENCE Hardge,T., Schellander,K. and Wimmers,K.
AUTHORS Genetic markers for the diagnosis of the expression of inverted nipples in pets, breeding animals and domestic cattle
TITLE
JOURNAL Patent: WO 03066891-A 90 14-AUG-2003;
Foerderverein Biotechnologieforschung der deutschen Schweineproduktion e.V. (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="Sus scrofa"
/mol_type="unassigned DNA"
/db_xref="taxon:9823"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 300 TTGTTGTTTCTGCCTTTG 317
Db 1 TTGCTGCTGTGCCTTTG 18

RESULT 308
AX837801/c
LOCUS AX837801 18 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 4925 from Patent EP1347046.
ACCESSION AX837801
VERSION AX837801.1 GI:39921493
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
1
REFERENCE Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,

Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.
Full-length cDNA sequences
Patent: EP 1347046-A 4925 24-SEP-2003;
Research Association for Biotechnology (JP)
Location/Qualifiers
FEATURES source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of Artificial Sequence: an artificially synthesized primer se q"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 314 TTGGATTTCCTGTTATT 331
Db 18 TCTGGAGTTGCTGTTATT 1

RESULT 309
BD065371/c
LOCUS BD065371 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065371
VERSION BD065371.1 GI:22610974
KEYWORDS JP 2001511000-A/6.
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 18)
REFERENCE Schlingensiepen,K.H. and Brysch,W.
AUTHORS An antisense oligonucleotide preparation method
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 6 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/6
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH key
Location/Qualifiers
FT source 1..18
/organism='Unknown'.
Location/Qualifiers
FEATURES source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCCCATCCC 213
Db 18 CGCCGCCTCCCCCATGCC 1

RESULT 310
AR028977/c
LOCUS AR028977 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5858981.
ACCESSION AR028977
VERSION AR028977.1 GI:5940950
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Schreiber,A.D. and Park,J.-G.
TITLE Method of inhibiting phagocytosis
JOURNAL Patent: US 5858981-A 16 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGGC 79
Db 16 AGACATGGCGGGC 4

RESULT 311
AR156859/c
LOCUS AR156859 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 16 from patent US 6242427.
ACCESSION AR156859
VERSION AR156859.1 GI:15125563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schreiber,A.D. and Park,J.-G.
TITLE Methods of inhibiting phagocytosis
JOURNAL Patent: US 6242427-A 16 05-JUN-2001;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGGC 79
Db 16 AGACATGGCGGGC 4

RESULT 312
AR412057/c
LOCUS AR412057 16 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6638764.
ACCESSION AR412057
VERSION AR412057.1 GI:40164606
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schreiber,A.D. and Park,J.-G.
TITLE Methods of inhibiting phagocytosis
JOURNAL Patent: US 6638764-A 16 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 AGACATGGCGGGC 79
Db 16 AGACATGGCGGGC 4

RESULT 313
BD258394/c
LOCUS BD258394 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258394
VERSION BD258394.1 GI:33068164
KEYWORDS JP 2002541795-A/6187.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6187 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/6187
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES Location/Qualifiers
source 1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCAGGCAATGCAG 392
Db 15 GCAGGCAATGCAG 3

RESULT 314
AX216369
LOCUS AX216369 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1811 from Patent WO0159103.
ACCESSION AX216369
VERSION AX216369.1 GI:15526430
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 1811 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
Mcswiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCAGT 61
Db 4 CCGCGGCCCCAGT 16

RESULT 315
AX216945
LOCUS AX216945 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2387 from Patent WO0159103.
ACCESSION AX216945
VERSION AX216945.1 GI:15527006
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2387 16-AUG-2001; Blatt, Lawrence (US) ; RIBOZYME PHARMACEUTICALS, INC. (US) ; Chowrira, Bharat M. (US) McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCAGT 61
Db 5 CCGCGGCCCCAGT 17

RESULT 316
AX226887/c
LOCUS AX226887 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 259 from Patent WO0157206.
ACCESSION AX226887
VERSION AX226887.1 GI:15556028
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 259 09-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAAGCC 40
Db 17 GTGGCAGGAAGCC 5

RESULT 317
AX226888/c
LOCUS AX226888 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 260 from Patent WO0157206.
ACCESSION AX226888
VERSION AX226888.1 GI:15556029
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 260 09-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAAGCC 40
Db 16 GTGGCAGGAAGCC 4

RESULT 318
AX227245/c
LOCUS AX227245 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 617 from Patent WO0157206.
ACCESSION AX227245
VERSION AX227245.1 GI:15556386
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 617 09-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGGCAGGAAGCC 40
Db 15 GTGGCAGGAAGCC 3

RESULT 319
AX227246/c
LOCUS AX227246 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 618 from Patent WO0157206.
ACCESSION AX227246
VERSION AX227246.1 GI:15556387
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 618 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTGGCAGGAAGCC 40
| | | | | | | | | |
Db 14 GTGGCAGGAAGCC 2

RESULT 320
AX227395/c
LOCUS AX227395 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 767 from Patent WO0157206.
ACCESSION AX227395
VERSION AX227395.1 GI:15556536
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 767 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTGGCAGGAAGCC 40
| | | | | | | | | |
Db 13 GTGGCAGGAAGCC 1

RESULT 321
AX735823
LOCUS AX735823 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1413 from Patent WO03025177.
ACCESSION AX735823
VERSION AX735823.1 GI:30515100
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 1413 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 981 GATCCAAAGGAGT 993
| | | | | | | | | |
Db 1 GATCCAAAGGAGT 13

RESULT 322
AX758667/c
LOCUS AX758667 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1988 from Patent WO03040369.
ACCESSION AX758667
VERSION AX758667.1 GI:32253283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 1988 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 796 TGGAGAGGCAGAT 808
| | | | | | | | | |
Db 14 TGGAGAGGCAGAT 2

RESULT 323
AX760253
LOCUS AX760253 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3574 from Patent WO03040369.
ACCESSION AX760253
VERSION AX760253.1 GI:32254869
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3574 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 CTTATATTGGAA 434

Fri Aug 19 10:59:59 2005

DEFINITION Sequence 4476 from Patent WO03025176.
ACCESSION AX726789
VERSION AX726789.1 GI:30506132
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4476 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 1.1%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 522 CATGTGCACATG 533
Db 16 CATGTGCACATG 5
Search completed: August 19, 2005, 10:52:32
Job time : 7 secs

Db
|||||
4 CTTATATTGGAA 16
RESULT 324
AX822240/c
LOCUS AX822240 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 132 from Patent EP1340818.
ACCESSION AX822240
VERSION AX822240.1 GI:39748868
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
AUTHORS Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: EP 1340818-A 132 03-SEP-2003;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AGCCGGAAGCAGC 49
Db 13 AGCCGGAAGCAGC 1

RESULT 325
AX825880/c
LOCUS AX825880 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 132 from Patent WO03072821.
ACCESSION AX825880
VERSION AX825880.1 GI:39751394
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
AUTHORS Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: WO 03072821-A 132 04-SEP-2003;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AGCCGGAAGCAGC 49
Db 13 AGCCGGAAGCAGC 1

RESULT 326
AX726789/c
LOCUS AX726789 17 bp DNA linear PAT 08-MAY-2003

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:37:46 ; Search time 0.001 Seconds
(without alignments)
352.024 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctggttgccaggctgc.....gttacctgctcattgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 9 seqs, 158 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 9 summaries

Database : estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| C 1 | 15.6 | 1.4 | 22 | 1 AZ457101 | ACCESSION:AZ457101 |
| C 2 | 14.8 | 1.3 | 19 | 1 D44776 | ACCESSION:D44776 |
| C 3 | 14.8 | 1.3 | 19 | 1 AZ579189 | ACCESSION:AZ579189 |
| C 4 | 14.8 | 1.3 | 20 | 1 AU060353 | ACCESSION:AU060353 |
| C 5 | 12.8 | 1.1 | 16 | 1 AI446372 | ACCESSION:AI446372 |
| C 6 | 12.8 | 1.1 | 18 | 1 AJ588273 | ACCESSION:AJ588273 |
| C 7 | 12.4 | 1.1 | 14 | 1 BH169716 | ACCESSION:BH169716 |
| C 8 | 12.4 | 1.1 | 15 | 1 CA851710 | ACCESSION:CA851710 |
| C 9 | 12 | 1.1 | 15 | 1 AJ727978 | ACCESSION:AJ727978 |

ALIGNMENTS

RESULT 1
AZ457101/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

1M0260J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0260J17 F, genomic survey sequence.

AZ457101
AZ457101.1 GI:10615226
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0260 row: J column: 17
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

1. .22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0260J17"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 920 TAGAGCCTTATTAGAAATGCAG 941
Db 22 TGGAGGCTTTTGAGAAATGCAG 1

RESULT 2
D44776/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

D44776
HUMSUPY214 Human brain cDNA Homo sapiens cdna clone MF51-S-2, mRNA sequence.
D44776
D44776.1 GI:1572251
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)
Hadano,S., Ishida,Y., Tomiyasu,H., Yamamoto,K., Bates,G.P. and Ikeda,J.
Transcript map of the human chromosome 4p16.3 consisting of 627 cDNA clones derived from 1 Mb of the Huntington's disease locus
DNA Res. 3 (4), 239-255 (1996)
97101646
8946164

COMMENT Contact: Shinji Hadano
Japan Science and Technology Corporation, NeuroGenes Project, ICORP
Univ. of Tokai School of Med.
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-5095
Fax: 81-463-91-4993
Email: shinji@nga.med.u-tokai.ac.jp.

FEATURES Location/Qualifiers
source
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MF51-S-2"
/tissue_type="brain"
/clone_lib="Human brain cDNA"

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 390 CAGTCATTTTCCCTTACAA 407
|||||
Db 19 CAGTCATTTTCCCCACAA 2

RESULT 3
AZ579189
LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0363I12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0363I12 F, genomic survey sequence.

ACCESSION AZ579189
VERSION AZ579189.1 GI:11693534
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: I column: 12
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363I12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 198 CCATCTCCCCCATCCCC 215
|||
Db 2 CCTCTCCCCCTCCCC 19

RESULT 4

AU060353

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PROJECT = Dictyostelium discoideum cDNA project in Japan.

Location/Qualifiers

1. .20

/organism="Dictyostelium discoideum"

/mol_type="mRNA"

/strain="AX4"

/db_xref="taxon:44689"

/clone="SLJ384"

/dev_stage="slug"

/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"

Query Match 1.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.8;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 TTGTTTGGCTGTTTCATGT 702

|||||

Db 3 TTGTTTGGCTGTGAATGT 20

RESULT 5

AI446372

LOCUS

DEFINITION

similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;contains

AI446372

LOCUS

DEFINITION

similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;contains

AI446372

LOCUS

DEFINITION

similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;contains

AI446372

LOCUS

DEFINITION

similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;contains

ACCESSION AI446372
VERSION AI446372.1 GI:4294748
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 16)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1948 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2141098"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 CCCCCATCCCCCATTT 219
||||| ||||||||
Db 1 CCCCCCCCCCCCCATT 16

RESULT 6
AJ588273/c
LOCUS AJ588273
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 529E06, genomic survey sequence.
ACCESSION AJ588273
VERSION AJ588273.1 GI:37937897
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535

element MSR1 repetitive element ;, mRNA sequence.
AI446372
AI446372.1 GI:4294748
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1948 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2141098"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 1.1%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 CCCCCATCCCCCATTT 219
||||| ||||||||
Db 1 CCCCCCCCCCCCCATT 16

RESULT 6
AJ588273/c
LOCUS AJ588273
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 529E06, genomic survey sequence.
ACCESSION AJ588273
VERSION AJ588273.1 GI:37937897
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535

PUBMED 12446565
REFERENCE 2 (bases 1 to 18)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
FEATURES
source
1..18
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="529E06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1..18
/note="T-DNA flanking sequence
right border"

Query Match 1.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 18 TGCCCGGGCGGTGGCAGG 35
||||| ||||||| ||||
Db 18 TGNCCCGGGCGGGNAGG 1

RESULT 7
BH169716
LOCUS BH169716
DEFINITION SALK 001788 Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK_001788, genomic survey sequence.
ACCESSION BH169716
VERSION BH169716.1 GI:15905091
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1 (bases 1 to 14)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..14
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"

db_xref="taxon:3702"

clone_lib="SALK_001788"

note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

Query Match

Best Local Similarity

Matches

1.1%;

Score 12.4;

DB 1;

Length 14;

92.9%;

Pred. No. 3.5;

0;

Mismatches

1;

Indels

0;

Gaps

0;

QY

16

GCTGCCCGGGCGGT

29

DB

1

GCAGCCCGGGCGGT

14

RESULT 8

CA851710

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CA851710

D16F12_L24_12_ab1_cDNA_Peking_library_2_4_day_SCN3_Glycine_max

cDNA_clone_D16F12_5', mRNA sequence.

CA851710

CA851710.1

GI:33388503

EST.

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 15)

Alkharouf,N.W., Khan,R. and Matthews,B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharon@ba.ars.usda.gov.

FEATURES

source

1..15

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="D16F12"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 2, 4 day SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

Query Match

Best Local Similarity

Matches

1.1%;

Score 12.4;

DB 1;

Length 15;

92.9%;

Pred. No. 3.8;

0;

Mismatches

1;

Indels

0;

Gaps

0;

QY

1046

CCCAACTTCCTTAT

1059

DB

2

CCCACTTCCTTAT

15

RESULT 9

AJ727978/c

LOCUS

DEFINITION

ACCESSION

AJ727978

AJ727978

riken1 Gallus gallus cDNA clone 32b13s8, mRNA sequence.

AJ727978

db_xref="taxon:3702"

clone_lib="SALK_001788"

note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

Query Match

Best Local Similarity

Matches

1.1%;

Score 12;

DB 1;

Length 15;

100.0%;

Pred. No. 4.5;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

966

AGGACATTTTGA

977

DB

13

AGGACATTTTGA

2

Search completed: August 19, 2005, 10:37:47

Job time : 0.001 secs

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AJ727978.1

GI:53893388

EST.

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 15)

Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Biagodatski,A., Kostovska,D., Koter,M., Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.

Full-length cDNAs from bursal lymphocytes to facilitate gene function analysis

Unpublished (2004)

Contact: Caldwell RB

GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie

Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.

Location/Qualifiers

1..15

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="32b13s8"

/cell_type="bursal lymphocyte"

/dev_stage="2-3 weeks old"

/clone_lib="riken1"

/note="CB inbred strain"

Query Match

Best Local Similarity

Matches

1.1%;

Score 12;

DB 1;

Length 15;

100.0%;

Pred. No. 4.5;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

966

AGGACATTTTGA

977

DB

13

AGGACATTTTGA

2

Search completed: August 19, 2005, 10:37:47

Job time : 0.001 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2005, 10:56:24 ; Search time 8 Seconds
(without alignments)
2.891 Million cell updates/sec

Title: US-10-774-721-21
Perfect score: 1114
Sequence: 1 gtctggcttgccaggctgc.....gttacctgctcatttgttta 1114

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 536 seqs, 10381 residues

Total number of hits satisfying chosen parameters: 1072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 537 summaries

Database : ngsdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1 | 60 | 5.4 | 60 | 1 | ACA56897 Human cDNA encodin |
| C 2 | 51 | 4.6 | 51 | 1 | AAH90177 Human clone cg4392 |
| C 3 | 49.4 | 4.4 | 51 | 1 | AAH90178 Human clone cg4392 |
| C 4 | 22 | 2.0 | 22 | 1 | ADR27689 OB-RGRP antisense |
| C 5 | 21 | 1.9 | 21 | 1 | ADT71352 Reverse primer for |
| C 6 | 20.2 | 1.8 | 25 | 1 | ACK10810 Human microarray D |
| C 7 | 20 | 1.8 | 20 | 1 | AAV17684 PCR primer p1 used |
| C 8 | 20 | 1.8 | 20 | 1 | AAV17685 PCR primer p2 used |
| C 9 | 20 | 1.8 | 20 | 1 | AAK95054 Human cDNA clone-s |
| C 10 | 20 | 1.8 | 20 | 1 | ADL32266 Clone specific PCR |
| C 11 | 20 | 1.8 | 20 | 1 | ADR27690 OB-RGRP antisense |
| C 12 | 20 | 1.8 | 20 | 1 | ADR27680 OB-RGRP antisense |
| C 13 | 20 | 1.8 | 20 | 1 | ADR27685 OB-RGRP antisense |
| C 14 | 20 | 1.8 | 20 | 1 | ADR27653 OB-RGRP antisense |
| C 15 | 20 | 1.8 | 20 | 1 | ADR27682 OB-RGRP antisense |
| C 16 | 20 | 1.8 | 20 | 1 | ADR27688 OB-RGRP antisense |
| C 17 | 20 | 1.8 | 20 | 1 | ADR27681 OB-RGRP antisense |
| C 18 | 20 | 1.8 | 20 | 1 | ADR27687 OB-RGRP antisense |
| C 19 | 20 | 1.8 | 20 | 1 | ADR27679 OB-RGRP antisense |
| C 20 | 20 | 1.8 | 20 | 1 | ADR27692 OB-RGRP antisense |
| C 21 | 20 | 1.8 | 20 | 1 | ADR27683 OB-RGRP antisense |
| C 22 | 20 | 1.8 | 20 | 1 | ADR27686 OB-RGRP antisense |
| C 23 | 20 | 1.8 | 20 | 1 | ADR27684 OB-RGRP antisense |
| C 24 | 20 | 1.8 | 20 | 1 | ADR27691 OB-RGRP antisense |
| C 25 | 20 | 1.8 | 20 | 1 | ADT71351 Forward primer for |
| C 26 | 19.8 | 1.8 | 25 | 1 | ABK39905 Human Parathyroid |
| C 27 | 19 | 1.7 | 19 | 1 | AAT64982 Human OB receptor |
| C 28 | 18.6 | 1.7 | 25 | 1 | ACK10811 Human microarray D |
| C 29 | 18.2 | 1.6 | 25 | 1 | ACI63081 Human microarray D |
| C 30 | 18 | 1.6 | 18 | 1 | AAT64981 Human OB receptor |
| C 31 | 18 | 1.6 | 18 | 1 | AAT85600 Sense oligonucleot |
| C 32 | 18 | 1.6 | 18 | 1 | AAT85601 Antisense oligonuc |
| C 33 | 18 | 1.6 | 18 | 1 | ACA75490 Human WSX receptor |

| | | | | | |
|-------|------|-----|----|---|------------------------------|
| 34 | 18 | 1.6 | 18 | 1 | ACA75491 Human WSX receptor |
| 35 | 18 | 1.6 | 18 | 1 | ACH66797 Human WSX receptor |
| C 36 | 18 | 1.6 | 18 | 1 | ACH66796 Human WSX receptor |
| C 37 | 18 | 1.6 | 18 | 1 | ADC08932 Human WSX receptor |
| C 38 | 18 | 1.6 | 18 | 1 | ADC08931 Human WSX receptor |
| C 39 | 17.6 | 1.6 | 24 | 1 | AAD38375 Human BAT-25 locus |
| C 40 | 17.6 | 1.6 | 24 | 1 | ABT03742 Human Phox2b gene |
| C 41 | 17.6 | 1.6 | 24 | 1 | AAD36414 Human BAT-25 loci |
| C 42 | 17.6 | 1.6 | 24 | 1 | ADD31191 Human microsatelli |
| C 43 | 17.6 | 1.6 | 25 | 1 | ACI87101 Human microarray D |
| C 44 | 17 | 1.5 | 17 | 1 | ADI51286 Human tumour suppr |
| C 45 | 16.8 | 1.5 | 20 | 1 | ADJ25095 Human endothelial |
| C 46 | 16.8 | 1.5 | 20 | 1 | ADJ25250 Human endothelial |
| C 47 | 16.8 | 1.5 | 21 | 1 | AAA50752 PCR primer 1F used |
| C 48 | 16.8 | 1.5 | 24 | 1 | AAT89716 PCR primer used fo |
| C 49 | 16.8 | 1.5 | 24 | 1 | ABA99037 Rat PDGF-associate |
| C 50 | 16.6 | 1.5 | 23 | 1 | AAS03279 Candida albicans G |
| C 51 | 16.6 | 1.5 | 23 | 1 | ABZ30445 Murine fancg/xrcc9 |
| C 52 | 16.6 | 1.5 | 23 | 1 | ADK67738 Chromosome 11 (loc |
| C 53 | 16.2 | 1.5 | 21 | 1 | AAQ82600 Primer #2 to ampli |
| C 54 | 16.2 | 1.5 | 21 | 1 | AAT65977 Human multidrug re |
| C 55 | 16.2 | 1.5 | 21 | 1 | ABS98440 Human TGR342 RT-PC |
| C 56 | 16.2 | 1.5 | 23 | 1 | ABK86295 EKN1-1R human-spec |
| C 57 | 16.2 | 1.5 | 23 | 1 | ADB16943 Leptin receptor re |
| C 58 | 16 | 1.4 | 16 | 1 | ADR27674 Human tumour suppr |
| C 59 | 16 | 1.4 | 17 | 1 | ADI52070 Human SAC1 gene-sp |
| C 60 | 16 | 1.4 | 20 | 1 | AAS97676 Human SAC1 gene-sp |
| C 61 | 16 | 1.4 | 20 | 1 | AAS97674 Human G-coupled re |
| C 62 | 16 | 1.4 | 20 | 1 | ADJ93118 Human SAC1 DNA PCR |
| C 63 | 16 | 1.4 | 20 | 1 | ADM16016 Endogenous caroten |
| C 64 | 16 | 1.4 | 20 | 1 | ADM16014 Human BCL2 s1NA up |
| C 65 | 15.8 | 1.4 | 19 | 1 | ADE78595 Human BCL2 s1NA up |
| C 66 | 15.8 | 1.4 | 19 | 1 | ADP50077 Campylobacter fetu |
| C 67 | 15.8 | 1.4 | 19 | 1 | ADF49663 Fox specific PCR p |
| C 68 | 15.8 | 1.4 | 20 | 1 | AAT36558 Human PPAR antisen |
| C 69 | 15.8 | 1.4 | 20 | 1 | ADG37263 Human PPAR antisen |
| C 70 | 15.8 | 1.4 | 20 | 1 | ADG86812 Oligonucleotide as |
| C 71 | 15.8 | 1.4 | 20 | 1 | ADJ61530 Human endothelial |
| C 72 | 15.8 | 1.4 | 20 | 1 | ADJ24889 Human endothelial |
| C 73 | 15.8 | 1.4 | 20 | 1 | ADJ23864 Human endothelial |
| C 74 | 15.8 | 1.4 | 20 | 1 | ADL34750 Antisense oligonuc |
| C 75 | 15.8 | 1.4 | 20 | 1 | ADL34750 Human PPAR-delta t |
| C 76 | 15.8 | 1.4 | 20 | 1 | ADL34898 Human oligonucleot |
| C 77 | 15.8 | 1.4 | 20 | 1 | ADO46920 Control PCR primer |
| C 78 | 15.8 | 1.4 | 21 | 1 | ABV76832 PCR primer #1 for |
| C 79 | 15.8 | 1.4 | 21 | 1 | ADA73990 Primer A #15 used |
| C 80 | 15.8 | 1.4 | 22 | 1 | AAS23701 Candida albicans G |
| C 81 | 15.8 | 1.4 | 22 | 1 | ABZ29880 H. pylori vaca pro |
| C 82 | 15.6 | 1.4 | 22 | 1 | AAV73536 Novel human nuclei |
| C 83 | 15.6 | 1.4 | 22 | 1 | ADH42586 DNA molecule prepa |
| C 84 | 15.6 | 1.4 | 22 | 1 | ADS75784 STS marker seconda |
| C 85 | 15.6 | 1.4 | 22 | 1 | ADS08410 Human ERG hammehe |
| C 86 | 15.4 | 1.4 | 17 | 1 | ABK18401 Tumour suppression |
| C 87 | 15.4 | 1.4 | 17 | 1 | ABT38549 Tumour suppression |
| C 88 | 15.4 | 1.4 | 17 | 1 | ADB42880 Human biallelic ma |
| C 89 | 15.4 | 1.4 | 18 | 1 | AAZ77304 Human CYP2D6 C100T |
| C 90 | 15.4 | 1.4 | 18 | 1 | ADD24780 Ribozyme target se |
| C 91 | 15.4 | 1.4 | 19 | 1 | AAQ81302 Cyclin B1 ribozyme |
| C 92 | 15.4 | 1.4 | 19 | 1 | AAA85723 Cyclin B1 ribozyme |
| C 93 | 15.4 | 1.4 | 19 | 1 | AAH60885 Probe #13 for inte |
| C 94 | 15.4 | 1.4 | 20 | 1 | AAT50899 TRA-8 heavy and li |
| C 95 | 15.4 | 1.4 | 20 | 1 | AAS97050 Mouse anti-human D |
| C 96 | 15.4 | 1.4 | 20 | 1 | AAL60465 Single nucleotide |
| C 97 | 15.4 | 1.4 | 20 | 1 | ADF87587 TRA-8 antibody PCR |
| C 98 | 15.4 | 1.4 | 20 | 1 | ADJ79773 Human endothelial |
| C 99 | 15.4 | 1.4 | 20 | 1 | ADJ25296 Chimeric phosphoro |
| C 100 | 15.4 | 1.4 | 20 | 1 | ADJ24880 Chimeric phosphoro |
| C 101 | 15.4 | 1.4 | 20 | 1 | ADP78840 Chimeric phosphoro |
| C 102 | 15.4 | 1.4 | 20 | 1 | ADP78598 Chimeric phosphoro |
| C 103 | 15.4 | 1.4 | 20 | 1 | ADP78693 Chimeric phosphoro |
| C 104 | 15.4 | 1.4 | 20 | 1 | ADP78666 Chimeric phosphoro |
| C 105 | 15.4 | 1.4 | 21 | 1 | ABK53793 DMS:acceptor oxido |
| C 106 | 15.2 | 1.4 | 20 | 1 | AAAX96738 PCR primer used to |

| | | | | | | |
|-------|------|-----|----|---|----------|--------------------|
| C 107 | 15.2 | 1.4 | 20 | 1 | AAC67691 | Oligonucleotide #2 |
| 108 | 15.2 | 1.4 | 20 | 1 | AAF23345 | Oligonucleotide fo |
| 109 | 15.2 | 1.4 | 20 | 1 | AAD20131 | Human histone deac |
| 110 | 15.2 | 1.4 | 20 | 1 | AAF92365 | PCR primer specifi |
| 111 | 15.2 | 1.4 | 20 | 1 | ABV73091 | Human HDAC-8 mRNA |
| C 112 | 15.2 | 1.4 | 20 | 1 | ABK87739 | Capture oligonucle |
| 113 | 15.2 | 1.4 | 20 | 1 | ABK87739 | Human histone deac |
| C 114 | 15.2 | 1.4 | 20 | 1 | ABV74507 | Human histone deac |
| 115 | 15.2 | 1.4 | 20 | 1 | ADC21719 | Human alphainterfe |
| 116 | 15.2 | 1.4 | 20 | 1 | ADC79289 | Human HDAC-8 antis |
| 117 | 15.2 | 1.4 | 20 | 1 | ABZ76492 | 5'-RACE primer for |
| 118 | 15.2 | 1.4 | 20 | 1 | ADH50696 | Human HDAC8 mRNA t |
| C 119 | 15.2 | 1.4 | 20 | 1 | ADH50625 | Human IRAK-1 DNA t |
| C 120 | 15.2 | 1.4 | 20 | 1 | ADJ45254 | Human IRAK-1 DNA, |
| 121 | 15.2 | 1.4 | 20 | 1 | ADJ45325 | Hepatoma-derived g |
| 122 | 15.2 | 1.4 | 20 | 1 | ADI34745 | Hepatoma-derived g |
| 123 | 15.2 | 1.4 | 20 | 1 | ADJ96374 | Human HDAC8-specif |
| C 124 | 15.2 | 1.4 | 20 | 1 | ADJ23397 | Human breast cance |
| 125 | 15.2 | 1.4 | 20 | 1 | ADJ96440 | Human breast cance |
| 126 | 15.2 | 1.4 | 20 | 1 | ADJ23397 | Human endothelial |
| 127 | 15.2 | 1.4 | 20 | 1 | ADJ23964 | Human endothelial |
| 128 | 15.2 | 1.4 | 20 | 1 | ADO07539 | Human histone deac |
| 129 | 15.2 | 1.4 | 20 | 1 | ADR20736 | Human histone deac |
| C 130 | 15.2 | 1.4 | 21 | 1 | AAT66953 | Asialoglycoprotein |
| C 131 | 15.2 | 1.4 | 21 | 1 | AAF95925 | Human gene single |
| 132 | 15.2 | 1.4 | 21 | 1 | AAF96968 | Human gene single |
| C 133 | 15.2 | 1.4 | 21 | 1 | ABK82248 | Human Atp-binding |
| 134 | 15.2 | 1.4 | 21 | 1 | ABK82248 | Human acetyl choli |
| 135 | 15.2 | 1.4 | 21 | 1 | ADH68383 | Rosa sp forward PC |
| C 136 | 15 | 1.3 | 20 | 1 | AAX79744 | BAPF siRNA sense s |
| C 137 | 15 | 1.3 | 20 | 1 | ADJ33553 | PCR primer H5528 f |
| 138 | 14.8 | 1.3 | 18 | 1 | AAH73748 | PCR primer used to |
| C 139 | 14.8 | 1.3 | 19 | 1 | ADE29652 | Mitogen activated |
| 140 | 14.8 | 1.3 | 19 | 1 | ADE29489 | Mitogen activated |
| 141 | 14.8 | 1.3 | 19 | 1 | ADQ27277 | RNA interference t |
| 142 | 14.8 | 1.3 | 19 | 1 | ADR27528 | Human single nucle |
| C 143 | 14.8 | 1.3 | 20 | 1 | AAT36153 | PCR primer for det |
| C 144 | 14.8 | 1.3 | 20 | 1 | AAI72504 | Human Int6 exon 3 |
| 145 | 14.8 | 1.3 | 20 | 1 | AAZ03074 | PCR primer used to |
| 146 | 14.8 | 1.3 | 20 | 1 | AAZ03074 | Mouse IL-5R antis |
| 147 | 14.8 | 1.3 | 20 | 1 | AAZ03074 | Mouse interleukin- |
| 148 | 14.8 | 1.3 | 20 | 1 | AAZ03074 | Mouse IL-5R antis |
| 149 | 14.8 | 1.3 | 20 | 1 | ABL45391 | Human chromosome 2 |
| C 150 | 14.8 | 1.3 | 20 | 1 | AAZ03074 | Alpha-V integrin-s |
| C 151 | 14.8 | 1.3 | 20 | 1 | AAZ03074 | Nod2 related olig |
| 152 | 14.8 | 1.3 | 20 | 1 | ABT05772 | Mouse Interleukin |
| 153 | 14.8 | 1.3 | 20 | 1 | ABX04453 | PKA regulatory sub |
| C 154 | 14.8 | 1.3 | 20 | 1 | ABZ81557 | Human PLSR4 antis |
| C 155 | 14.8 | 1.3 | 20 | 1 | ADZ57723 | Human TLR1 related |
| 156 | 14.8 | 1.3 | 20 | 1 | ABZ93663 | Human oligonucleot |
| 157 | 14.8 | 1.3 | 20 | 1 | ABD29893 | T74688-derived oli |
| 158 | 14.8 | 1.3 | 20 | 1 | ADJ86050 | Nucleic acid anal |
| C 159 | 14.8 | 1.3 | 20 | 1 | ADJ54494 | Human B7-2 DNA ant |
| 160 | 14.8 | 1.3 | 20 | 1 | ADJ23824 | Human endothelial |
| 161 | 14.8 | 1.3 | 20 | 1 | ADJ22770 | Human endothelial |
| 162 | 14.8 | 1.3 | 20 | 1 | ADJ23294 | Human endothelial |
| C 163 | 14.8 | 1.3 | 20 | 1 | ADK19749 | Mouse cDNA clone C |
| C 164 | 14.8 | 1.3 | 20 | 1 | ADO56167 | Cyclin-dependent k |
| 165 | 14.8 | 1.3 | 20 | 1 | ADO56108 | Cyclin-dependent k |
| C 166 | 14.8 | 1.3 | 20 | 1 | ADN31001 | Human Int6 cDNA PC |
| C 167 | 14.8 | 1.3 | 20 | 1 | ADP64695 | Human interleukin- |
| 168 | 14.8 | 1.3 | 20 | 1 | ADP64751 | Human interleukin- |
| 169 | 14.8 | 1.3 | 20 | 1 | ADR12130 | Murine interleukin |
| 170 | 14.8 | 1.3 | 21 | 1 | AAQ52344 | Sequence of synthe |
| 171 | 14.8 | 1.3 | 21 | 1 | ABS66964 | Human MRP-1 polymo |
| C 172 | 14.8 | 1.3 | 21 | 1 | ABS66965 | Human MRP-1 polymo |
| 173 | 14.8 | 1.3 | 21 | 1 | ABS66966 | Human MRP-1 polymo |
| 174 | 14.8 | 1.3 | 21 | 1 | ABS66966 | Human MRP-1 polymo |
| C 175 | 14.8 | 1.3 | 21 | 1 | ABS66967 | Human MRP-1 polymo |
| C 176 | 14.8 | 1.3 | 21 | 1 | ABS66969 | Human MRP-1 polymo |
| C 177 | 14.8 | 1.3 | 21 | 1 | ACF62467 | Cancer based on CY |
| 178 | 14.8 | 1.3 | 21 | 1 | ACF62464 | Cancer based on CY |
| C 179 | 14.8 | 1.3 | 21 | 1 | ACF62465 | Cancer based on CY |

| | | | | | | |
|-------|------|-----|----|---|----------|---------------------|
| 180 | 14.8 | 1.3 | 21 | 1 | ACF62466 | Cancer based on CY |
| 181 | 14.8 | 1.3 | 21 | 1 | ADB21135 | MRP1 based cancer |
| C 182 | 14.8 | 1.3 | 21 | 1 | ADB21136 | MRP1 based cancer |
| C 183 | 14.8 | 1.3 | 21 | 1 | ADB21137 | MRP1 based cancer |
| 184 | 14.8 | 1.3 | 21 | 1 | ADB21137 | MRP1 based cancer |
| C 185 | 14.8 | 1.3 | 21 | 1 | ADB88225 | Human UGT1A1 varia |
| C 186 | 14.8 | 1.3 | 21 | 1 | ADB88227 | Human UGT1A1 varia |
| 187 | 14.8 | 1.3 | 21 | 1 | ADB88226 | Human UGT1A1 varia |
| 188 | 14.8 | 1.3 | 21 | 1 | ADB88226 | Human UGT1A1 varia |
| 189 | 14.8 | 1.3 | 21 | 1 | ADB97207 | Human MRP1 variant |
| C 190 | 14.8 | 1.3 | 21 | 1 | ADB97210 | Human MRP1 variant |
| 191 | 14.8 | 1.3 | 21 | 1 | ADB97208 | Human MRP1 variant |
| C 192 | 14.8 | 1.3 | 21 | 1 | ADB97209 | Human MRP1 variant |
| C 193 | 14.8 | 1.3 | 21 | 1 | ADB92401 | Human MRP1 variant |
| C 194 | 14.8 | 1.3 | 21 | 1 | ADB92399 | Human MRP1 variant |
| 195 | 14.8 | 1.3 | 21 | 1 | ADB92398 | Human MRP1 variant |
| 196 | 14.8 | 1.3 | 21 | 1 | ADB92400 | Human MRP1 variant |
| C 197 | 14.8 | 1.3 | 21 | 1 | ADF87704 | Single nucleotide |
| C 198 | 14.8 | 1.3 | 21 | 1 | ADP46739 | Human c-Cbl siRNA |
| 199 | 14.8 | 1.3 | 21 | 1 | ADP46857 | Human c-Cbl siRNA |
| 200 | 14.8 | 1.3 | 21 | 1 | ADR18488 | Human GOBLIN siRNA |
| C 201 | 14.8 | 1.3 | 21 | 1 | ADR18487 | Human GOBLIN siRNA |
| 202 | 14.6 | 1.3 | 15 | 1 | ABL52014 | Human SLC18A2 alle |
| 203 | 14.6 | 1.3 | 15 | 1 | ABK27525 | Human CTIA4 gene a |
| 204 | 14.4 | 1.3 | 16 | 1 | ABQ78935 | Mouse intermediate |
| 205 | 14.4 | 1.3 | 17 | 1 | AAA18571 | Human TIE-2 substr |
| C 206 | 14.4 | 1.3 | 17 | 1 | ABN02574 | Human GDMPLP-1 17-m |
| C 207 | 14.4 | 1.3 | 17 | 1 | ABN02573 | Human GDMPLP-1 17-m |
| 208 | 14.4 | 1.3 | 17 | 1 | ABK19407 | Human ERG Amberzym |
| 209 | 14.4 | 1.3 | 17 | 1 | ABK17677 | Human ERG hammerhe |
| 210 | 14.4 | 1.3 | 17 | 1 | ACD52117 | HBV inozyme substr |
| 211 | 14.4 | 1.3 | 17 | 1 | ACC67229 | Murine oligonucleo |
| C 212 | 14.4 | 1.3 | 17 | 1 | ADB45885 | Tumour suppression |
| 213 | 14.4 | 1.3 | 17 | 1 | ADB30660 | Cholesterol homeos |
| C 214 | 14.4 | 1.3 | 17 | 1 | ADI50064 | Human tumour suppr |
| C 215 | 14.4 | 1.3 | 17 | 1 | ACC53731 | Human tumour suppr |
| 216 | 14.4 | 1.3 | 17 | 1 | ADM58814 | Hepatitis B virus |
| C 217 | 14.4 | 1.3 | 17 | 1 | ACN65663 | Human GDMPLP-1 prob |
| C 218 | 14.4 | 1.3 | 17 | 1 | ACN65664 | Human GDMPLP-1 prob |
| C 219 | 14.4 | 1.3 | 17 | 1 | AAA85722 | Cyclin B1 ribozyme |
| C 220 | 14.4 | 1.3 | 19 | 1 | AAH60884 | Cyclin B1 ribozyme |
| 221 | 14.4 | 1.3 | 19 | 1 | ABA82563 | Zmax1 gene region |
| 222 | 14.4 | 1.3 | 19 | 1 | ABK23360 | Human Zmax1 CDNA r |
| 223 | 14.4 | 1.3 | 19 | 1 | ACC45943 | Human HBM STS mark |
| 224 | 14.4 | 1.3 | 19 | 1 | ADB98641 | Sequence tagged si |
| 225 | 14.4 | 1.3 | 19 | 1 | ADR17506 | Human chromosome 1 |
| 226 | 14.4 | 1.3 | 19 | 1 | ADR48157 | Human chromosome 1 |
| C 227 | 14.4 | 1.3 | 20 | 1 | AAZ92502 | PCR primer used to |
| 228 | 14.4 | 1.3 | 20 | 1 | AAA96394 | Primer used to amp |
| 229 | 14.4 | 1.3 | 20 | 1 | AAZ72439 | Human biallelic ma |
| 230 | 14.4 | 1.3 | 20 | 1 | AAA47500 | Primer for amplify |
| 231 | 14.4 | 1.3 | 20 | 1 | ABK85315 | Human PTP1B antise |
| 232 | 14.4 | 1.3 | 20 | 1 | ACC86742 | Human VEGFR-1 chim |
| C 233 | 14.4 | 1.3 | 20 | 1 | ADB68675 | Microsomal triglyc |
| C 234 | 14.4 | 1.3 | 20 | 1 | ACF36599 | Col11a2 cDNA ampli |
| 235 | 14.4 | 1.3 | 20 | 1 | ADI14044 | Antisense DNA olig |
| 236 | 14.4 | 1.3 | 20 | 1 | ADJ25024 | Human endothelial |
| C 237 | 14.4 | 1.3 | 20 | 1 | ADN61693 | Corn chromosome 6 |
| 238 | 14.4 | 1.3 | 20 | 1 | ADN01882 | Human HIP1 antisen |
| C 239 | 14.4 | 1.3 | 20 | 1 | ADN01807 | Human HIP1 antisen |
| C 240 | 14.4 | 1.3 | 20 | 1 | ADN01806 | Human HIP1 antisen |
| 241 | 14.4 | 1.3 | 20 | 1 | ADN01883 | Chimeric phosphoro |
| 242 | 14.4 | 1.3 | 20 | 1 | ADP78871 | Chimeric phosphoro |
| 243 | 14.4 | 1.3 | 20 | 1 | ADP78738 | CAPN3/DYSF PCR pri |
| 244 | 14.4 | 1.3 | 20 | 1 | ADQ14074 | PCR primer used to |
| C 245 | 14.4 | 1.3 | 20 | 1 | ADQ91206 | Target nucleic aci |
| 246 | 14.2 | 1.3 | 19 | 1 | AAT30234 | Human breast cance |
| C 247 | 14.2 | 1.3 | 19 | 1 | AAV10771 | PCR primer used to |
| 248 | 14.2 | 1.3 | 19 | 1 | AAA46190 | Stabilising reagen |
| 249 | 14.2 | 1.3 | 19 | 1 | ABT23695 | RTQ PCR primer #2 |
| 250 | 14.2 | 1.3 | 19 | 1 | ADI82218 | RNA interference t |
| 251 | 14.2 | 1.3 | 19 | 1 | ADQ27747 | Anti-NR2E1 siRNA r |
| C 252 | 14.2 | 1.3 | 19 | 1 | ADQ61744 | Anti-NR2E1 siRNA r |

| | | | | | | |
|--|--|--|--|--|--|---------------------|
| | | | | | | Cancer based on CY |
| | | | | | | MRP1 based cancer |
| | | | | | | MRP1 based cancer |
| | | | | | | MRP1 based cancer |
| | | | | | | MRP1 based cancer |
| | | | | | | Human UGT1A1 varia |
| | | | | | | Human UGT1A1 varia |
| | | | | | | Human UGT1A1 varia |
| | | | | | | Human UGT1A1 varia |
| | | | | | | Human MRP1 variant |
| | | | | | | Human MRP1 variant |
| | | | | | | Human MRP1 variant |
| | | | | | | Human MRP1 variant |
| | | | | | | Human MRP1 variant |
| | | | | | | Human MRP1 variant |
| | | | | | | Human MRP1 variant |
| | | | | | | Single nucleotide |
| | | | | | | Human c-Cbl siRNA |
| | | | | | | Human c-Cbl siRNA |
| | | | | | | Human GOBLIN siRNA |
| | | | | | | Human GOBLIN siRNA |
| | | | | | | Human SLC18A2 alle |
| | | | | | | Human CTLA4 gene a |
| | | | | | | Mouse intermediate |
| | | | | | | Human TIE-2 substr |
| | | | | | | Human GDMPLP-1 17-m |
| | | | | | | Human GDMPLP-1 17-m |
| | | | | | | Human ERG Amberzym |
| | | | | | | Human ERG hammerhe |
| | | | | | | HBV inozyme substr |
| | | | | | | Murine oligonucleo |
| | | | | | | Tumour suppression |
| | | | | | | Cholesterol homeos |
| | | | | | | Human tumour suppr |
| | | | | | | Human tumour suppr |
| | | | | | | Hepatitis B virus |
| | | | | | | Human GDMPLP-1 prob |
| | | | | | | Human GDMPLP-1 prob |
| | | | | | | Cyclin B1 ribozyme |
| | | | | | | Cyclin B1 ribozyme |
| | | | | | | Zmax1 gene region |
| | | | | | | Human Zmax1 CDNA r |
| | | | | | | Human HBM STS mark |
| | | | | | | Sequence tagged si |
| | | | | | | Human chromosome 1 |
| | | | | | | Human chromosome 1 |
| | | | | | | PCR primer used to |
| | | | | | | Primer used to amp |
| | | | | | | Human biallelic ma |
| | | | | | | Primer for amplify |
| | | | | | | Human PTP1B antise |
| | | | | | | Human VEGFR-1 chim |
| | | | | | | Microsomal triglyc |
| | | | | | | Col11a2 cDNA ampli |
| | | | | | | Antisense DNA olig |
| | | | | | | Human endothelial |
| | | | | | | Corn chromosome 6 |
| | | | | | | Human HIP1 antisen |
| | | | | | | Human HIP1 antisen |
| | | | | | | Human HIP1 antisen |
| | | | | | | Human HIP1 antisen |
| | | | | | | Chimeric phospho |
| | | | | | | Chimeric phospho |
| | | | | | | CAPN3/DYSF PCR pri |
| | | | | | | PCR primer used to |
| | | | | | | Target nucleic aci |
| | | | | | | Human breast cance |
| | | | | | | PCR primer used to |
| | | | | | | Stabilising reagen |
| | | | | | | RTQ PCR primer #2 |
| | | | | | | RNA interference t |
| | | | | | | Anti-NR2E1 siRNA r |

| | | | | | | |
|-------|------|-----|----|---|-----------|--------------------|
| C 253 | 14.2 | 1.3 | 19 | 1 | ADR70528 | Reverse RTQ primer |
| C 254 | 14.2 | 1.3 | 19 | 1 | ADR75949 | Human apolipoprote |
| C 255 | 14.2 | 1.3 | 19 | 1 | ADR78567 | Human apolipoprote |
| C 256 | 14.2 | 1.3 | 19 | 1 | ADR76227 | Human apolipoprote |
| C 257 | 14.2 | 1.3 | 19 | 1 | ADR78845 | Human apolipoprote |
| C 258 | 14.2 | 1.3 | 20 | 1 | AAQ35765 | M segment 5' fragm |
| C 259 | 14.2 | 1.3 | 20 | 1 | AAQ53275 | CTV primer 5' . Sy |
| C 260 | 14.2 | 1.3 | 20 | 1 | AAQ97957 | PNA oligomer targe |
| C 261 | 14.2 | 1.3 | 20 | 1 | AAQ84260 | PKC-epsilon coding |
| C 262 | 14.2 | 1.3 | 20 | 1 | AAV01278 | Guanylate cyclase |
| C 263 | 14.2 | 1.3 | 20 | 1 | AAAX22647 | Human protein kina |
| C 264 | 14.2 | 1.3 | 20 | 1 | AAAX76903 | H2-1 Pagl gene dir |
| C 265 | 14.2 | 1.3 | 20 | 1 | AAAX78609 | Human PKC-epsilon |
| C 266 | 14.2 | 1.3 | 20 | 1 | AAAX83735 | Human protein kina |
| C 267 | 14.2 | 1.3 | 20 | 1 | AAAX92824 | PCR primer used to |
| C 268 | 14.2 | 1.3 | 20 | 1 | AAAX94795 | PCR primer used to |
| C 269 | 14.2 | 1.3 | 20 | 1 | AAAX95833 | PCR primer used to |
| C 270 | 14.2 | 1.3 | 20 | 1 | AAAX97255 | Primer used to amp |
| C 271 | 14.2 | 1.3 | 20 | 1 | AAAX95840 | PCR primer used to |
| C 272 | 14.2 | 1.3 | 20 | 1 | AAAX19212 | Human PKC-epsilon |
| C 273 | 14.2 | 1.3 | 20 | 1 | AAZ227351 | Human protein kina |
| C 274 | 14.2 | 1.3 | 20 | 1 | AAZ75053 | Human biallelic ma |
| C 275 | 14.2 | 1.3 | 20 | 1 | AAA64912 | Antisense oligonuc |
| C 276 | 14.2 | 1.3 | 20 | 1 | AAF62444 | A thaliana VRN1 ge |
| C 277 | 14.2 | 1.3 | 20 | 1 | AAF23509 | Primer cadP-R1C. |
| C 278 | 14.2 | 1.3 | 20 | 1 | AAAC92586 | Human nucleolin ph |
| C 279 | 14.2 | 1.3 | 20 | 1 | AAI65644 | Primer for microsa |
| C 280 | 14.2 | 1.3 | 20 | 1 | ABA82285 | Zmax1 gene region |
| C 281 | 14.2 | 1.3 | 20 | 1 | AAI46974 | Cell cycle regulat |
| C 282 | 14.2 | 1.3 | 20 | 1 | ABL90939 | Human protein kina |
| C 283 | 14.2 | 1.3 | 20 | 1 | AAI45924 | Murine dystrophin- |
| C 284 | 14.2 | 1.3 | 20 | 1 | ABL45469 | Human chromosome 2 |
| C 285 | 14.2 | 1.3 | 20 | 1 | ABL44467 | Human chromosome 1 |
| C 286 | 14.2 | 1.3 | 20 | 1 | ABT06471 | NES-1 gene methyl |
| C 287 | 14.2 | 1.3 | 20 | 1 | ABQ62452 | Mouse syntaxin 4 i |
| C 288 | 14.2 | 1.3 | 20 | 1 | ABK23082 | Human Zmax1 CDNA r |
| C 289 | 14.2 | 1.3 | 20 | 1 | ABS68905 | Human RecQ protein |
| C 290 | 14.2 | 1.3 | 20 | 1 | AAD41640 | Human interleukin- |
| C 291 | 14.2 | 1.3 | 20 | 1 | ADE31838 | Solid surface asse |
| C 292 | 14.2 | 1.3 | 20 | 1 | ABT21432 | Multiplex group PC |
| C 293 | 14.2 | 1.3 | 20 | 1 | ABX10661 | Reverse PCR primer |
| C 294 | 14.2 | 1.3 | 20 | 1 | ACC45665 | Human HBM STS mark |
| C 295 | 14.2 | 1.3 | 20 | 1 | ABZ80435 | Human protein PP13 |
| C 296 | 14.2 | 1.3 | 20 | 1 | ACH11218 | Human protein kina |
| C 297 | 14.2 | 1.3 | 20 | 1 | ACA62693 | RIZ(A)8 tract prim |
| C 298 | 14.2 | 1.3 | 20 | 1 | ABT44202 | Chimeric antisense |
| C 299 | 14.2 | 1.3 | 20 | 1 | ADB98363 | Sequence tagged si |
| C 300 | 14.2 | 1.3 | 20 | 1 | ADD20426 | Oreochromis niloti |
| C 301 | 14.2 | 1.3 | 20 | 1 | ADD90778 | S. pneumoniae vncs |
| C 302 | 14.2 | 1.3 | 20 | 1 | ACH00690 | Mammalian inverted |
| C 303 | 14.2 | 1.3 | 20 | 1 | ABZ91305 | Human oligonucleot |
| C 304 | 14.2 | 1.3 | 20 | 1 | ABZ99318 | Human PDE4C oligon |
| C 305 | 14.2 | 1.3 | 20 | 1 | ABZ88740 | Human oligonucleot |
| C 306 | 14.2 | 1.3 | 20 | 1 | ABQ84375 | DPPI0 PCR primer # |
| C 307 | 14.2 | 1.3 | 20 | 1 | ABZ77118 | Human stearoyl-CoA |
| C 308 | 14.2 | 1.3 | 20 | 1 | ABV99953 | Coriolus versicolo |
| C 309 | 14.2 | 1.3 | 20 | 1 | ADM83692 | Serine protease-li |
| C 310 | 14.2 | 1.3 | 20 | 1 | ADM83766 | Serine protease-li |
| C 311 | 14.2 | 1.3 | 20 | 1 | ABD27535 | AA486238-derived o |
| C 312 | 14.2 | 1.3 | 20 | 1 | ABD24970 | AI138216-derived o |
| C 313 | 14.2 | 1.3 | 20 | 1 | ABD32349 | Human PDE4C-derive |
| C 314 | 14.2 | 1.3 | 20 | 1 | ADH47993 | Protein kinase C e |
| C 315 | 14.2 | 1.3 | 20 | 1 | ADH58845 | Human CDC-like kin |
| C 316 | 14.2 | 1.3 | 20 | 1 | ADH58791 | Human CDC-like kin |
| C 317 | 14.2 | 1.3 | 20 | 1 | ADH65127 | Human glucocortico |
| C 318 | 14.2 | 1.3 | 20 | 1 | ADH65989 | Human glucocortico |
| C 319 | 14.2 | 1.3 | 20 | 1 | ADH65276 | Human glucocortico |
| C 320 | 14.2 | 1.3 | 20 | 1 | ADH64643 | Human glucocortico |
| C 321 | 14.2 | 1.3 | 20 | 1 | ADH65757 | Human glucocortico |
| C 322 | 14.2 | 1.3 | 20 | 1 | ADH65015 | Human glucocortico |
| C 323 | 14.2 | 1.3 | 20 | 1 | ADI79588 | Human HMG-CoA redu |
| C 324 | 14.2 | 1.3 | 20 | 1 | ADI79785 | Human HMG-CoA redu |
| C 325 | 14.2 | 1.3 | 20 | 1 | ADI44833 | Human cystic fibro |

| | | | | | | |
|-------|------|-----|----|---|-----------|--------------------|
| C 326 | 14.2 | 1.3 | 20 | 1 | ADJ61611 | Oligonucleotide as |
| C 327 | 14.2 | 1.3 | 20 | 1 | ADJ61203 | Oligonucleotide as |
| C 328 | 14.2 | 1.3 | 20 | 1 | ADJ19254 | Antisense 2-MOB ga |
| C 329 | 14.2 | 1.3 | 20 | 1 | ADJ18790 | Antisense DNA olig |
| C 330 | 14.2 | 1.3 | 20 | 1 | ADJ18263 | Antisense DNA olig |
| C 331 | 14.2 | 1.3 | 20 | 1 | ADJ18084 | Antisense DNA olig |
| C 332 | 14.2 | 1.3 | 20 | 1 | ADJ17966 | Antisense DNA olig |
| C 333 | 14.2 | 1.3 | 20 | 1 | ADJ24119 | Human endothelial |
| C 334 | 14.2 | 1.3 | 20 | 1 | ADJ24136 | Human endothelial |
| C 335 | 14.2 | 1.3 | 20 | 1 | ADJ24120 | Human endothelial |
| C 336 | 14.2 | 1.3 | 20 | 1 | ADK80500 | Chimeric phosphoro |
| C 337 | 14.2 | 1.3 | 20 | 1 | ADK80983 | Chimeric phosphoro |
| C 338 | 14.2 | 1.3 | 20 | 1 | ADL97965 | Msx2 probe, SEQ ID |
| C 339 | 14.2 | 1.3 | 20 | 1 | ADO46593 | Human oligonucleot |
| C 340 | 14.2 | 1.3 | 20 | 1 | ADO47001 | Human oligonucleot |
| C 341 | 14.2 | 1.3 | 20 | 1 | ADP12146 | Taqman probe set 2 |
| C 342 | 14.2 | 1.3 | 20 | 1 | ADP68640 | Human PPAR-alpha a |
| C 343 | 14.2 | 1.3 | 20 | 1 | ADR27036 | Human single nucle |
| C 344 | 14.2 | 1.3 | 20 | 1 | ADR17228 | Human chromosome 1 |
| C 345 | 14.2 | 1.3 | 20 | 1 | ADK67431 | PCR primer used to |
| C 346 | 14.2 | 1.3 | 20 | 1 | ADR47879 | Human chromosome 1 |
| C 347 | 14.2 | 1.3 | 20 | 1 | ADS31697 | Gene expression in |
| C 348 | 14.2 | 1.3 | 20 | 1 | ADS31698 | Gene expression in |
| C 349 | 14 | 1.3 | 14 | 1 | ADR27673 | Leptin receptor re |
| C 350 | 14 | 1.3 | 15 | 1 | AAT54666 | Mouse IL-5 hammerh |
| C 351 | 14 | 1.3 | 15 | 1 | AAZ63871 | Substrate for hamm |
| C 352 | 14 | 1.3 | 15 | 1 | ABX00924 | Hepatitis C virus |
| C 353 | 14 | 1.3 | 17 | 1 | ABT39781 | Tumour suppression |
| C 354 | 14 | 1.3 | 18 | 1 | AAZ71197 | Human biallelic ma |
| C 355 | 14 | 1.3 | 20 | 1 | AAZ69829 | Human biallelic ma |
| C 356 | 14 | 1.3 | 20 | 1 | AAZ71268 | Human biallelic ma |
| C 357 | 14 | 1.3 | 20 | 1 | AAD34452 | Human TREK2 CDNA s |
| C 358 | 14 | 1.3 | 20 | 1 | ABN79739 | Human Fas target o |
| C 359 | 14 | 1.3 | 20 | 1 | AAI42518 | Alpha-V integrin-s |
| C 360 | 14 | 1.3 | 20 | 1 | ACH00628 | Mammalian inverted |
| C 361 | 14 | 1.3 | 20 | 1 | ADH77414 | Human PTPN12 antis |
| C 362 | 14 | 1.3 | 20 | 1 | ADL27795 | Human Fas cDNA, an |
| C 363 | 14 | 1.3 | 20 | 1 | ADM53567 | Human Fas antisens |
| C 364 | 13.8 | 1.2 | 17 | 1 | AAQ40912 | C-erb-B2 sense oli |
| C 365 | 13.8 | 1.2 | 17 | 1 | AAQ40911 | C-erb-B2 antisense |
| C 366 | 13.8 | 1.2 | 17 | 1 | AAT05984 | COX II forward pri |
| C 367 | 13.8 | 1.2 | 17 | 1 | AAA18772 | Human TIE-2 substr |
| C 368 | 13.8 | 1.2 | 17 | 1 | AAF04220 | Hammerhead ribozym |
| C 369 | 13.8 | 1.2 | 17 | 1 | ABK02567 | Hammerhead ribozym |
| C 370 | 13.8 | 1.2 | 17 | 1 | AAF69066 | Human NOGO Amberzy |
| C 371 | 13.8 | 1.2 | 17 | 1 | AAF69066 | COXII PCR primer # |
| C 372 | 13.8 | 1.2 | 17 | 1 | AAF690629 | COXII PCR primer # |
| C 373 | 13.8 | 1.2 | 17 | 1 | AAF69063 | COXII PCR primer # |
| C 374 | 13.8 | 1.2 | 17 | 1 | AAF69064 | COXII PCR primer # |
| C 375 | 13.8 | 1.2 | 17 | 1 | AAF69018 | COXII PCR primer # |
| C 376 | 13.8 | 1.2 | 17 | 1 | ABL46970 | Human GRID zinzyme |
| C 377 | 13.8 | 1.2 | 17 | 1 | AAI65652 | Primer for studyin |
| C 378 | 13.8 | 1.2 | 17 | 1 | ABN06757 | Human GDMLP-1 17-m |
| C 379 | 13.8 | 1.2 | 17 | 1 | ABN02571 | Human GDMLP-1 17-m |
| C 380 | 13.8 | 1.2 | 17 | 1 | ABN02572 | Human GDMLP-1 17-m |
| C 381 | 13.8 | 1.2 | 17 | 1 | ABV82997 | Human HTPL scannin |
| C 382 | 13.8 | 1.2 | 17 | 1 | ABK19408 | Human ERG Amberzym |
| C 383 | 13.8 | 1.2 | 17 | 1 | ABL31405 | Human HLA genotypi |
| C 384 | 13.8 | 1.2 | 17 | 1 | ADA49961 | Human mitochondria |
| C 385 | 13.8 | 1.2 | 17 | 1 | ADA50007 | Human mitochondria |
| C 386 | 13.8 | 1.2 | 17 | 1 | ADA49972 | Human mitochondria |
| C 387 | 13.8 | 1.2 | 17 | 1 | ADA50009 | Human mitochondria |
| C 388 | 13.8 | 1.2 | 17 | 1 | ADA50006 | Human mitochondria |
| C 389 | 13.8 | 1.2 | 17 | 1 | ADA50271 | Human PCR primer 9 |
| C 390 | 13.8 | 1.2 | 17 | 1 | ADL46684 | Human NOGO recepto |
| C 391 | 13.8 | 1.2 | 17 | 1 | ADM09493 | Human NOGO recepto |
| C 392 | 13.8 | 1.2 | 17 | 1 | ADM54293 | Human GRID mRNA su |
| C 393 | 13.8 | 1.2 | 17 | 1 | ADL82299 | Human ER+ breast c |
| C 394 | 13.8 | 1.2 | 17 | 1 | ACN69847 | Human GDMLP-1 prob |
| C 395 | 13.8 | 1.2 | 17 | 1 | ACN65662 | Human GDMLP-1 prob |
| C 396 | 13.8 | 1.2 | 17 | 1 | ACN65661 | Human GDMLP-1 prob |
| C 397 | 13.8 | 1.2 | 18 | 1 | AAV44608 | Human uncoupling p |
| C 398 | 13.8 | 1.2 | 18 | 1 | AAZ00111 | HEV US-1 amplifyin |

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|-------|------|-----|----|---|----------|--------------------|
| C 399 | 13.8 | 1.2 | 18 | 1 | AAZ76902 | Hs-1 Pagl gene dir |
| C 400 | 13.8 | 1.2 | 18 | 1 | AAZ71685 | Human biallelic ma |
| C 401 | 13.8 | 1.2 | 18 | 1 | AAZ76996 | Human biallelic ma |
| C 402 | 13.8 | 1.2 | 18 | 1 | AAZ70376 | Human biallelic ma |
| C 403 | 13.8 | 1.2 | 18 | 1 | ABL54891 | PCR primer BV-b5. |
| C 404 | 13.8 | 1.2 | 18 | 1 | ACF63028 | Human progesterone |
| C 405 | 13.8 | 1.2 | 18 | 1 | ACF63026 | Human progesterone |
| C 406 | 13.8 | 1.2 | 18 | 1 | ADM06379 | Human PCR primer S |
| C 407 | 13.8 | 1.2 | 18 | 1 | ADJ65208 | Human connexin gen |
| C 408 | 13.8 | 1.2 | 18 | 1 | ADN35818 | Human NSCLC gene a |
| C 409 | 13.8 | 1.2 | 18 | 1 | ADS90119 | Oligonucleotide of |
| C 410 | 13.8 | 1.2 | 19 | 1 | AAA83453 | cdk8 ribozyme bind |
| C 411 | 13.8 | 1.2 | 19 | 1 | AAA83063 | cdk6 ribozyme bind |
| C 412 | 13.8 | 1.2 | 19 | 1 | AAH56706 | Streptococcus pyog |
| C 413 | 13.8 | 1.2 | 19 | 1 | AAH58225 | Cell-cycle depende |
| C 414 | 13.8 | 1.2 | 19 | 1 | AAH58615 | Cell-cycle depende |
| C 415 | 13.8 | 1.2 | 19 | 1 | AAF74684 | P. furiosus thermo |
| C 416 | 13.8 | 1.2 | 19 | 1 | ADF1834 | Human IGF-1R siNA |
| C 417 | 13.8 | 1.2 | 19 | 1 | ADF31557 | Human IGF-1R trans |
| C 418 | 13.8 | 1.2 | 19 | 1 | ADF88498 | Single nucleotide |
| C 419 | 13.8 | 1.2 | 19 | 1 | ADI57146 | Oryza minuta Pi9 1 |
| C 420 | 13.8 | 1.2 | 19 | 1 | ADN75775 | TCPTP associated s |
| C 421 | 13.8 | 1.2 | 19 | 1 | ADN75774 | TCPTP associated s |
| C 422 | 13.8 | 1.2 | 19 | 1 | ADQ27278 | RNA interference t |
| C 423 | 13.8 | 1.2 | 19 | 1 | ADP48850 | Mouse Myo1c target |
| C 424 | 13.8 | 1.2 | 19 | 1 | ADP48849 | Mouse beta actin P |
| C 425 | 13.4 | 1.2 | 15 | 1 | ABK15072 | Human |
| C 426 | 13.4 | 1.2 | 15 | 1 | ADJ82300 | KLMSY-encoding nuc |
| C 427 | 13.4 | 1.2 | 15 | 1 | ADJ82292 | KLMSY-encoding nuc |
| C 428 | 13.4 | 1.2 | 15 | 1 | ADJ82304 | KLMSY-encoding nuc |
| C 429 | 13.4 | 1.2 | 15 | 1 | ADG13597 | Human HER1-4 hamme |
| C 430 | 13.4 | 1.2 | 16 | 1 | AAH77878 | PCR primer used to |
| C 431 | 13.4 | 1.2 | 16 | 1 | ADO49843 | H. pylori strain J |
| C 432 | 13.4 | 1.2 | 16 | 1 | ADO50267 | H. pylori strain J |
| C 433 | 13.4 | 1.2 | 17 | 1 | AAF04357 | Hammerhead ribozym |
| C 434 | 13.4 | 1.2 | 17 | 1 | AAF04805 | Hammerhead ribozym |
| C 435 | 13.4 | 1.2 | 17 | 1 | AAF04219 | Hammerhead ribozym |
| C 436 | 13.4 | 1.2 | 17 | 1 | AAF04667 | Hammerhead ribozym |
| C 437 | 13.4 | 1.2 | 17 | 1 | AAF02422 | Hammerhead ribozym |
| C 438 | 13.4 | 1.2 | 17 | 1 | ABK00818 | Human NOGO inozyme |
| C 439 | 13.4 | 1.2 | 17 | 1 | ABK02566 | Human NOGO inozyme |
| C 440 | 13.4 | 1.2 | 17 | 1 | ABK00819 | Human GDMLP-1 17-m |
| C 441 | 13.4 | 1.2 | 17 | 1 | ABN06296 | Human GDMLP-1 17-m |
| C 442 | 13.4 | 1.2 | 17 | 1 | ABN06295 | Human GDMLP-1 17-m |
| C 443 | 13.4 | 1.2 | 17 | 1 | ABN06297 | Human GDMLP-1 17-m |
| C 444 | 13.4 | 1.2 | 17 | 1 | ABN02575 | Human GDMLP-1 17-m |
| C 445 | 13.4 | 1.2 | 17 | 1 | ABV82999 | Human HTPL scannin |
| C 446 | 13.4 | 1.2 | 17 | 1 | ABV82998 | Human HTPL scannin |
| C 447 | 13.4 | 1.2 | 17 | 1 | ABK18400 | Human ERG hammerhe |
| C 448 | 13.4 | 1.2 | 17 | 1 | ABT39733 | Tumour suppression |
| C 449 | 13.4 | 1.2 | 17 | 1 | ABT35826 | Tumour suppression |
| C 450 | 13.4 | 1.2 | 17 | 1 | ADA99778 | Human MDZ3 scannin |
| C 451 | 13.4 | 1.2 | 17 | 1 | ADA99779 | Human MDZ3 scannin |
| C 452 | 13.4 | 1.2 | 17 | 1 | ACD52118 | HBV inozyme substr |
| C 453 | 13.4 | 1.2 | 17 | 1 | ACD53199 | HBV G-cleaver subs |
| C 454 | 13.4 | 1.2 | 17 | 1 | ACC68460 | Murine oligonucleo |
| C 455 | 13.4 | 1.2 | 17 | 1 | ACC64249 | Murine oligonucleo |
| C 456 | 13.4 | 1.2 | 17 | 1 | ADB42997 | Tumour suppression |
| C 457 | 13.4 | 1.2 | 17 | 1 | ADC38464 | Human AMLP1b scann |
| C 458 | 13.4 | 1.2 | 17 | 1 | ADC38465 | Human AMLP1b scann |
| C 459 | 13.4 | 1.2 | 17 | 1 | ADC38463 | Human AMLP1b scann |
| C 460 | 13.4 | 1.2 | 17 | 1 | ADB45002 | Tumour suppression |
| C 461 | 13.4 | 1.2 | 17 | 1 | ADI51662 | Human tumour suppr |
| C 462 | 13.4 | 1.2 | 17 | 1 | ADI49509 | Human tumour suppr |
| C 463 | 13.4 | 1.2 | 17 | 1 | ACC54318 | Human tumour suppr |
| C 464 | 13.4 | 1.2 | 17 | 1 | ADL82512 | Human ER+ breast c |
| C 465 | 13.4 | 1.2 | 17 | 1 | ADM59349 | Hepatitis B virus |
| C 466 | 13.4 | 1.2 | 17 | 1 | ACN69387 | Hepatitis B virus |
| C 467 | 13.4 | 1.2 | 17 | 1 | ADM58815 | Human GDMLP-1 prob |
| C 468 | 13.4 | 1.2 | 17 | 1 | ACN69387 | Human GDMLP-1 prob |
| C 469 | 13.4 | 1.2 | 17 | 1 | ACN69386 | Human GDMLP-1 prob |
| C 470 | 13.4 | 1.2 | 17 | 1 | ACN69385 | Human GDMLP-1 prob |
| C 471 | 13.4 | 1.2 | 17 | 1 | ACN65665 | Human GDMLP-1 prob |

| | | | | | | |
|-------|------|-----|----|---|-----------|---------------------|
| 472 | 13.4 | 1.2 | 18 | 1 | AAZ90709 | Forward primer for |
| 473 | 13.4 | 1.2 | 18 | 1 | AAZ71388 | Human biallelic ma |
| C 474 | 13.4 | 1.2 | 18 | 1 | AAZ71139 | Human biallelic ma |
| C 475 | 13.4 | 1.2 | 18 | 1 | AAZ98939 | Human long QT synd |
| C 476 | 13.4 | 1.2 | 18 | 1 | AAA66260 | Dog genomic marker |
| C 477 | 13.4 | 1.2 | 18 | 1 | AAAC89949 | Human KVLQTI exon |
| C 478 | 13.4 | 1.2 | 18 | 1 | AAAS05095 | Neurofibromatosis |
| C 479 | 13.4 | 1.2 | 18 | 1 | AAAS05039 | Neurofibromatosis |
| C 480 | 13.4 | 1.2 | 18 | 1 | ABV72174 | PCR primer used to |
| C 481 | 13.4 | 1.2 | 18 | 1 | ABV76827 | PCR primer used to |
| C 482 | 13.4 | 1.2 | 18 | 1 | ADK13869 | Human cyclin-depen |
| C 483 | 13.4 | 1.2 | 18 | 1 | ADN35810 | Human NSCLC gene a |
| C 484 | 13.4 | 1.2 | 18 | 1 | ADO56517 | Human cyclin-depen |
| C 485 | 13.4 | 1.2 | 18 | 1 | ADRO5071 | PCR primer 2 used |
| C 486 | 13.4 | 1.2 | 18 | 1 | ADS90284 | Oligonucleotide of |
| C 487 | 13.4 | 1.2 | 19 | 1 | AAV23538 | Mouse beta defensin |
| C 488 | 13.4 | 1.2 | 19 | 1 | AAZ01215 | PCR primer for PGL |
| C 489 | 13.4 | 1.2 | 19 | 1 | AAA86085 | Cdc 25 hs ribozyme |
| C 490 | 13.4 | 1.2 | 19 | 1 | AAZ70031 | Human biallelic ma |
| C 491 | 13.4 | 1.2 | 19 | 1 | AAZ76970 | Human biallelic ma |
| C 492 | 13.4 | 1.2 | 19 | 1 | ABA95463 | Thermus thermophil |
| C 493 | 13.4 | 1.2 | 19 | 1 | AAH61247 | Cdc25 hs ribozyme |
| C 494 | 13.4 | 1.2 | 19 | 1 | ABL43540 | Human chromosome 1 |
| C 495 | 13.4 | 1.2 | 19 | 1 | ADF85077 | Human ERG2-targete |
| C 496 | 13.4 | 1.2 | 19 | 1 | ADF85253 | Human ERG2-targete |
| C 497 | 13.4 | 1.2 | 19 | 1 | ADN75949 | Human ERG2-targete |
| C 498 | 13.4 | 1.2 | 19 | 1 | ADN75950 | TCPTP2 siRNA #1. |
| C 499 | 13.4 | 1.2 | 19 | 1 | ADO18480 | TCPTP2 siRNA #2. |
| C 500 | 13.4 | 1.2 | 19 | 1 | ADO18573 | Analytical probe c |
| C 501 | 13.4 | 1.2 | 19 | 1 | ADR79444 | Analytical probe c |
| C 502 | 13.4 | 1.2 | 19 | 1 | ADR77809 | Human apolipoprote |
| C 503 | 13.2 | 1.2 | 18 | 1 | AAQ91053 | Human apolipoprote |
| C 504 | 13.2 | 1.2 | 18 | 1 | AAV48417 | HHV-6 associated M |
| C 505 | 13.2 | 1.2 | 18 | 1 | AAZ76549 | Collagen gene prom |
| C 506 | 13.2 | 1.2 | 18 | 1 | AAZ22179 | Transforming growt |
| C 507 | 13.2 | 1.2 | 18 | 1 | AAZ22147 | Human WISP-2 PCR p |
| C 508 | 13.2 | 1.2 | 18 | 1 | AAZ22147 | Human c-IAP-1 mRNA |
| C 509 | 13.2 | 1.2 | 18 | 1 | AAZ01825 | Murine tRNA gene f |
| C 510 | 13.2 | 1.2 | 18 | 1 | AAZ01825 | Mouse tRNA-Ala(g) |
| C 511 | 13.2 | 1.2 | 18 | 1 | AAZ01825 | Murine Ala tRNA 3' |
| C 512 | 13.2 | 1.2 | 18 | 1 | AAZ01825 | Human genomic SNP |
| C 513 | 13.2 | 1.2 | 18 | 1 | AAZ98709 | Collagen promoter |
| C 514 | 13.2 | 1.2 | 18 | 1 | AAZ97374 | CMV GlyB detection |
| C 515 | 13.2 | 1.2 | 18 | 1 | AAZ08213 | Murine tRNA oligon |
| C 516 | 13.2 | 1.2 | 18 | 1 | AAZ71352 | Human biallelic ma |
| C 517 | 13.2 | 1.2 | 18 | 1 | AAZ75603 | Human biallelic ma |
| C 518 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | TM7XN1 cDNA antise |
| C 519 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | PCR primer used to |
| C 520 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Reverse primer #96 |
| C 521 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Human mGluR1beta G |
| C 522 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Human HCN1 DNA amp |
| C 523 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Human glial cell d |
| C 524 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Haematopoietic cel |
| C 525 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Haematopoietic cel |
| C 526 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | DNA fragment B amp |
| C 527 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | PGC-1 mutational a |
| C 528 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | TCV RdRP mutagenic |
| C 529 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Xenopus axis dupli |
| C 530 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Mammalian inverted |
| C 531 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Human PCR primer S |
| C 532 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Human ciAP-1 DNA a |
| C 533 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Human MD-1 RP105-a |
| C 534 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | CENPC1 extend prim |
| C 535 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Nitrile hydratase |
| C 536 | 13.2 | 1.2 | 18 | 1 | AAZ75986 | Nitrile hydratase |
| C 537 | 12 | 1.1 | 17 | 1 | AAZ75986 | MGB-probe to deter |
| C 537 | 12 | 1.1 | 17 | 1 | AAZ75986 | Murine oligonucleo |

ALIGNMENTS

RESULT 1
ACA56897

| | | |
|---|---|------------------------|
| ID | ACA56897 | standard; cDNA; 60 BP. |
| XX | | |
| AC | ACA56897; | |
| XX | | |
| DT | 10-JUN-2003 | (first entry) |
| XX | | |
| DE | Human cDNA encoding an adipocyte bait protein, OBRGP_v2. | |
| XX | | |
| KW | Human; ss; gene; bait; adipocyte; SID; selected interacting domain; | |
| KW | anorectic; antidiabetic; protein-protein interaction; diabetes; | |
| KW | yeast 2-hybrid assay; metabolic disorder; obesity. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | W0200286122-A2. | |
| XX | | |
| PD | 31-OCT-2002. | |
| XX | | |
| PF | 14-MAR-2002; 2002WO-EP003768. | |
| XX | | |
| PR | 14-MAR-2001; 2001US-0275734P. | |
| XX | | |
| PA | (HYBR-) HYBRIGENICS. | |
| XX | | |
| PI | Legrain P, Daviet L; | |
| XX | | |
| DR | WPI; 2003-103412/09. | |
| DR | P-PSDB; ABU70363. | |
| XX | | |
| PT | New complex between two interacting proteins in adipocyte cells, useful | |
| PT | for identifying selected interacting domains that modulate protein | |
| PT | interactions, or for preventing or treating metabolic disorders such as | |
| PT | obesity or diabetes. | |
| XX | | |
| PS | Claim 1; Page 41; 382pp; English. | |
| XX | | |
| CC | The invention relates to a complex between two interacting proteins in | |
| CC | adipocyte cells, given in the specification. The proteins are identified | |
| CC | by selecting a bait protein from a known adipocyte marker and then | |
| CC | performing a yeast 2-hybrid selection to isolate prey proteins encoded by | |
| CC | members of an adipocyte cDNA library. The proteins are designated SID | |
| CC | (RTM) (selected interacting domains) proteins. Also included are a | |
| CC | polynucleotide encoding a polypeptide in the adipocyte cells, a | |
| CC | recombinant host cell expressing at least one of the interacting | |
| CC | polypeptides of the complex, selecting a modulating compound in adipocyte | |
| CC | cells, a SID (RTM) polypeptide comprising any of the 738 amino acid | |
| CC | sequences given in the specification (including its fragment or variant), | |
| CC | a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences | |
| CC | given in the specification (including its fragment or variant), a vector | |
| CC | comprising the SID (RTM) polynucleotide, a recombinant host cell | |
| CC | comprising the vector, a protein chip comprising the polypeptides and a | |
| CC | record comprising all or part of the data, listed in the specification. | |
| CC | The complex, polypeptides, polynucleotides and compounds are useful for | |
| CC | preventing or treating metabolic disorders such as obesity or diabetes. | |
| CC | The polynucleotides are useful as probes or primers. The complex is | |
| CC | particularly useful for identifying selected interacting domains (SID | |
| CC | (RTM)) for screening drugs that modulate the protein interaction, thus | |
| CC | exhibiting the therapeutic effect. The present sequence encodes a bait | |
| CC | protein used to generate the complexes of the invention | |
| XX | | |
| SQ | Sequence 60 BP; 18 A; 15 C; 15 G; 12 T; 0 U; 0 Other; | |
| Query Match 5.4%; Score 60; DB 1; Length 60; | | |
| Best Local Similarity 100.0%; Pred. No. 1.5e-06; | | |
| Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| QY | 221 ATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTGCGGAAC | TGGCA 280 |
| DB | 1 ATTGCCAAAGAGTCACCTATGACTCAGATGCAACCAAGTAGTGCTGTGCGGAAC | TGGCA 60 |
| RESULT 2 | | |
| AAH90177/c | | |

| | | |
|---|---|--|
| ID | AAH90177 | standard; cDNA; 51 BP. |
| XX | | |
| AC | AAH90177; | |
| XX | | |
| DT | 08-OCT-2001 | (first entry) |
| XX | | |
| DE | Human clone cg43922807 | SNP site, SEQ ID NO:57. |
| XX | | |
| KW | Human; single nucleotide polymorphism; SNP; chromosome 1; detection; | |
| KW | identification; gene therapy; genetic disorder; ss. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | variation | replace(26,T) |
| FT | | /*tag= a |
| FT | | /standard_name= "single nucleotide polymorphism" |
| XX | | |
| PN | W0200147942-A2. | |
| XX | | |
| PD | 05-JUL-2001. | |
| XX | | |
| PF | 27-DEC-2000; 2000WO-US035387. | |
| XX | | |
| PR | 27-DEC-1999; 99US-00472865. | |
| XX | | |
| PA | (CURA-) CURAGEN CORP. | |
| XX | | |
| PI | Shimkets RA, Leach M; | |
| XX | | |
| DR | WPI; 2001-425617/45. | |
| XX | | |
| PT | New polynucleotides containing single nucleotide polymorphisms, for | |
| PT | detecting the presence of polymorphism, detecting a polymorphic site, and | |
| PT | treating a patient suffering from a pathology ascribed to the | |
| PT | polymorphism. | |
| XX | | |
| PS | Claim 1; Page 69; 295pp; English. | |
| XX | | |
| CC | Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which | |
| CC | contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568 | |
| CC | (AAH90121-AAH90688) are consecutive pairs of nucleotides which contain | |
| CC | silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive | |
| CC | pairs of nucleotides containing SNPs which result in changes in the | |
| CC | corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in | |
| CC | sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino acid | |
| CC | changes, while those in sequences 575 to 578 (AAH90695-AAH90698) result | |
| CC | in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699- | |
| CC | AAH90700) generates a frameshift mutation. The invention also relates to | |
| CC | a method of detecting a polymorphic site in a nucleic acid and a method | |
| CC | of determining the relatedness of two nucleic acids. It also encompasses | |
| CC | peptides containing polymorphic sites, antibodies raised against such | |
| CC | peptides, and a method of detecting polymorphic proteins/ peptides using | |
| CC | the antibodies. The nucleic acids are useful for gene therapy of an | |
| CC | individual having, suspected of having, or at risk of developing a | |
| CC | pathological condition due to the presence of a sequence polymorphism. | |
| CC | Such treatment would comprise administration of the wild-type nucleic | |
| CC | acid sequence. Antibodies raised against polymorphic peptides can also be | |
| CC | used in the treatment of such individuals | |
| XX | | |
| SQ | Sequence 51 BP; 13 A; 17 C; 13 G; 8 T; 0 U; 0 Other; | |
| Query Match 4.6%; Score 51; DB 1; Length 51; | | |
| Best Local Similarity 100.0%; Pred. No. 6.1e-05; | | |
| Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| QY | 820 AGGCTCTCATGACCCAGGAGCCGGGGTGGATCCCTCTTTGTGTGTAG | 870 |
| DB | .51 AGGCTCTCATGACCCAGGAGCCGGGGTGGATCCCTCTTTGTGTGTAG | 1 |
| RESULT 3 | | |
| AAH90178/c | | |

ID XX AAH90178 standard; cDNA; 51 BP.
AC XX AAH90178;
XX 08-OCT-2001 (first entry)
XX Human clone cg43922807 SNP site, SEQ ID NO:58.
DE XX Human; single nucleotide polymorphism; SNP; chromosome 1; detection;
KW KW identification; gene therapy; genetic disorder; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT variation replace(26,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX WO200147942-A2.
PN XX
XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-US035387.
XX PR 27-DEC-1999; 99US-00472865.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX WPI; 2001-425617/45.
DR New polynucleotides containing single nucleotide polymorphisms, for
XX detecting the presence of polymorphism, detecting a polymorphic site, and
PT treating a patient suffering from a pathology ascribed to the
PT polymorphism.
XX Claim 1; Page 69; 295pp; English.
XX Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568
CC (AAH90121-AAH90688) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in
CC sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino acid
CC changes, while those in sequences 575 to 578 (AAH90695-AAH90698) result
CC in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699-
CC AAH90700) generates a frameshift mutation. The invention also relates to
CC a method of detecting a polymorphic site in a nucleic acid and a method
CC of determining the relatedness of two nucleic acids. It also encompasses
CC peptides containing polymorphic sites, antibodies raised against such
CC peptides, and a method of detecting polymorphic proteins/ peptides using
CC the antibodies. The nucleic acids are useful for gene therapy of an
CC individual having, suspected of having, or at risk of developing a
CC pathological condition due to the presence of a sequence polymorphism.
CC Such treatment would comprise administration of the wild-type nucleic
CC acid sequence. Antibodies raised against polymorphic peptides can also be
CC used in the treatment of such individuals
XX Sequence 51 BP; 13 A; 16 C; 13 G; 9 T; 0 U; 0 Other;
SQ Query Match 4.4%; Score 49.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.00012;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 820 AGGCCTCTCATGACCCAGGAGCCGGGGTGGATCCCTCTTTGTGTGTAG 870
|||||
Db 51 AGGCCTCTCATGACCCAGGAGCCAGGGTGGATCCCTCTTTGTGTGTAG 1
|||||
RESULT 4
ADR27689/c

ID XX ADR27689 standard; DNA; 22 BP.
AC XX ADR27689;
XX 04-NOV-2004 (first entry)
XX OB-RGRP antisense oligonucleotide, AS 11.
DE XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX Synthetic.
OS Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 18..22
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX FR2850971-A1.
XX 13-AUG-2004.
XX 10-FEB-2003; 2003FR-00001543.
XX 10-FEB-2003; 2003FR-00001543.
XX (AVET) AVENTIS PHARMA SA.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX Example 6; Fig 1; 104pp; French.
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (yfp) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.

Fri Aug 19 11:00:00 2005

Db 1 TTCATCCTGAGTTTCCACGCCGTCT 25

RESULT 7
AAV17684/c
ID AAV17684 standard; DNA; 20 BP.
XX
AC AAV17684;
XX
DT 10-JUL-1998 (first entry)
XX
DE PCR primer P1 used to amplify a leptin receptor gene-related protein.
XX
KW Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703;
KW treatment; cancer; connective tissue disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9805792-A2.
XX
PD 12-FEB-1998.
XX
PF 25-JUL-1997; 97WO-US014191.
XX
PR 01-AUG-1996; 96US-00691071.
PR 15-APR-1997; 97US-00843370.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Akerblom IE;
XX
WPI; 1998-145624/13.
XX
PD 12-FEB-1998.
XX
PF 25-JUL-1997; 97WO-US014191.
XX
PR 01-AUG-1996; 96US-00691071.
PR 15-APR-1997; 97US-00843370.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Akerblom IE;
XX
WPI; 1998-145624/13.
XX
PT DNA encoding human leptin receptor gene-related protein - useful for,
PT e.g. screening for drugs used in treatment of metabolic, reproductive,
PT developmental and connective tissue disorders or cancer.
XX
PS Disclosure; Page 36; 60pp; English.
XX
CC PCR primers AAV17684-87 are used in a reverse transcriptase PCR (RT-PCR)
CC reaction to amplify DNA encoding human leptin receptor gene-related
CC protein (LRGRP). The cDNA sequence was first isolated in Incyte clone
CC 492703 from the hNT2 cell line cDNA library through a computer generated
CC search for amino acid sequence alignments. The LRGRP protein has some
CC homology to the membrane associated proteins of Caenorhabditis elegans
CC ORF C30B.2 and Saccharomyces cerevisiae ORF YJR044c. The agonists of LRGRP
CC can be used to treat metabolic, reproductive and developmental disorders,
CC whilst antagonists of LRGRP can be used for treatment of cancer or
CC connective tissue disorders e.g. rheumatoid arthritis and Sjogren's
CC syndrome. Polynucleotides which hybridise to the LRGRP nucleotide
CC sequence can be used for detection
XX
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 354 AATGGGGAGCCTGCGGCCTT 373
Db 20 AATGGGGAGCCTGCGGCCTT 1

RESULT 8
AAV17685
ID AAV17685 standard; DNA; 20 BP.
XX
AC AAV17685;
XX
DT 10-JUL-1998 (first entry)
XX
DE PCR primer P2 used to amplify a leptin receptor gene-related protein.

XX Human; leptin receptor gene-related protein; LRGRP; Incyte clone 492703;
KW treatment; cancer; connective tissue disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9805792-A2.
XX
PD 12-FEB-1998.
XX
PF 25-JUL-1997; 97WO-US014191.
XX
PR 01-AUG-1996; 96US-00691071.
PR 15-APR-1997; 97US-00843370.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Akerblom IE;
XX
WPI; 1998-145624/13.
XX
PD DNA encoding human leptin receptor gene-related protein - useful for,
PT e.g. screening for drugs used in treatment of metabolic, reproductive,
PT developmental and connective tissue disorders or cancer.
XX
PS Disclosure; Page 36; 60pp; English.
XX
CC PCR primers AAV17684-87 are used in a reverse transcriptase PCR (RT-PCR)
CC reaction to amplify DNA encoding human leptin receptor gene-related
CC protein (LRGRP). The cDNA sequence was first isolated in Incyte clone
CC 492703 from the hNT2 cell line cDNA library through a computer generated
CC search for amino acid sequence alignments. The LRGRP protein has some
CC homology to the membrane associated proteins of Caenorhabditis elegans
CC ORF C30B.2 and Saccharomyces cerevisiae ORF YJR044c. The agonists of LRGRP
CC can be used to treat metabolic, reproductive and developmental disorders,
CC whilst antagonists of LRGRP can be used for treatment of cancer or
CC connective tissue disorders e.g. rheumatoid arthritis and Sjogren's
CC syndrome. Polynucleotides which hybridise to the LRGRP nucleotide
CC sequence can be used for detection
XX
SQ Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 AGCAGCCGCGGCCCCAGTTC 63
Db 1 AGCAGCCGCGGCCCCAGTTC 20

RESULT 9
AAK95054/c
ID AAK95054 standard; DNA; 20 BP.
XX
AC AAK95054;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone-specific primer, SEQ ID NO: 4299.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.

Fri Aug 19 11:00:00 2005

PI Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
DR
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
PS
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 CGGGAAGTGGCATATTTCTT 288
Db 20 CGGGAAGTGGCATATTTCTT 1

RESULT 12
ADR27680/c
ID ADR27680 standard; DNA; 20 BP.
XX
AC ADR27680;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 02.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT
FT modified_base 16..20

FT /*tag= c
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT 20
FT modified_base
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3, triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
PI WPI; 2004-595751/58.
XX
DR New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
PS
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CCCAGTTCGGGAGACATGGC 75
Db 20 CCCAGTTCGGGAGACATGGC 1

RESULT 13
ADR27685/c
ID ADR27685 standard; DNA; 20 BP.
XX
XX ADR27685;
AC
XX
XX 04-NOV-2004 (first entry)
DT
XX
DE OB-RGRP antisense oligonucleotide, AS 07.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3, triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
DR
XX
PT New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 143 TGTGCCTTAGAGGATTATGG 162
Db 20 TGTGCCTTAGAGGATTATGG 1
RESULT 14
ADR27653/c
ID ADR27653 standard; DNA; 20 BP.
XX
AC ADR27653;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, SEQ ID 2.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW ss.
XX
OS Synthetic.
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
DR
XX
PT New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Claim 4; SEQ ID NO 2; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 ACATGTGCACATCGGCATT 540
|||||
Db 20 ACATGTGCACATCGGCATT 1

RESULT 15
ADR27682/c
ID ADR27682 standard; DNA; 20 BP.
XX
AC ADR27682;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 04.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX

Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
XX WPI; 2004-595751/58.
DR
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a

triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
(iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
protein (YFP) for detecting compounds that modify the interaction between
the leptin receptor and OB-RGRP proteins, which can be used to prevent or
treat leptin-related disorders. ON, also related interfering RNA, are
used for prevention and/or treatment of leptin-related disorders, e.g.
osteoporosis (or other conditions involving reduced bone density);
calcification; obesity; diabetes; anorexia; disorders of sexual maturity;
haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
and inflammation, fetal development and cancer. The present OB-RGRP
antisense oligonucleotide was used to illustrate the invention.

XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 ATGCGGGCGGTTAAAGCTCT 90
|||||
Db 20 ATGCGGGCGGTTAAAGCTCT 1

RESULT 16
ADR27688/c
ID ADR27688 standard; DNA; 20 BP.
XX
AC ADR27688;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 10.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX

Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX

PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PI Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
DR
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
PS
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 262 TGCCTGTCGGGAAGTGGCAT 281
Db 20 TGCCTGTCGGGAAGTGGCAT 1
RESULT 17
ADR27681/c
ID ADR27681 standard; DNA; 20 BP.
XX
AC ADR27681;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 03.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a

FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
XX 13-AUG-2004.
PD
XX
XX 10-FEB-2003; 2003FR-00001543.
PF
XX 10-FEB-2003; 2003FR-00001543.
PR
XX (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
DR
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 63 CGGAGACATGGCGGCGGT 82
Db 20 CGGAGACATGGCGGCGGT 1
RESULT 18
ADR27687/c
ID ADR27687 standard; DNA; 20 BP.
XX
AC ADR27687;
XX
DT 04-NOV-2004 (first entry)
XX

Fri Aug 19 11:00:00 2005

DE OB-RGRP antisense oligonucleotide, AS 09.

XX Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

KW Leptin receptor related protein; OB-RGRP; leptin receptor;

KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;

KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;

KW thrombus formation; immunity; inflammation; fetal development; cancer;

KW antisense; ss.

XX Synthetic.

OS

XX

FH Key Location/Qualifiers

FT modified_base 1. .20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Optional thioester"

FT modified_base 1. .5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 16. .20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 20

FT /*tag= d

FT /mod_base= OTHER

FT /note= "3' triethyleneglycol spacer"

XX

PN FR2850971-A1.

XX

XX 13-AUG-2004.

XX

PF 10-FEB-2003; 2003FR-00001543.

XX

PR 10-FEB-2003; 2003FR-00001543.

XX

XX (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

PI Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

DR

XX

PT New oligonucleotides that inhibit expression of the leptin receptor

PT related protein, useful for treatment and prevention of e.g.

PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and

PT angiogenesis.

XX

PS Example 6; Fig 1; 104pp; French.

XX

CC The present invention relates to a leptin receptor related protein (OB-

CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CC specifically with and inhibits the expression of ADR27652. The ON

CC promotes expression of leptin receptors on the cell surface and may

CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a

CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA

CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit

CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their

CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of

CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that

CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent

CC protein (YFP) for detecting compounds that modify the interaction between

CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or

CC treat leptin-related disorders. ON, also related interfering RNA, are

CC used for prevention and/or treatment of leptin-related disorders, e.g.

CC osteoporosis (or other conditions involving reduced bone density);

CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,

CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity

CC and inflammation, fetal development and cancer. The present OB-RGRP

CC antisense oligonucleotide was used to illustrate the invention.

XX

SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GCGTTTACTGGCCCTTATT 180

Db 20 GCGTTTACTGGCCCTTATT 1

||||||||||||||||||||

RESULT 19

ADR27679/c

ID ADR27679 standard; DNA; 20 BP.

XX

AC ADR27679;

XX

DT 04-NOV-2004 (first entry)

XX

DE OB-RGRP antisense oligonucleotide, AS 01.

XX

KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;

KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;

KW leptin receptor related protein; OB-RGRP; leptin receptor;

KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;

KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;

KW thrombus formation; immunity; inflammation; fetal development; cancer;

KW antisense; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1. .20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Optional thioester"

FT modified_base 1. .5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 16. .20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2' O-methylation"

FT modified_base 20

FT /*tag= d

FT /mod_base= OTHER

FT /note= "3' triethyleneglycol spacer"

XX

PN FR2850971-A1.

XX

XX 13-AUG-2004.

XX

PF 10-FEB-2003; 2003FR-00001543.

XX

PR 10-FEB-2003; 2003FR-00001543.

XX

PA (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

PI Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

DR

XX

PT New oligonucleotides that inhibit expression of the leptin receptor

PT related protein, useful for treatment and prevention of e.g.

PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and

PT angiogenesis.

XX

PS Example 6; Fig 1; 104pp; French.

XX

CC The present invention relates to a leptin receptor related protein (OB-

CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises

CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.

XX
SQ Sequence 20 BP; 1 A; 9 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGGCCGTGGCAGGAAGC 39
Db 20 CCCGGCCGTGGCAGGAAGC 1

RESULT 20
ADR27692/c
ID ADR27692 standard; DNA; 20 BP.
XX
AC ADR27692;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 14.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.

Key Location/Qualifiers
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FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3, triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.

XX 10-FEB-2003; 2003FR-00001543.
PR (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
DR
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
XX
CC The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.

XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 ACATGTGCACATGCGGCATT 540
Db 20 ACATGTGCACATGCGGCATT 1

RESULT 21
ADR27683/c
ID ADR27683 standard; DNA; 20 BP.
XX
AC ADR27683;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 05.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW Leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER

Fri Aug 19 11:00:00 2005

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FT modified_base /note= "Optional thioester"
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FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
PN FR2850971-A1.
XX
XX 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and their
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis; thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 84 AAGCTCTCGTGGCATTATCC 103
XX ||||||||||||||||
DB 20 AAGCTCTCGTGGCATTATCC 1
XX
XX RESULT 22
XX ADR27686/c
XX ID ADR27686 standard; DNA; 20 BP.
XX
XX AC ADR27686;
```

```
XX
DT
XX
XX 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 08.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
XX
FH Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2' O-methylation"
FT 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3' triethyleneglycol spacer"
XX
XX FR2850971-A1.
XX
XX 13-AUG-2004.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX 10-FEB-2003; 2003FR-00001543.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX
XX New oligonucleotides that inhibit expression of the leptin receptor
XX related protein, useful for treatment and prevention of e.g.
XX osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
XX angiogenesis.
XX
XX Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
XX RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
XX specifically with and inhibits the expression of ADR27652. The ON
XX promotes expression of leptin receptors on the cell surface and may
XX contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
XX triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
XX (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and their
XX expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
XX coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
XX the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
XX is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
XX protein (YFP) for detecting compounds that modify the interaction between
XX the leptin receptor and OB-RGRP proteins, which can be used to prevent or
XX treat leptin-related disorders. ON, also related interfering RNA, are
XX used for prevention and/or treatment of leptin-related disorders, e.g.
XX osteoporosis (or other conditions involving reduced bone density);
XX calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
XX haematopoiesis, angiogenesis; thrombus formation, regulation of immunity
XX and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 84 AAGCTCTCGTGGCATTATCC 103
XX ||||||||||||||||
DB 20 AAGCTCTCGTGGCATTATCC 1
XX
XX RESULT 22
XX ADR27686/c
XX ID ADR27686 standard; DNA; 20 BP.
XX
XX AC ADR27686;
```



```
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 GAGGATTATGGCGTTTACTG 171
Db 20 GAGGATTATGGCGTTTACTG 1

RESULT 23
ADR27684/c
ID ADR27684 standard; DNA; 20 BP.
XX
AC ADR27684;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 06.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3, triethyleneglycol spacer"
XX
FN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.
XX
PR 10-FEB-2003; 2003FR-00001543.
XX
PA (AVET ) AVENTIS PHARMA SA.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Jockers R, Couturier C, Uhlmann E;
XX
DR WPI; 2004-595751/58.
XX
PT New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
```

```
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
CC antisense oligonucleotide was used to illustrate the invention.
XX
SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match      1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 CTTATGCTGGGATGTGCCTT 150
Db 20 CTTATGCTGGGATGTGCCTT 1

RESULT 24
ADR27691/c
ID ADR27691 standard; DNA; 20 BP.
XX
AC ADR27691;
XX
DT 04-NOV-2004 (first entry)
XX
DE OB-RGRP antisense oligonucleotide, AS 13.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW antisense; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optional thioester"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2, O-methylation"
FT modified_base 20
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3, triethyleneglycol spacer"
XX
FN FR2850971-A1.
```


PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-000001543.
XX
XX 10-FEB-2003; 2003FR-000001543.
PR
XX (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Jockers R, Couturier C, Uhlmann E;
PI
XX WPI; 2004-595751/58.
DR
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX
PS Example 6; Fig 1; 104pp; French.
XX
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present OB-RGRP
XX antisense oligonucleotide was used to illustrate the invention.
SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 CCTTGTGTTGGCAGGCAATG 389
Db 20 CCTTGTGTTGGCAGGCAATG 1

RESULT 25
ADT71351
ID ADT71351 standard; DNA; 20 BP.
XX
AC ADT71351;
XX
DT 16-DEC-2004 (first entry)
XX
DE Forward primer for amplifying OB-RGRP, seq id 14.
XX
KW Antidiabetic; anorectic; weight loss; weight gain; diabetes; LEPROTL1;
KW leptin receptor overlapping transcript-like 1; OB-RGRP;
KW leptin receptor gene related protein; intracellular transport; obesity;
KW PCR; primer; ss.
XX
XX Unidentified.
OS
XX FR2852397-A1.
PN
XX 17-SEP-2004.
PD
XX

PF 10-MAR-2003; 2003FR-00002931.
XX
PR 10-MAR-2003; 2003FR-00002931.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Bailleul B, Rouille Y, Seron K, Belouzard S;
XX
XX WPI; 2004-671009/66.
XX
XX Identifying compounds useful for treating loss or gain of weight or
PT diabetes, from their ability to modulate expression or transport of
PT proteins related to the leptin receptor.
XX
PS Example 3; SEQ ID NO 14; 38pp; French.
XX
XX The invention relates to a method for identifying compounds (I) that are
CC active against loss or gain of weight or diabetes in humans or animals.
CC The method comprises measuring the effect of a test compound on the
CC expression of at least one of the genes LEPROTL1 (leptin receptor
CC overlapping transcript-like 1) or OB-RGRP (leptin receptor gene related
CC protein). Alternatively the method comprises measuring the effect of the
CC compound on intracellular transport as far as the cell membrane (CM), the
CC presence at CM, and internalisation from the membrane of proteins (X)
CC encoded by the specified genes, or parts of them. Compounds of the
CC invention are used to treat or prevent obesity, weight loss and diabetes.
CC The current sequence represents a primer for the amplification of OB-
CC RGRP.
XX
SQ Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 1.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 AGCAGCGCGGCCCCCAGTTC 63
Db 1 AGCAGCGCGGCCCCCAGTTC 20

RESULT 26
ABK39905/c
ID ABK39905 standard; DNA; 25 BP.
XX
AC ABK39905;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human Parathyroid hormone 3' RT-PCR primer.
XX
KW Human; ss; PCR; embryonic stem cell; differentiation; primer;
KW transplantation; heart muscle damage; kidney tissue degeneration;
KW skin damage; liver degeneration; brain degeneration; spinal cord injury;
KW anaemia; immunodeficiency; adrenal degeneration;
KW biomedical engineering human development.
XX
OS Homo sapiens.
XX
PN WO200210347-A2.
XX
PD 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-IB001719.
PF
XX 01-AUG-2000; 2000US-0222160P.
PR
PR 09-FEB-2001; 2001US-0267559P.
XX
XX (YISS) YISSUM RES & DEV CO.
PA
XX Benvenisty N;
PI
XX WPI; 2002-180078/23.
DR
XX

PT Mapping a pathway of or directing differentiation of human embryonic
PT cells, comprises exposing cells to an exogenous factor and measuring gene
PT expression products characteristic of the particular cell type or
XX lineage.
PS Example 1; Fig 5; 52pp; English.
XX
CC The invention relates to mapping a pathway of differentiation of a
CC population of embryonic cells, comprising (a) selecting: (i) a set of
CC gene expression products, where each gene expression product in the set
CC is characteristic of a cell type that has undergone differentiation, so
CC that several differentiated cell types are represented in the set and
CC (ii) an exogenous factor from a library of exogenous factors, (b)
CC applying the exogenous factor to the population of embryonic cells, (c)
CC characterising the effect of the exogenous factor on the differentiation
CC pathway of the population of cells by determining gene expression
CC products in the set and (d) mapping the pathway of differentiation of the
CC cells. The method is useful for directing differentiation of embryonic
CC stem cells. The method is particularly useful for manipulating
CC differentiation of human embryonic stem cells to provide a uniform
CC population of precursors and differentiated cells of a desired lineage.
CC The differentiated cells may be used for treating a medical condition in
CC a human, e.g. as a source of cells for transplantation in numerous human
CC pathologies, (e.g. heart muscle damage, kidney tissue degeneration, skin
CC damage, liver degeneration, brain degeneration, spinal cord injury,
CC anaemia, immunodeficiency, and adrenal degeneration) or as a component in
CC biomedical engineering as well as providing clues on early stages of
CC human development. The present sequence is an RT-PCR (reverse
CC transcriptase PCR) primer used to amplify the one member of the set of
CC expression products from embryonic stem cells in the method of the
XX invention
SQ Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 794 CTTGGAGAGGCAGATAACGCTGA 816
Db 23 CTTGGAGAGGCAGACAAAGCTGA 1

RESULT 27
AAT64982
ID AAT64982 standard; DNA; 19 BP.
XX
AC AAT64982;
XX
DT 23-FEB-1998 (first entry)
XX
DE Human OB receptor 5' untranslated region PCR primer HOBR 1F-2.
XX
KW Ob receptor; obesity; leptin; rat; rodent; animal model; ligand; fatty;
KW fa mutation; therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9731015-A1.
XX
PD 28-AUG-1997.
XX
PF 18-FEB-1997; 97WO-US002397.
XX
PR 22-FEB-1996; 96US-0090405P.
PR 22-MAR-1996; 96US-0013969P.
PR 25-APR-1996; 96GB-00008473.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hess JW, Caskey CT, Liu Q, Phillips MS;
XX

DR WPI; 1997-435085/40.
XX
PT Rat wild-type and mutant ob receptor protein - useful in identification
PT of new ligands for prevention and treatment of obesity.
XX
PS Example 6; Page 13; 35pp; English.
XX
CC This oligonucleotide comprises forward PCR primer HOBR 1F-2, which is
CC based on the 5' untranslated region (5'UTR) of the human ob receptor (OB-
CC R) sequence. Primers HOBR 1F (AAT64981) and HOBR 1F-2 were paired with
CC rat OB-R specific reverse primers ROBR 11 (AAT64983) or ROBR 12
CC (AAT64984) to amplify the 5' end of rat OB-R cDNA. The largest product,
CC obtained with HOBR 1F-2 and ROBR11, was a 500 bp fragment that covered
CC the 5' region and included a Met codon. Full-length sequences for lean
CC rat OB-R cDNA (AAT64961) and fatty (fa) mutant rat OB-R cDNA (AAT64062),
CC which differ by only 1 bp, were subsequently obtained
XX
SQ Sequence 19 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 TCGTGGCATTATCCTTCAG 108
Db 1 TCGTGGCATTATCCTTCAG 19

RESULT 28
ACK10811
ID ACK10811 standard; DNA; 25 BP.
XX
AC ACK10811;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 110792.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 110792; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more

Fri Aug 19 11:00:00 2005

CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 179 TTCGTCCTCGATTTTCACGCCATCT 203
||| ||||| | ||||| |||||
Db 1 TTCATCCTGAGTATCCACGCGTCT 25

RESULT 29
ACI63081/c
ID ACI63081 standard; DNA; 25 BP.
XX
AC ACI63081;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 63072.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 63072; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring

CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 8 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 271 GGAACCTGGCATATTTCTTCACTA 293
||||| ||||| ||||| |||||
Db 24 GGAACCTGACATATCTTCTCATTA 2

RESULT 30
AAT64981
ID AAT64981 standard; DNA; 18 BP.
XX
AC AAT64981;
XX
DT 23-FEB-1998 (first entry)
XX
DE Human OB receptor 5' untranslated region PCR primer HOBR 1F.
XX
KW Ob receptor; obesity; leptin; rat; rodent; animal model; ligand; fatty;
KW fa mutation; therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9731015-A1.
XX
PD 28-AUG-1997.
XX
PF 18-FEB-1997; 97WO-US002397.
XX
PR 22-FEB-1996; 96US-0090405P.
PR 22-MAR-1996; 96US-0013969P.
PR 25-APR-1996; 96GB-00008473.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hess JW, Caskey CT, Liu Q, Phillips MS;
XX
DR WPI; 1997-435085/40.
XX
PT Rat wild-type and mutant ob receptor protein - useful in identification
PT of new ligands for prevention and treatment of obesity.
XX
PS Example 6; Page 13; 35pp; English.
XX
CC This oligonucleotide comprises forward PCR primer HOBR 1F, which is based
CC on the 5' untranslated region (5'UTR) of the human ob receptor (OB-R)
CC sequence. Primers HOBR 1F and HOBR 1F-2 (AAT64982) were paired with rat
CC OB-R specific reverse primers ROBR 11 (AAT64983) or ROBR 12 (AAT64984) to
CC amplify the 5' end of rat OB-R cDNA. Full- length sequences for lean rat
CC OB-R cDNA (AAT64961) and fatty (fa) mutant rat OB-R cDNA (AAT64062),
XX which differ by only 1 bp, were subsequently obtained
SQ Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 CTTATGCTGGGATGTGCC 148
Db 1 CTTATGCTGGGATGTGCC 18

RESULT 31
AAT85600/c
ID AAT85600 standard; DNA; 18 BP.
XX
AC AAT85600;
XX
DT 17-MAR-1998 (first entry)
XX
DE Sense oligonucleotide -47 for human WSX receptor cDNA.
XX
KW Human; WSX receptor; identification; purification; ligand; activator;
KW antibody; agonist; proliferation; obesity; differentiation; anaemia;
KW treatment; neoplasia; arteriosclerosis; Type II diabetes;
KW polycystic ovarian disease; cardiovascular disease; osteoarthritis;
KW dermatological disorder; hypertension; insulin resistance;
KW hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis;
KW sense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
PF 07-JAN-1997; 97WO-US0000325.
XX
PR 08-JAN-1996; 96US-00585005.
PR 20-JUN-1996; 96US-00667197.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX
DR WPI; 1997-372864/34.
XX
PT WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving haematopoiesis or
PT for treating tumours.
XX
PS Example 8; Fig 7; 219pp; English.
XX
CC The present sequence is the sense oligonucleotide -47 for the human WSX
CC receptor cDNA. The receptor can be used to identify and purify ligands
CC and activators. An anti-WSX receptor antibody can be used as an agonist
CC to activate the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also be
CC used to decrease body weight and/or fat-depot weight and/or food intake
CC in an obese mammal. WSX receptor ligands can be used to enhance
CC proliferation or differentiation of lymphoid, myeloid or erythroid blood
CC cell lineages. This is useful when a mammal, especially a human, is
CC suffering from decreased blood cell levels, i.e. anaemia, caused by
CC chemotherapy, radiation therapy or bone marrow transplantation therapy.
CC It can also be used to repopulate blood cells in a mammal. The products
CC can also be used to treat, e.g. neoplastic disorders, arteriosclerosis,
CC Type II diabetes, polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and
CC cholelithiasis
XX
SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTGCCTTAGA 153
Db 18 GCTGGGATGTGCCTTAGA 1

RESULT 32
AAT85601
ID AAT85601 standard; DNA; 18 BP.
XX
AC AAT85601;
XX
DT 17-MAR-1998 (first entry)
XX
DE Antisense oligonucleotide -47 for human WSX receptor cDNA.
XX
KW Human; WSX receptor; identification; purification; ligand; activator;
KW antibody; agonist; proliferation; obesity; differentiation; anaemia;
KW treatment; neoplasia; arteriosclerosis; Type II diabetes;
KW polycystic ovarian disease; cardiovascular disease; osteoarthritis;
KW dermatological disorder; hypertension; insulin resistance;
KW hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis;
KW antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
PF 07-JAN-1997; 97WO-US0000325.
XX
PR 08-JAN-1996; 96US-00585005.
PR 20-JUN-1996; 96US-00667197.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX
DR WPI; 1997-372864/34.
XX
PT WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving haematopoiesis or
PT for treating tumours.
XX
PS Example 8; Fig 7; 219pp; English.
XX
CC The present sequence is the antisense oligonucleotide +85 for the human
CC WSX receptor cDNA. The receptor can be used to identify and purify
CC ligands and activators. An anti-WSX receptor antibody can be used as an
CC agonist to activate the WSX receptor, leading to enhanced proliferation
CC or differentiation of a cell expressing the WSX receptor. It can also be
CC used to decrease body weight and/or fat-depot weight and/or food intake
CC in an obese mammal. WSX receptor ligands can be used to enhance
CC proliferation or differentiation of lymphoid, myeloid or erythroid blood
CC cell lineages. This is useful when a mammal, especially a human, is
CC suffering from decreased blood cell levels, i.e. anaemia, caused by
CC chemotherapy, radiation therapy or bone marrow transplantation therapy.
CC It can also be used to repopulate blood cells in a mammal. The products
CC can also be used to treat, e.g. neoplastic disorders, arteriosclerosis,
CC Type II diabetes, polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and
CC cholelithiasis
XX
SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC immune (autoimmune) thrombocytopenic purpura (ITP) and HIV induced ITP),
CC myeloproliferative thrombocytotic diseases, thrombocytosis from
CC inflammatory conditions and in iron deficiency, obesity or diabetes, for
CC enhancing repopulation of mature blood cell lineages in cells having
CC undergone chemo- or radiation therapy or bone marrow transplantation
CC therapy, or for promoting kidney, liver and lung growth and/or repair.
CC The WSX receptor is useful for producing anti-WSX receptor antibodies,
CC for affinity purification of WSX ligand, for competitive screening of
CC potential agonists or antagonists for binding to the WSX receptor, as
CC molecular weight markers, as reagents for mechanism studies of the WSX
CC receptor or its ligands, to study the role of the WSX receptor and WSX
CC ligand in normal growth and development, as well as abnormal growth and
CC development, e.g., in malignancies, or as standards or controls in assays
CC for WSX receptor. A composition comprising the WSX polypeptide is useful
CC as an antagonist for reducing activation of endogenous WSX receptor, and
CC to treat metabolic disorders (e.g. anorexia or steroid-induced
CC truncalobesity), stem cell tumours and other tumours which express WSX
CC receptor. The present sequence represents a human WSX receptor probe used
CC in an antisense inhibition assay
XX
SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18

RESULT 35
ACH66797
ID ACH66797 standard; DNA; 18 BP.
XX
AC ACH66797;

XX
DT 06-NOV-2003 (first entry)
XX
DE Human WSX receptor antisense oligonucleotide for position -47.
XX
KW Leptin receptor; WSX receptor; metabolic disorder; ITP; ss; antisense;
KW anorexia; steroid-induced truncalobesity; stem cell tumour; tumour; DIC;
KW anaemia; thrombocytopenia; hypoplasia; myelodysplasia; HIV-induced ITP;
KW disseminated intravascular coagulation; immune thrombocytopenic purpura;
KW myeloproliferative thrombocytotic disease; thrombocytosis;
KW inflammatory condition; iron deficiency; diabetes; renal failure;
KW haematopoietic cell proliferation; bone marrow transplantation.
XX
OS Homo sapiens.
XX
PN US6541604-B1.
XX
PD 01-APR-2003.
XX
PF 08-JAN-1997; 97US-00780562.
XX
PR 08-JAN-1996; 96US-0064855P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Matthews W;
XX
DR WPI; 2003-539731/51.
XX
PT New WSX receptor, useful for preparing a composition for treating
PT diseases mediated by WSX receptor e.g., diabetes or obesity.
XX
PS Example 8; Fig 7; 142pp; English.
XX

CC The invention relates to an isolated leptin/WSX receptor comprising a
CC sequence of mature human WSX receptor variant 12.1. Also disclosed are
CC the 13.2 and 6.4 WSX receptor variants (and DNA molecules encoding all 3
CC proteins), a partial mouse WSX receptor and its encoding DNA sequence.
PS Example 8; Fig 7; 142pp; English.
XX
CC The invention relates to an isolated leptin/WSX receptor comprising a
CC sequence of mature human WSX receptor variant 12.1. Also disclosed are
CC the 13.2 and 6.4 WSX receptor variants (and DNA molecules encoding all 3

CC proteins), a partial mouse WSX receptor and its encoding DNA sequence.
CC The WSX receptor is useful for preparing a composition for treating
CC diseases mediated by WSX receptor, especially diseases characterised by a
CC decrease in haematopoietic cells, e.g., anaemia, thrombocytopenia,
CC hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia,
CC immune (autoimmune) thrombocytopenic purpura (ITP), and HIV induced ITP.
CC The WSX receptor is also useful for treating metabolic disorders such as
CC anorexia, obesity (e.g. steroid-induced truncalobesity) tumours such as
CC stem cell tumours, inflammatory conditions, iron deficiency, diabetes,
CC renal failure, conditions related to haematopoietic cell proliferation
CC (such as in bone marrow transplantation and for promoting kidney, lung
CC and liver growth and/or repair. An experiment was performed to show
CC antisense inhibition of human and mouse WSX receptors. The present
CC sequence is an antisense oligonucleotide used in the experiment
XX
SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18

RESULT 36
ACH66796/C
ID ACH66796 standard; DNA; 18 BP.
XX
AC ACH66796;

XX
DT 06-NOV-2003 (first entry)
XX
DE Human WSX receptor sense oligonucleotide for position -47.
XX
KW Leptin receptor; WSX receptor; metabolic disorder; ITP; ss; anorexia;
KW steroid-induced truncalobesity; stem cell tumour; tumour; DIC; anaemia;
KW thrombocytopenia; hypoplasia; myelodysplasia; HIV-induced ITP;
KW disseminated intravascular coagulation; immune thrombocytopenic purpura;
KW myeloproliferative thrombocytotic disease; thrombocytosis;
KW inflammatory condition; iron deficiency; diabetes; renal failure;
KW haematopoietic cell proliferation; bone marrow transplantation.
XX
OS Homo sapiens.
XX
PN US6541604-B1.
XX
PD 01-APR-2003.
XX
PF 08-JAN-1997; 97US-00780562.
XX
PR 08-JAN-1996; 96US-0064855P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett B, Matthews W;
XX
DR WPI; 2003-539731/51.
XX
PT New WSX receptor, useful for preparing a composition for treating
PT diseases mediated by WSX receptor e.g., diabetes or obesity.
XX
PS Example 8; Fig 7; 142pp; English.
XX

CC The invention relates to an isolated leptin/WSX receptor comprising a
CC sequence of mature human WSX receptor variant 12.1. Also disclosed are
CC the 13.2 and 6.4 WSX receptor variants (and DNA molecules encoding all 3
CC proteins), a partial mouse WSX receptor and its encoding DNA sequence.
CC The WSX receptor is useful for preparing a composition for treating
CC diseases mediated by WSX receptor, especially diseases characterised by a
CC decrease in haematopoietic cells, e.g., anaemia, thrombocytopenia,
CC hypoplasia, disseminated intravascular coagulation (DIC), myelodysplasia,

CC immune (autoimmune) thrombocytopenic purpura (ITP), and HIV induced ITP.
CC The WSX receptor is also useful for treating metabolic disorders such as
CC anorexia, obesity (e.g. steroid-induced truncalobesity) tumours such as
CC stem cell tumours, inflammatory conditions, iron deficiency, diabetes,
CC renal failure, conditions related to haematopoietic cell proliferation
CC (such as in bone marrow transplantation and for promoting kidney, lung
CC and liver growth and/or repair. An experiment was performed to show
CC antisense inhibition of human and mouse WSX receptors. The present
CC sequence is a sense (control) oligonucleotide used in the experiment
XX
SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 18 GCTGGGATGTCCTTAGA 1

RESULT 37
ADC08932
ID ADC08932 standard; DNA; 18 BP.

XX
AC ADC08932;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human WSX receptor DNA antisense oligonucleotide #8.

XX Human; WSX receptor; ss; weight reduction; obesity; bulimia;
KW metabolic disorder; diabetes; insulin level reduction; food consumption;
KW type II adult onset diabetes; infertility; hypercholesterolaemia;
KW hyperlipidaemia; cardiovascular disease; arteriosclerosis;
KW polycystic ovarian disease; osteoarthritis; dermatological disorder;
KW insulin resistance; hypertriglyceridaemia; cancer; cholelithiasis;
KW hypertension; kidney ailment; lung dysfunction; emphysema; haemorrhage;
KW anaemia; thrombocytopenia; hypoplasia; cachexia; anorexia; appetite loss;
KW tumour; antisense.

XX Homo sapiens.
XX US2002193571-A1.
XX
PD 19-DEC-2002.
XX
PF 07-JAN-1997; 97US-00779457.
XX
PR 08-JAN-1996; 96US-00585005.
PR 20-JUN-1996; 96US-00667197.

XX (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.

XX Carter PJ, Chiang NY, Kim KJ, Matthews W, Rodrigues ML;
PI
XX WPI; 2003-657237/62.

XX Novel agonist antibody useful for activating WSX receptor and for
PT enhancing proliferation or differentiation of a cell comprising WSX
PT receptor, which specifically binds to the WSX receptor.

XX Example 8; SEQ ID NO 31; 140pp; English.

XX The invention relates to agonist antibodies which specifically bind to
CC the human WSX receptor. The agonist antibodies are useful for activating
CC the WSX receptor and for enhancing proliferation or differentiation of a
CC cell comprising the WSX receptor, by exposing the cell to an antibody.
CC The antibodies are also useful for reducing weight, specifically in the

CC treatment of obesity, bulimia and other disorders associated with
CC abnormal expression or functions of WSX receptor genes, for treating
CC metabolic disorders such as diabetes, for reducing excessive levels of
CC insulin in human patients and for treating patients suffering from food
CC consumption and related pathological conditions such as type II adult
CC onset diabetes, infertility, hypercholesterolaemia, hyperlipidaemia,
CC cardiovascular diseases, arteriosclerosis, polycystic ovarian disease,
CC osteoarthritis, dermatological disorders, insulin resistance, The
CC hypertriglyceridaemia, cancer, cholelithiasis and hypertension. The
CC antibodies are also useful for treating kidney ailments, lung
CC dysfunctions such as emphysema, haemorrhages, diseases characterised by
CC decrease in blood cells such as anaemia, thrombocytopenia, hypoplasia,
CC metabolic disorders such as cachexia, anorexia and loss of appetite, and
CC other tumour related disorders. This sequence represents a human WSX
CC receptor DNA antisense oligonucleotide.

XX
SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 1 GCTGGGATGTCCTTAGA 18

RESULT 38
ADC08931/c
ID ADC08931 standard; DNA; 18 BP.

XX
AC ADC08931;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human WSX receptor DNA antisense oligonucleotide #7.

XX Human; WSX receptor; ss; weight reduction; obesity; bulimia;
KW metabolic disorder; diabetes; insulin level reduction; food consumption;
KW type II adult onset diabetes; infertility; hypercholesterolaemia;
KW hyperlipidaemia; cardiovascular disease; arteriosclerosis;
KW polycystic ovarian disease; osteoarthritis; dermatological disorder;
KW insulin resistance; hypertriglyceridaemia; cancer; cholelithiasis;
KW hypertension; kidney ailment; lung dysfunction; emphysema; haemorrhage;
KW anaemia; thrombocytopenia; hypoplasia; cachexia; anorexia; appetite loss;
KW tumour; antisense.

XX Homo sapiens.
XX
PN US2002193571-A1.
XX
PD 19-DEC-2002.

XX 07-JAN-1997; 97US-00779457.
XX
PR 08-JAN-1996; 96US-00585005.
PR 20-JUN-1996; 96US-00667197.

XX (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.

XX Carter PJ, Chiang NY, Kim KJ, Matthews W, Rodrigues ML;
PI
XX WPI; 2003-657237/62.

XX Novel agonist antibody useful for activating WSX receptor and for
PT enhancing proliferation or differentiation of a cell comprising WSX
PT receptor, which specifically binds to the WSX receptor.

XX Example 8; SEQ ID NO 30; 140pp; English.

XX The invention relates to agonist antibodies which specifically bind to
CC the human WSX receptor. The agonist antibodies are useful for activating
CC the WSX receptor and for enhancing proliferation or differentiation of a
CC cell comprising the WSX receptor, by exposing the cell to an antibody.
CC The antibodies are also useful for reducing weight, specifically in the
CC treatment of obesity, bulimia and other disorders associated with
CC abnormal expression or functions of WSX receptor genes, for treating
CC metabolic disorders such as diabetes, for reducing excessive levels of
CC insulin in human patients and for treating patients suffering from food
CC consumption and related pathological conditions such as type II adult
CC onset diabetes, infertility, hypercholesterolaemia, hyperlipidaemia,
CC cardiovascular diseases, arteriosclerosis, polycystic ovarian disease,
CC osteoarthritis, dermatological disorders, insulin resistance,
CC hypertriglyceridaemia, cancer, cholelithiasis and hypertension. The
CC antibodies are also useful for treating kidney ailments, lung
CC dysfunctions such as emphysema, haemorrhages, diseases characterised by
CC decrease in blood cells such as anaemia, thrombocytopenia, hypoplasia,
CC metabolic disorders such as cachexia, anorexia and loss of appetite, and
CC other tumour related disorders. This sequence represents a human WSX
CC receptor DNA antisense oligonucleotide.
XX
SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 GCTGGGATGTCCTTAGA 153
Db 18 GCTGGGATGTCCTTAGA 1
|||||

RESULT 39
AAD38375/c
ID AAD38375 standard; DNA; 24 BP.
XX
AC AAD38375;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human BAT-25 locus amplifying PCR primer #3.
XX
KW Human; microsatellite loci; tumour; familial tumour predisposition;
KW microsatellite instability; MSI; cancer; gastrointestinal system;
KW endometrium; BAT-25 locus; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002058265-A1.
XX
PD 16-MAY-2002.
XX
PF 24-APR-2001; 2001US-00841366.
XX
PR 15-SEP-2000; 2000US-00663020.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Bacher JW, Flanagan L, Nassif N;
XX
DR WPI; 2002-443805/47.
XX
PT Analyzing microsatellite loci for detecting microsatellite instability
PT that can be used for prognostic tumor diagnosis, comprises coamplifying a
PT mononucleotide repeat locus and two tetranucleotide repeat loci.
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for analysing microsatellite
CC loci. The method involves coamplifying a set of 3 microsatellite loci,
CC comprising a specific mononucleotide repeat locus selected from the group
CC consisting of BAT-25, BAT-26, BAT-40, MONO-11 and MONO-15 and two

CC tetranucleotide repeat loci selected from FGA, D1S518, D17S1299 etc from
CC a sample of genomic DNA and determining the size of the amplified
CC fragments. The method is useful for analysing microsatellite loci and for
CC detecting microsatellite instability (MSI) in genomic DNA. The
CC instability in the set of microsatellite loci are used in prognostic
CC tumour diagnosis for the diagnosis of familial tumour predisposition. It
CC is also used to detect cancerous tumours in the gastrointestinal system
CC and of the endometrium. The cancerous tumours are preferably from a
CC colorectal cancer. The present DNA sequence is a PCR primer which is used
CC for amplifying human BAT-25 locus. This primer is used in the
CC exemplification of the invention
XX
SQ Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 921 AGAGCCTTATTAGAAATGCAGAAT 944
Db 24 AGAGCCATAGTTAAATGCAGAAT 1
|||||

RESULT 40
ABT03742
ID ABT03742 standard; DNA; 24 BP.
XX
AC ABT03742;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human Phox2b gene PCR primer SEQ ID NO: 263.
XX
KW Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
KW transcription factor; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200240716-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US043461.
XX
PR 16-NOV-2000; 2000US-0249508P.
XX
PA (CEMI-) CEMINES LLC.
XX
PI Palm K;
XX
DR WPI; 2002-537346/57.
XX
PT Determining the presence of neoplastic molecular markers, by identifying
PT the presence of markers in host test sample using array of neoplastic
PT molecular marker specific reagents and analyzing the array of the
PT reagents.
XX
PS Example 1; Page 18; 41pp; English.
XX
CC The present invention relates to a method for determining the presence of
CC neoplastic molecular markers in a host, involving the use of neoplastic
CC molecular marker specific reagents to detect such markers and analysing
CC the array of reagents, allowing the identification of the neoplastic
CC disease present. This can be used to determine the best treatment for
CC cancers, in particular neural cell, lung and prostate tumours. The
CC present sequence is a PCR primer useful for detecting the coding
CC sequences of markers of the invention
XX
SQ Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Fri Aug 19 11:00:00 2005

```

QY      834 CCAGGAGCGCGGGTGGATCCCT 857
      ||||| ||||| ||||| ||||| |||||
Db      1 CCAGTATGCGCGGGATGGATACCT 24

RESULT 41
AAD36414/c
ID  AAD36414 standard; DNA; 24 BP.
XX
AC  AAD36414;
XX
DT  09-AUG-2002 (first entry)
XX
DE  Human BAT-25 loci amplifying primer #3.
XX
KW  Human; microsatellite locus; microsatellite instability; MSI; tumour;
KW  cancer; primer; ss.
XX
OS  Homo sapiens.
XX
PN  WO200222879-A2.
XX
PD  21-MAR-2002.
XX
PF  14-SEP-2001; 2001WO-US028647.
XX
PR  15-SEP-2000; 2000US-00663020.
XX
PA  (PROM-) PROMEGA CORP.
XX
PI  Bacher JW, Flanagan L, Nassif N;
XX
DR  WPI; 2002-393975/42.
XX
PT  Analyzing micro-satellite loci for detecting or diagnosing cancer, by co-
PT  amplifying set of three microsatellite loci from DNA sample in multiplex
PT  reaction using primers, and determining size of amplified fragments.
XX
PS  Claim 6; Page 73; 73pp; English.
XX
CC  The present invention relates to a method of analysing microsatellite
CC  loci. The method involves co-amplifying a set of three microsatellite
CC  loci comprising at least one mononucleotide repeat locus and at least two
CC  tetra-nucleotide repeat loci from a sample of genomic DNA in a multiplex
CC  amplification reaction using primers and determining the size of the
CC  amplified DNA fragments obtained. The method is useful for analysing
CC  microsatellite loci and for detecting microsatellite instability (MSI) in
CC  genomic DNA microsatellite loci of the second genomic DNA, where the MSI
CC  results are useful in prognostic tumour diagnosis, in diagnosis of
CC  familial tumour predisposition, to detect cancerous tumours of the
CC  gastrointestinal system and of the endometrium, where the cancerous
CC  tumours are tumours from a colorectal cancer. The method is useful for
CC  detecting or diagnosing diseases associated with MSI such as certain
CC  types of cancer and predisposition for cancer and in diagnostic assays to
CC  be used to determine treatment and prognosis of disease. The present DNA
CC  sequence is a primer which is used for amplifying human BAT-25 locus.
CC  This primer is used in the method of the invention
XX
SQ  Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921 AGAGCCTTATTAGAAATGCAGAAT 944
      ||||| ||| ||||| |||||
Db      24 AGAGCCATAGTTAAATGCAGAAT 1

RESULT 42
ADD31191/c
ID  ADD31191 standard; DNA; 24 BP.
XX
SQ  Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921 AGAGCCTTATTAGAAATGCAGAAT 944
      ||||| ||| ||||| |||||
Db      24 AGAGCCATAGTTAAATGCAGAAT 1

RESULT 43
ACI87101/c
ID  ACI87101 standard; DNA; 25 BP.
XX
AC  ACI87101;
XX
DT  14-OCT-2003 (first entry)
XX
DE  Human microarray DNA oligonucleotide SEQ ID NO 87092.
XX
KW  EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW  genetic variation; biallelic marker; polymorphism; human;
KW  cross-species comparison.
XX
OS  Homo sapiens.
XX
PN  US2003104410-A1.
XX
PD  05-JUN-2003.

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```

XX
AC  ADD31191;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human microsatellite locus PCR primer #60.
XX
KW  ss; PCR; primer; human; microsatellite locus;
KW  prognostic tumour diagnosis; familial tumour predisposition;
KW  cancerous tumour; gastrointestinal cancer; endometrial cancer;
KW  colorectal cancer.
XX
OS  Homo sapiens.
XX
PN  US2003180758-A1.
XX
PD  25-SEP-2003.
XX
PF  09-DEC-2002; 2002US-00314810.
XX
PR  15-SEP-2000; 2000US-00663020.
XX
PR  24-APR-2001; 2001US-00841366.
XX
PA  (PROM-) PROMEGA CORP.
XX
PI  Bacher JW, Flanagan L, Nassif N;
XX
DR  WPI; 2003-830985/77.
XX
PT  Analyzing microsatellite instability by amplification of multiple loci
PT  including mono-nucleotide and tetra-nucleotide repeats useful to detect
PT  cancerous gastrointestinal or endometrium tumors particularly colorectal
PT  cancer.
XX
PS  Claim 4; SEQ ID NO 60; 48pp; English.
XX
CC  The invention relates to a method of analysing microsatellite loci. The
CC  invention is used to detect microsatellite instability in prognostic
CC  tumour diagnosis, particularly a familial tumour predisposition,
CC  especially to detect cancerous tumours of the gastrointestinal system or
CC  endometrium, most particularly colorectal cancer. The present sequence
CC  represents a human microsatellite locus PCR primer.
XX
SQ  Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match      1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      921 AGAGCCTTATTAGAAATGCAGAAT 944
      ||||| ||| ||||| |||||
Db      24 AGAGCCATAGTTAAATGCAGAAT 1

RESULT 43
ACI87101/c
ID  ACI87101 standard; DNA; 25 BP.
XX
AC  ACI87101;
XX
DT  14-OCT-2003 (first entry)
XX
DE  Human microarray DNA oligonucleotide SEQ ID NO 87092.
XX
KW  EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW  genetic variation; biallelic marker; polymorphism; human;
KW  cross-species comparison.
XX
OS  Homo sapiens.
XX
PN  US2003104410-A1.
XX
PD  05-JUN-2003.

```

XX 15-MAR-2002; 2002US-00098263.
PF
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
PI Mittmann MP;
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 87092; 9pp; English.
PS
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 2 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 652 CAATTTAGATTATGTTACTCAA 675
||||||| | ||||| |||||
Db 24 CAATTTAAACTATGTCAC TGAA 1

RESULT 44
ADI51286
ID ADI51286 standard; DNA; 17 BP.
XX
AC ADI51286;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID3789.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytosstatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
XX 27-MAR-2003.
PD
XX

PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 3789; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 6 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGTTGTA 997
||||||| | ||||| |||||
Db 1 GATCCAAAGGAGTTGTA 17

RESULT 45
ADJ25095
ID ADJ25095 standard; DNA; 20 BP.
XX
AC ADJ25095;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3493.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
PD 29-JAN-2004.

Fri Aug 19 11:00:00 2005

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XX PF 18-JUL-2003; 2003WO-US022410.
XX PR 19-JUL-2002; 2002US-0397106P.
XX PA (PHAA ) PHARMACIA CORP.
XX PI Bhat BG;
XX DR WPI; 2004-132912/13.
XX PT New antisense oligonucleotide for modulating endothelial lipase
XX PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX PS Claim 3; SEQ ID NO 3493; 1007pp; English.
XX CC The present invention relates to antisense oligonucleotides (ADJ21603-
XX CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX SQ Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 CCCGGCCGTGGCAGGAGC 39
DB 1 CCCGGCCGTGGCAGGAGC 20

RESULT 46
ADJ25250
ID ADJ25250 standard; DNA; 20 BP.
XX AC ADJ25250;
XX DT 20-MAY-2004 (first entry)
XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3648.
XX KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
XX KW cardiovascular disorder; metabolic syndrome X; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /mod_base= a
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX WO2004009541-A2.
XX PD 29-JAN-2004.
XX PF 18-JUL-2003; 2003WO-US022410.
XX PR 19-JUL-2002; 2002US-0397106P.
XX PA (PHAA ) PHARMACIA CORP.

XX PI Bhat BG;
XX DR WPI; 2004-132912/13.
XX PT New antisense oligonucleotide for modulating endothelial lipase
XX PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX PS Claim 3; SEQ ID NO 3648; 1007pp; English.
XX CC The present invention relates to antisense oligonucleotides (ADJ21603-
XX CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX SQ Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GCCCGGCCGTGGCAGGAAG 38
DB 1 GCCCGGCCGTGGCAGGAAG 20

RESULT 47
AAA50752/c
ID AAA50752 standard; DNA; 21 BP.
XX AC AAA50752;
XX DT 01-SEP-2000 (first entry)
XX DE PCR primer 1F used in FIS2 gene identification.
XX KW Seed; development; FIS; endosperm; autonomous embryogenesis;
XX KW transgenic plant; seedless fruit; parthenocarpic; citrus fruit;
XX KW stone fruit; PCR primer; ss.
XX OS Arabidopsis thaliana.
XX PN WO200016609-A1.
XX PD 30-MAR-2000.
XX PF 21-SEP-1999; 99WO-AU0000805.
XX PR 21-SEP-1998; 98US-0101184P.
XX PR 22-SEP-1998; 98AU-00006061.
XX PR 22-SEP-1998; 98AU-00006062.
XX PR 22-SEP-1998; 98AU-00006063.
XX PR 01-JUL-1999; 99AU-00001345.
XX PR 01-JUL-1999; 99AU-00001346.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Bilodeau P, Chaudhury AM, Dennis ES, Koltunow AMG, Luo M;
XX PI Peacock WJ;
XX DR WPI; 2000-283392/24.
XX PT Induction of seed development in plants in the absence of fertilization
XX PT by inhibiting or preventing the expression of a negative regulator of
XX PT seed formation for production of seedless or soft-seeded fruit.
XX PS Example 13; Page 107; 207pp; English.
```


XX The present invention relates to a method of inducing the development of
CC seeds in a plant, comprising inhibiting, interrupting or reducing the
CC expression of a negative regulator of seed formation in one or more
CC female reproductive cells, tissues, or organs of the plant or a
CC progenitor cell, tissue or organ. The negative regulator is a
CC polypeptide. The FIS family of genes are known to be capable of
CC regulating autonomous endosperm development and/or autonomous
CC embryogenesis. In the invention the reduced expression of the negative
CC regulator is achieved by the introduction of a transgene which comprises
CC a FIS genetic sequence, which may inhibit FIS activity. The present
CC sequence represents a PCR primer used to identify the FIS2 gene. Plants
CC produced using the method of the invention produce parthenocarpic fruit
CC or soft-seeded fruit, where the fruit are made parthenocarpic or have
CC soft seed by a process comprising expressing the introduced nucleic acid
CC molecule in a tissue or organ of the fruit. The plant produces seed
CC independent of fertilization. The isolated FIS nucleic acid molecules are
CC used in the production of an antisense molecule, a ribozyme, a co-
CC suppression molecule, a gene-targeting molecule, a gene-silencing
CC molecule and a dominant-negative sense molecule where the member is used
CC for the production of a transformed plant. The transformed plant is
CC apomictic or produces soft-seeded or parthenocarpic fruit. Production of
CC soft-seeded fruit has large economic value, since it makes the fruit more
CC desirable to customers. Examples include stone fruits such as apricots
CC and peaches, citrus fruits such as oranges, lemons, grapefruit and
CC mandarins and other fruits such as grapes, apples, melons, pears and
CC berries. The plants which undergo autonomous seed formation do not
CC require fertilization to reproduce, and may express desirable
CC characteristics stably between generations. Antibodies produced to the
CC FIS polypeptides can be used to detect the peptides of the invention and
CC can be used in an enzyme linked immunosorbant assay (ELISA),
CC radioimmunoassay or histochemical tests
XX
SQ Sequence 21 BP; 4 A; 5 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 606 ACTTCATAAGTAGGAGATGA 625
Db 20 ACTTCATAAGGAAGATGA 1
|||||||
|||

RESULT 48
AAT89716
ID AAT89716 standard; DNA; 24 BP.
XX
AC AAT89716;
XX
DT 05-FEB-1998 (first entry)
XX
DE PCR primer used for hepatitis C virus genotyping.
XX
KW Hepatitis C virus; HCV; genotype determination; 1a; 1b; 2a; 2b; 3a; 3b;
KW 4; 5a; 6a; 6b; diagnosis; amplification; PCR; primer; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
FN JP09234072-A.
XX
PD 09-SEP-1997.
XX
PF 01-FEB-1996; 96JP-00038875.
XX
PR 01-FEB-1995; 95JP-00035997.
PR 30-DEC-1995; 95JP-000352511.
XX
PA (SRLS-) SRL KK.
XX
DR WPI; 1997-497313/46.
XX

PT Primers used for determining hepatitis C virus genotype - provide a rapid
PT and accurate method of hepatitis C virus genotyping.
XX
PS Claim 28; Page 15; 33pp; Japanese.
XX
CC AAT89689-T89744 are individually claimed oligonucleotides used as PCR
CC (polymerase chain reaction) primers for the discrimination of the
CC genotype of hepatitis C virus (HCV). Classification of the genotype of
CC HCV can be achieved precisely and simply according to the International
CC Standardisation of Classification. The primers can be used to distinguish
CC between HCV genotypes 1a, 1b, 2a, 2b, 3a, 3b, 4, 5a, 6a and 6b
XX
SQ Sequence 24 BP; 3 A; 8 C; 8 G; 4 T; 0 U; 1 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 70;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 TGGGCAGGCTGCCCGGGCGCTG 30
|||
|||
Db 1 TCGACAGGCKGCCCGGGCGCTG 22
|||||
|||

RESULT 49
ABA99037
ID ABA99037 standard; DNA; 24 BP.
XX
AC ABA99037;
XX
DT 22-JUL-2002 (first entry)
XX
DE PCR primer corresponding to the plasmid backbone of pJK148.
XX
KW PCR; primer; site-specific gene replacement; irreversible recombinase;
KW irreversible recombination site; IRS; ss.
XX
OS Unidentified.
XX
PN WO200208409-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023049.
XX
PR 21-JUL-2000; 2000US-0220062P.
XX
PA (USDA) US DEPT OF AGRICULTURE.
XX
PI Ow DW;
XX
DR WPI; 2002-195874/25.
XX
PT Obtaining site-specific gene replacement, useful for obtaining specific
PT and stable integration of nucleic acids into chromosomes of eukaryotes,
PT by employing irreversible recombination sites (IRS) and irreversible
PT recombinases.
XX
PS Example 1; Page 32; 84pp; English.
XX
CC The sequence represents a PCR primer used in the invention to prepare the
CC attB-ura4-attB linear DNA, as a PCR product using pLT50 as a template.
CC The invention relates to a novel method for obtaining site-specific gene
CC replacement in a eukaryotic cell comprising employing irreversible
CC recombination sites (IRS) and irreversible recombinases. The method is
CC useful for obtaining specific and stable integration of nucleic acids
CC into chromosomes of eukaryotes or for obtaining site-specific replacement
CC of nucleic acids in a target construct. The method may also be used to
CC stably integrate a polynucleotide into any eukaryotic cell that can be
CC transformed by a polynucleotide
XX
SQ Sequence 24 BP; 3 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTCTTCTGCC 313
||| ||||| ||||| |||||
Db 5 CTGAAATTGTGCTTCTGCC 24

RESULT 50
AAS03279/c
ID AAS03279 standard; DNA; 23 BP.
XX
AC AAS03279;
XX
DT 07-SEP-2001 (first entry)
XX
DE Rat PDGF-associated protein, PRO, PCR primer Ag197#1.
XX
KW Rat; platelet-derived growth factor; PDGF; PRO; tumour; cancer;
KW PDGF-associated disorder; myofibroblast development; wound healing;
KW angiogenesis; cancer; tumour; muscle wasting disease; PCR primer; ss.
XX
OS Rattus sp.
XX
PN WO200131010-A1.
XX
PD 03-MAY-2001.
XX
PF 25-OCT-2000; 2000WO-US029391.
XX
PR 25-OCT-1999; 99US-0161315P.
PR 24-OCT-2000; 2000US-00695366.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess C, Rastelli L;
XX
DR WPI; 2001-308644/32.
XX
PT Polypeptides related to platelet-derived growth factor-associated
PT proteins, useful for increasing muscle mass and to treat wasting
PT diseases.
XX
PS Example 1; Page 75; 95pp; English.
XX
CC The sequence represents a PCR primer used to isolate nucleic acid
CC molecules encoding a platelet-derived growth factor (PDGF) associated
CC protein, PRO. Polypeptides, nucleic acids and antibodies of the invention
CC are used to treat or prevent a pathological state in a mammal,
CC particularly a PDGF-associated disorder in a human. Specifically, these
CC molecules can be used to control myofibroblast development, wound healing
CC or angiogenesis, for example in the treatment of cancer and tumours, or
CC muscle wasting diseases
XX
SQ Sequence 23 BP; 9 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 386 AATGCAGTCATTTTCTTACAAT 408
| ||||| || ||||| ||||| |||||
Db 23 ACTGCATTGCTTTCTTCTGACAAT 1

RESULT 51
ABZ30445/c
ID ABZ30445 standard; DNA; 23 BP.
XX
AC ABZ30445;
XX
DT 30-JAN-2003 (first entry)
XX

DE Candida albicans GRACE strain PCR primer SEQ ID NO 4596.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR WPI; 2002-566694/60.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 36; SEQ ID NO 4596; 167pp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 23 BP; 10 A; 6 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 477 TGATTACAGTGCATTGAATTCT 499
||| ||||| ||||| ||||| |||||
Db 23 TGATTGCAGTGCCTTGAATTTT 1

RESULT 52
ADK67738/c
ID ADK67738 standard; DNA; 23 BP.
XX
AC ADK67738;
XX
DT 06-MAY-2004 (first entry)
XX

XX Murine fancg/xrcc9 gene primer G34.
DE Transgenic; knockout; gene therapy; bacterial artificial chromosome;
XX mouse; fancg/xrcc9 gene; PCR; primer; ss.
KW Mus sp.
OS WO2004013299-A2.
PN 12-FEB-2004.
XX 01-AUG-2003; 2003WO-US024322.
PF 02-AUG-2002; 2002US-0400900P.
XX (GEO) GEN HOSPITAL CORP.
PR Seed B, Yang Y;
XX WPI; 2004-157118/15.
DR Producing a genetically modified mammalian cell, useful in producing
XX modified non-human mammal for screening compounds to treat or prevent
PT cancer, by inserting into mammalian cells an artificial chromosome
PT comprising a cassette.
XX Disclosure; SEQ ID NO 9; 80pp; English.
PS The present invention relates to methods for generating cell lines and
XX mammals with site-specific genetic modification. The methods use
CC homologous recombination between an artificial chromosome having the
CC modification and an endogenous chromosome of a cell. The resulting
CC modified cells can be used to generate genetically modified mammals
CC useful in screening methods to identify compounds of therapeutic
CC interest. Cells can also be modified to eliminate a mutation associated
CC with a disease, e.g. cancer, and then transplanted into patients for
CC treatment of the disease. In an example of the method, bacterial
CC artificial chromosomes (BACs) containing mutations in fancg/xrcc9 were
CC used to modify mouse embryonic stem (ES) cells for the generation of
CC fancg/xrcc9 knockout mice. The present primer, designated G34, was used
CC in a nested PCR to screen modified BAC clones for correct targeting
CC events.
XX Sequence 23 BP; 3 A; 9 C; 8 G; 3 T; 0 U; 0 Other;
SQ Query Match 1.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 20 CCCGGGCGGTGGCAGGAAGCCGG 42
Db 23 CCCGCTCCGTGGCTGGAAGACGG 1
RESULT 53
AAQ82600
ID AAQ82600 standard; DNA; 21 BP.
XX AAQ82600;
AC 25-MAR-2003 (revised)
XX 14-SEP-1995 (first entry)
DT Chromosome 11 (locus D11S870) STS primer 350.
XX sequence sampled mapping; genomic analysis; complex genome mapping;
KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX Synthetic.
OS WO9429486-A1.
PN
XX

PD 22-DEC-1994.
XX 15-JUN-1994; 94WO-US006810.
PF 15-JUN-1993; 93US-00078471.
PR 07-SEP-1993; 93US-00117952.
XX (SALK) SALK INST BIOLOGICAL STUDIES.
PA Evans GA, Smith MW;
XX WPI; 1995-036508/05.
PI Sequencing complex genomes, present as fragments in a cosmid library - by
XX sequencing end-specific nucleotides of each clone then correlating with
PT spatial relationship of cosmid, esp. for mammalian chromosomes.
PT Example 4; Page 89; 128pp; English.
XX Sequences were determined from the ends of chromosome 11-specific cosmids
CC by automated sequencing without intermediate subcloning. A sample of 371
CC DNA sequence fragments were determined and of these, 277 were suitable
CC for STS primer prediction by computer analysis (using the "Primer"
CC program available from E.Lander, MIT). The STSs and cosmids were mapped
CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
CC this method, 370 STSs specific for human chromosome 11 were generated and
CC most of them were regionally mapped. This procedure illustrates a novel
CC method for sequencing complex genomes, designated "sequence sampled
CC mapping". The sequence sampled mapping method is useful for the
CC completion of high density sequence-based maps, and ultimately, for the
CC complete sequencing of genomic DNA directly from cosmid clones. See
CC AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX Sequence 21 BP; 5 A; 3 C; 4 G; 9 T; 0 U; 0 Other;
SQ Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 513 ATCTGTATACATGTGCACATG 533
Db 1 ATCTGTATATATGTGTACCTG 21
RESULT 54
AAT65977
ID AAT65977 standard; DNA; 21 BP.
XX AAT65977;
AC 25-MAR-2003 (revised)
XX 18-JUN-1997 (first entry)
DT Primer #2 to amplify repeat sequence marker Mfd90.
XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX Synthetic.
OS US5582979-A.
XX 10-DEC-1996.
PN 04-APR-1994; 94US-00222177.
XX 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX (MARS-) MARSHFIELD CLINIC.
PA

XX Weber JL;
PI WPI; 1997-042299/04.
XX
DR
XX
XX
PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
PT using novel nucleic acid mols. as primers.
XX
XX
PS Disclosure; Col 11-12; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. Clones containing the
CC repeat sequences were isolated by hybridisation of chromosome-specific
CC phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100
CC repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR
CC amplify the inserts from the isolated clones containing the repeat
CC sequences. The primers AAT65976-7 were used to amplify the repeat
CC sequence marker clone Mfd90. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 21 BP; 5 A; 3 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTGCACATG 533
|||||||
Db 1 ATCTGTATATATGTGTACCTG 21

RESULT 55
ABS98440
ID ABS98440 standard; DNA; 21 BP.
XX
AC ABS98440;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance associated protein 3 polymorphic sequence #62.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX WO200257410-A2.
PN
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX

PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
XX Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
XX Example 24; Page 153; 714pp; English.
PS
XX This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GSTI2), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
CC ARNT, EPHX2, GSTI2, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 21 BP; 4 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 616 TAGGAGATGAGTTTATTCTC 636
|||||
Db 1 TAGTAGCTGAGTTTGATTCTC 21

RESULT 56
ABK86295/c
ID ABK86295 standard; DNA; 23 BP.
XX
XX
AC ABK86295;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human TGR342 RT-PCR primer #2.
XX
KW Human; TGR342; primer; ss; G-protein coupled receptor; GPCR; TGR; RT-PCR;

KW TGR-associated disorder; signal transduction; renal failure; nephritis;
KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
KW diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;
KW circadian rhythm; reverse transcriptase.
XX
OS Homo sapiens.
XX
XX
PN WO200242458-A2.
XX
XX 30-MAY-2002.
PD
XX
PF 21-NOV-2001; 2001WO-US043404.
XX
PR 22-NOV-2000; 2000US-0252841P.
PR 22-DEC-2000; 2000US-0257636P.
PR 12-JAN-2001; 2001US-0261377P.
PR 28-MAR-2001; 2001US-0279554P.
PR 29-MAR-2001; 2001US-0280696P.
XX
PA (TULA-) TULARIK INC.
XX
PI Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;
XX
XX WPI; 2002-463633/49.
DR
XX New isolated G-protein couple receptor polypeptide, termed TGR, for
PT diagnosis and treatment of diseases such as renal failure, nephritis,
PT hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.
XX
PS Example 2; Page 65; 98pp; English.
XX
XX The invention relates to a G-protein coupled receptor polypeptide (GPCR),
CC termed TGR, and its associated nucleic acid. The sequences of the
CC invention are useful for identifying a compound that modulates signal
CC transduction and for identifying a mammal having a TGR-associated
CC disorder. The proteins and nucleic acids are useful in diagnosis and
CC treatment of diseases or conditions such as renal failure, nephritis,
CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
CC diabetes insipidus, hyperprolactinaemia and disturbances of thirst,
CC sleep, temperature regulation, appetite, blood pressure or any other
CC syndrome or disease associated with the hypothalamus. The genetic markers
CC be used in regulation of circadian rhythms, for use as genetic markers
CC for the identification of mutations associated with diseases resulting
CC from GPCR inactivation in particular cell types and for identification of
CC modulators of GPCR signal transduction. This sequence represents a
CC reverse transcriptase PCR (RT-PCR) primer for human TGR342 DNA
XX
SQ Sequence 23 BP; 11 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 117 TTGGACTGACTTTCTTATGC 137
Db ||||| || ||||| ||||| ||
22 TTGGAATGCCTTTCTTATTC 2
RESULT 57
ADB16943
ID ADB16943 standard; DNA; 23 BP.
XX
AC ADB16943;
XX
DT 20-NOV-2003 (first entry)
XX
DE EKN1-1R human-specific intronic PCR primer for DYXC1.
XX
KW EKN1-1R; ss; human; DYXC1; dyslexia; neurological disorder;
KW reading disability; phonological processing; rapid naming;
KW verbal short-term memory; primer; PCR.
XX

OS Homo sapiens.
XX
PN WO2003068814-A1.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-FI000110.
XX
PR 12-FEB-2002; 2002US-0355782P.
XX
PA (LICN) LICENTIA LTD.
XX
PI Kere J, Taipale M, Nopola-Hemmi J, Kaminen N;
XX
XX WPI; 2003-646482/61.
DR
XX New isolated, purified DYXC1 nucleic acid for studying brain processes,
PT e.g. reading, phonological processing, rapid naming or verbal short-term
PT memory, or for diagnosing dyslexia or assessing the predisposition to
PT dyslexia.
XX
PS Disclosure; Page 23; 135pp; English.
XX
CC This invention relates to a novel isolated human gene DYXC1 that is
CC functionally related to dyslexia, more particularly it describes single
CC nucleotide polymorphisms thought to predispose an individual in to
CC developing dyslexia. This is a neurological disorder with a genetic basis
CC (DYXC1 has been isolated to chromosome 15q21), which manifests itself as
CC a specific reading disability. Specifically, DYXC1 is can be useful in
CC study of brain processes such as reading, phonological processing, rapid
CC naming and verbal short-term memory. Accordingly, the present invention
CC describes methods and materials for analysing allelic variations in the
CC DYXC1 gene, and also provides DYXC1 as an antigen for the production of
CC antibodies used in the diagnosis of dyslexia. This oligonucleotide is the
CC EKN1-1R PCR primer that is specific for human intronic DYXC1, and is used
CC to amplify exon 1 in an exemplification of the invention.
XX
SQ Sequence 23 BP; 9 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1000 CACATGAAAGTTTGAGAAGCA 1020
Db ||||| ||||| ||||| ||||| ||
1 CACACCAAAGTTTGAGAACCA 21
RESULT 58
ADR27674/c
ID ADR27674 standard; DNA; 16 BP.
XX
AC ADR27674;
XX
DT 04-NOV-2004 (first entry)
XX
DE Leptin receptor related protein, OB-RGRP, RT-PCR primer #2.
XX
KW Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW human; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN FR2850971-A1.
XX
PD 13-AUG-2004.
XX
PF 10-FEB-2003; 2003FR-00001543.

ngs.res

Fri Aug 19 11:00:00 2005

XX PR 10-FEB-2003; 2003FR-00001543.
XX PA (AVET) AVENTIS PHARMA SA.
XX PI (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX Jockers R, Couturier C, Uhlmann E;
XX WPI; 2004-595751/58.
XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and
PT angiogenesis.
XX Disclosure; Page 23; 104pp; French.
XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present sequence is a
CC RT-PCR primer used to illustrate the invention.
XX SQ Sequence 16 BP; 6 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 1.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 332 CTTGCTCGTGTGGCTG 347
DB 16 CTTGCTCGTGTGGCTG 1
RESULT 59
ADI52070
ID ADI52070 standard; DNA; 17 BP.
XX AC ADI52070;
XX 15-APR-2004 (first entry)
XX Human tumour suppression/reversion-related DNA sequence SeqID4573.
DE tumour suppression; tumour reversion; virus resistance;
KW cytosstatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; Gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX OS Homo sapiens.
XX WO2003025177-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002WO-IB004523.
XX PF 17-SEP-2001; 2001FR-00011980.
PR

XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313354/30.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX Disclosure; SEQ ID NO 4573; 30pp; French.
PS This invention relates to novel isolated nucleic acid sequences involved
XX in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration. The
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX SQ Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 981 GATCCAAAGGAGTTGT 996
DB 1 GATCCAAAGGAGTTGT 16
RESULT 60
AAS97676/c
ID AAS97676 standard; DNA; 20 BP.
XX AC AAS97676;
XX 12-MAR-2002 (first entry)
XX Human SAC1 gene-specific oligonucleotide PCR primer #37.
DE Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW protein replacement therapy.
XX OS Homo sapiens.
XX WO200183749-A2.
XX 08-NOV-2001.
XX 25-APR-2001; 2001WO-US013387.
XX 28-APR-2000; 2000US-0200794P.
XX 28-JUL-2000; 2000US-0221419P.
XX 10-NOV-2000; 2000US-0247443P.
XX (WARN) WARNER LAMBERT CO.
XX (MONE-) MONELL CHEM SENSES CENT.
XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
XX Ohmen JD, Reed DR, Ross D, Tordoff MG;
PI

XX WPI; 2002-075162/10.

XX

XX Novel isolated polypeptide comprising variant form of mouse or human SAC1

PT polypeptide, and is associated with altered preference for carbohydrates

PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

XX

PS Claim 14; Page 84; 239pp; English.

XX

CC The invention relates to an isolated polypeptide, comprising a variant

CC form of mouse or human SAC1 polypeptide. The variant form is associated

CC with altered preference for carbohydrates, other sweeteners or ethanol.

CC The polypeptide and its associated DNA sequence can be produced by

CC recombinant techniques and is useful for preventing obesity, diabetes or

CC alcoholism associated with SAC1 expression. The sequences are useful in

CC screening for drugs and sweeteners. Recombinant cell lines and transgenic

CC embryos may be used in screening for and identifying agents that induce

CC or repress function of SAC1. Predisposition to diabetes, obesity or

CC alcoholism can be ascertained by testing any fluid or tissue of a human

CC (such as blood, pancreas or tongue) for sequence variations of the SAC1

CC gene. A sequence variation of the SAC1 locus may indicate a

CC predisposition to diabetes, obesity and/or alcoholism and may provide a

CC diagnostic mark. The polynucleotide can be detected in a biological

CC sample by contacting the DNA with a probe to form a hybridisation complex

CC which is then detected. The sequences represent cDNA encoding human and

CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes

XX

SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107

Db |||||||||||||||

16 GGTGTTACCTGCTCAT 1

RESULT 61

AAS97674/c

ID AAS97674 standard; DNA; 20 BP.

XX

AC AAS97674;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human SAC1 gene-specific oligonucleotide PCR primer #35.

KW Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;

KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;

KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;

KW protein replacement therapy.

XX

OS Homo sapiens.

XX

PN WO200183749-A2.

PD

PD 08-NOV-2001.

XX

PF 25-APR-2001; 2001WO-US013387.

XX

PR 28-APR-2000; 2000US-0200794P.

PR 28-JUL-2000; 2000US-0221419P.

PR 10-NOV-2000; 2000US-0247443P.

XX

PA (WARN) WARNER LAMBERT CO.

PA (MONE-) MONELL CHEM SENSES CENT.

XX

PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;

PI Ohmen JD, Reed DR, Ross D, Tordoff MG;

XX

DR WPI; 2002-075162/10.

XX

PT Novel isolated polypeptide comprising variant form of mouse or human SAC1

PT polypeptide, and is associated with altered preference for carbohydrates

PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

XX

PS Claim 14; Page 84; 239pp; English.

XX

CC The invention relates to an isolated polypeptide, comprising a variant

CC form of mouse or human SAC1 polypeptide. The variant form is associated

CC with altered preference for carbohydrates, other sweeteners or ethanol.

CC The polypeptide and its associated DNA sequence can be produced by

CC recombinant techniques and is useful for preventing obesity, diabetes or

CC alcoholism associated with SAC1 expression. The sequences are useful in

CC screening for drugs and sweeteners. Recombinant cell lines and transgenic

CC embryos may be used in screening for and identifying agents that induce

CC or repress function of SAC1. Predisposition to diabetes, obesity or

CC alcoholism can be ascertained by testing any fluid or tissue of a human

CC (such as blood, pancreas or tongue) for sequence variations of the SAC1

CC gene. A sequence variation of the SAC1 locus may indicate a

CC predisposition to diabetes, obesity and/or alcoholism and may provide a

CC diagnostic mark. The polynucleotide can be detected in a biological

CC sample by contacting the DNA with a probe to form a hybridisation complex

CC which is then detected. The sequences represent cDNA encoding human and

CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes

XX

SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107

Db |||||||||||||||

16 GGTGTTACCTGCTCAT 1

RESULT 62

ADJ93118

ID ADJ93118 standard; DNA; 20 BP.

XX

AC ADJ93118;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human G-coupled receptor protein HGPBMY30 gene primer GPCR99-2s.

XX

KW immunosuppressive; cardiant; antiinflammatory; cytostatic; anti-HIV;

KW anti-rheumatic; antiarthritic; antibacterial; antiseborrheic;

KW dermatological; antipsoriatic; neuroprotective; nootropic;

KW antiparkinsonian; antidiabetic; ophthalmological; antiasthmatic;

KW antidepressant; neuroleptic; hypotensive; tranquilizer; hypertensive;

KW anorectic; metabolic; virucide; osteopathic; antiangular; vulnery;

KW gene therapy; G-protein coupled receptor protein; HGPBMY30;

KW immune disorder; cardiovascular disorder; inflammatory disorder;

KW metabolic disorder; reproductive disorder; testicular cancer;

KW neural disorder; endocrine disorder; gastrointestinal disorder;

KW Alzheimer's disease; Parkinson's diseases; diabetes; dwarfism; asthma;

KW schizophrenia; obesity; anorexia; osteoporosis; angina pectoris;

KW myocardial infarction; primer; ss.

XX

OS Homo sapiens.

XX

PN WO200296946-A1.

XX

PD 05-DEC-2002.

XX

PF 30-MAY-2002; 2002WO-US017085.

XX

PR 30-MAY-2001; 2001US-0294411P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder JN, Mintier GA, Ramanathan C;

XX

DR WPI; 2003-140445/13.

XX Novel human G-protein coupled receptor, HGPRBM30 polypeptide useful for

PT preventing and treating e.g. immune disorders, cardiovascular disorders

PT or inflammatory disorders.

XX Example 3; SEQ ID NO 21; 343pp; English.

PS

XX The invention relates to an isolated human G-protein coupled receptor,

CC HGPRBM30 polypeptide or a sequence having 95% identity to the above

CC mentioned sequences. (I) is useful for preventing or treating a medical

CC condition, selected from an immune disorder; a cardiovascular disorder;

CC an inflammatory disorder in which G-protein coupled receptors are either

CC directly, or indirectly, associated with the disorder; a metabolic

CC disorder; a reproductive disorder; a male reproductive disorder;

CC testicular cancer; a neural disorder; an endocrine disorder;

CC gastrointestinal disorder; (I) and (II) are also useful for detecting,

CC prognosing, preventing, treating, and/or ameliorating the diseases such

CC as hematopoietic and pulmonary disorders, Alzheimer's, Parkinson's

CC diseases, diabetes, dwarfism, color blindness, sleeplessness, hypertension, anxiety,

CC asthma, expression, schizophrenia, acute heart failure, hypotension, obesity,

CC stress, renal failure, HIV infections, osteoporosis, angina pectoris, and myocardial

CC anorexia, anorexia, and (II) are useful for modulating signal transduction

CC infarction. (I) and (II) are useful as an inhibitor of chemotaxis, as a

CC food additive or preservative, and for modifying the activities of (I).

CC (I) and (II) also useful to modulate mammalian characteristics, such as

CC body height, weight, hair color, eye color, skin, percentage of adipose

CC tissue, pigmentation, size and shape, to change a mammal's mental state

CC or physical state by influencing biorhythms, cardiac rhythms,

CC depression, tendency for violence, tolerance for pain, reproductive

CC capabilities, hormonal or endocrine levels, appetite, libido, memory,

CC stress, or other cognitive qualities. This sequence corresponds to a PCR

CC primer for the coding sequence for the novel HGPRBM30 protein.

XX

SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107

DB 5 GGTGTTACCTGCTCAT 20

RESULT 63

ADM16016/c

ID ADM16016 standard; DNA; 20 BP.

XX

AC ADM16016;

XX

DT 15-JUL-2004 (first entry)

XX

DE Human SAC1 DNA PCR primer #37.

XX

XX Human; SAC1; PCR; ss; carbohydrate; sweetener; ethanol; obesity;

KW diabetes; alcoholism; antidiabetic; alcohol; anorectic; antialcoholic;

KW primer.

XX

OS Homo sapiens.

XX

PN US2004081964-A1.

XX

PD 29-APR-2004.

XX

PF 25-OCT-2002; 2002US-00280183.

XX

XX 25-OCT-2002; 2002US-00280183.

PR

XX (BACH/) BACHMANOV A A.

PA (BEAU/) BEAUCHAMP G K.

PA (LISS/) LI S.

PA (LIXX/) LI X.

PA (REED/) REED D R.

PA (TORD/) TORDOFF M G.

PA (ROSS/) ROSS D A.

PA (OHMA/) OHMAN J D.

PA (CHAT/) CHATTERJEE A.

PA (DJON/) DE JONG P J.

XX

PI Bachmanov AA, Beauchamp GK, Li S, Li X, Reed DR, Tordoff MG;

PI Ross DA, Ohman JD, Chatterjee A, De Jong PJ;

XX

DR WPI; 2004-340133/31.

XX

PT New isolated polynucleotides for sensing carbohydrates, other sweeteners,

PT or ethanol, useful for screening drugs for inhibition or restoration of

PT gene function as antidiabetic, antioesity or antialcohol consumption

PT therapies.

PT

XX Example 12; SEQ ID NO 286; 148pp; English.

PS

XX The invention relates to SAC1 polypeptides and the polynucleotides

CC encoding them. The polynucleotides contain a variation associated with

CC sensing carbohydrates, other sweeteners or ethanol. The invention also

CC relates to a method for analysing a biomolecule in a biological sample,

CC comprising altering SAC1 activity in the sample and measuring the

CC activity, a method for analysing a polynucleotide in a biological sample,

CC comprising contacting a polynucleotide in a biological sample with a

CC probe where the probe hybridises to a SAC1 polynucleotide to form a

CC hybridisation complex and detecting the hybridisation complex, a method

CC of identifying susceptibility to obesity or diabetes comprising comparing

CC the nucleotide sequence of the suspected SAC1 allele with a wild type

CC and the wild-type sequence identifies a sequence variation of the SAC1

CC nucleotide sequence, where the difference between the suspected allele

CC nucleotide sequence, and a method of treating or preventing obesity,

CC diabetes or alcoholism associated with expression of SAC1, comprising

CC administering to a subject a pharmaceutical composition and a transgenic

CC animal that carries an altered SAC1 allele. The methods and compositions

CC of the invention are useful for screening drugs for inhibition or

CC restoration of gene function as antidiabetic, antioesity or antialcohol

CC consumption therapies and for identifying sweeteners and alcohols. This

CC sequence represents a PCR primer used to amplify human SAC1 DNA of the

CC invention.

XX

SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 GGTGTTACCTGCTCAT 1107

DB 16 GGTGTTACCTGCTCAT 1

RESULT 64

ADM16014/c

ID ADM16014 standard; DNA; 20 BP.

XX

AC ADM16014;

XX

DT 15-JUL-2004 (first entry)

XX

DE Human SAC1 DNA PCR primer #35.

XX

XX Human; SAC1; PCR; ss; carbohydrate; sweetener; ethanol; obesity;

KW diabetes; alcoholism; antidiabetic; alcohol; anorectic; antialcoholic;

KW primer.

XX

OS Homo sapiens.

XX

PN US2004081964-A1.

XX

PD 29-APR-2004.

XX 25-OCT-2002; 2002US-00280183.
PF (BACH/) BACHMANOV A A.
XX (BEAU/) BEAUCHAMP G K.
PR (LISS/) LI S.
XX (LIXX/) LI X.
PA (REED/) REED D R.
PA (TORD/) TORDOFF M G.
PA (ROSS/) ROSS D A.
PA (OHMA/) OHMAN J D.
PA (CHAT/) CHATTERJEE A.
PA (DJON/) DE JONG P J.
XX
PI Bachmanov AA, Beauchamp GK, Li S, Li X, Reed DR, Tordoff MG;
PI Ross DA, Ohman JD, Chatterjee A, De Jong PJ;
XX
DR WPI; 2004-340133/31.
XX
PT New isolated polynucleotides for sensing carbohydrates, other sweeteners,
PT or ethanol, useful for screening drugs for inhibition or restoration of
PT gene function as antidiabetic, antiobesity or antialcohol consumption
PT therapies.
XX
PS Example 12; SEQ ID NO 284; 148pp; English.
XX
CC The invention relates to SAC1 polypeptides and the polynucleotides
CC encoding them. The polynucleotides contain a variation associated with
CC sensing carbohydrates, other sweeteners or ethanol. The invention also
CC relates to a method for analysing a biomolecule in a biological sample,
CC comprising altering SAC1 activity in the sample and measuring the
CC activity, a method for analysing a polynucleotide in a biological sample,
CC comprising contacting a polynucleotide in a biological sample with a
CC probe where the probe hybridises to a SAC1 polynucleotide to form a
CC hybridisation complex and detecting the hybridisation complex, a method
CC of identifying susceptibility to obesity or diabetes comprising comparing
CC the nucleotide sequence of the suspected SAC1 allele with a wild type
CC nucleotide sequence, where the difference between the suspected allele
CC and the wild-type sequence identifies a sequence variation of the SAC1
CC nucleotide sequence, and a method of treating or preventing obesity,
CC diabetes or alcoholism associated with expression of SAC1, comprising
CC administering to a subject a pharmaceutical composition and a transgenic
CC animal that carries an altered SAC1 allele. The methods and compositions
CC of the invention are useful for screening drugs for inhibition or
CC restoration of gene function as antidiabetic, antiobesity or antialcohol
CC consumption therapies and for identifying sweeteners and alcohols. This
CC sequence represents a PCR primer used to amplify human SAC1 DNA of the
CC invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1092 GGTGTTACTGCTCAT 1107
Db 16 GGTGTTACTGCTCAT 1

RESULT 65
ADE78595
ID ADE78595 standard; DNA; 19 BP.
XX
AC ADE78595;
XX
DT 29-JAN-2004 (first entry)
XX
DE Endogenous carotenoid gene expression RT-PCR primer #19.
XX
KW metabolite; carotene; plant; carotene hydroxylase; lycopene beta-cyclase;

KW beta-carotene hydroxylase; zeaxanthin; beta-carotene;
KW oxygenated carotenoid; RT-PCR; primer; carotenoid; ss.
XX
OS Unidentified.
XX
PN EP1323825-A2.
XX
PD 02-JUL-2003.
XX
PF 08-NOV-2002; 2002EP-00425681.
XX
PR 09-NOV-2001; 2001IT-RM000670.
XX
PA (CNEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
PA (BIOJ) BIOGEN SRL.
XX
PI Giuliano G, Rosati C, Dharmapuri S, Pallara P, Camara B;
XX WPI; 2003-714401/68.
DR
XX
PT Increasing the metabolites of carotene content in a plant useful for
PT producing recombinant plants comprises upregulating a gene encoding
PT carotene hydroxylase activity.
XX
PS Example 1; Page 12; 21pp; English.
XX
CC The invention relates to a novel process for increasing the metabolites
CC of carotene content of a plant. The novel process comprises upregulating
CC at least one gene which encodes carotene hydroxylase activity. The
CC compositions of the novel process have lycopene beta-cyclase or a beta-
CC carotene hydroxylase activity. The process is useful for increasing the
CC metabolites of carotene content of a plant, comprising transforming a
CC plant cell from which viable plants may be recovered, using a plant
CC expression cassette, or a DNA construct, and generating viable plants
CC from the cell. The carotene metabolites are useful for increasing
CC zeaxanthin and beta-carotene, including oxygenated carotenoids. This
CC polynucleotide sequence represents an RT-PCR primer used in the process
CC for the expression of the introduced proteins and endogenous carotenoid
CC genes of the invention.
XX
SQ Sequence 19 BP; 6 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 435 GAGGAGATGATTTTAGCTG 453
Db 1 GAGGAGAAGAGTTTAGCTG 19

RESULT 66
ADF50077/c
ID ADF50077 standard; RNA; 19 BP.
XX
AC ADF50077;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human BCL2 siNA upper sequence SEQ ID NO:805.
XX
KW ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
OS Homo sapiens.
XX
PN WO2003070969-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-US004908.
XX


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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Beigelman L;
PI
XX WPI; 2003-712622/67.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
PS Example 3; SEQ ID NO 805; 148pp; English.
XX
CC The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 19 BP; 8 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ACAGTGCATTGAATTTCTT 500
Db ||||| ||||| ||||| |||||
19 ACAGTGGATTGCATTTCTT 1

RESULT 67
ADF49663
ID ADF49663 standard; RNA; 19 BP.
XX
AC ADF49663;
XX
XX 12-FEB-2004 (first entry)
DT
XX Human BCL2 siNA upper sequence SEQ ID NO:391.
DE
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
OS
XX WO2003070969-A2.
PN
XX 28-AUG-2003.
PD
XX 18-FEB-2003; 2003WO-US004908.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Beigelman L;
PI
XX WPI; 2003-712622/67.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
PS Example 3; SEQ ID NO 805; 148pp; English.
XX
CC The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 19 BP; 8 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ACAGTGCATTGAATTTCTT 500
Db ||||| ||||| ||||| |||||
19 ACAGTGGATTGCATTTCTT 1

RESULT 67
ADF49663
ID ADF49663 standard; RNA; 19 BP.
XX
AC ADF49663;
XX
XX 12-FEB-2004 (first entry)
DT
XX Human BCL2 siNA upper sequence SEQ ID NO:391.
DE
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
OS
XX WO2003070969-A2.
PN
XX 28-AUG-2003.
PD
XX 18-FEB-2003; 2003WO-US004908.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Beigelman L;
PI
XX WPI; 2003-712622/67.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
PS Example 3; SEQ ID NO 805; 148pp; English.
XX
CC The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 19 BP; 8 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
```

```
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Beigelman L;
PI
XX WPI; 2003-712622/67.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
PS Example 3; SEQ ID NO 391; 148pp; English.
XX
CC The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 19 BP; 4 A; 3 C; 4 G; 0 T; 8 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 95;
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 482 ACAGTGCATTGAATTTCTT 500
Db ||||| ||||| ||||| |||||
1 ACAGUGGAUUGCAUUUCUU 19

RESULT 68
AAT36558
ID AAT36558 standard; DNA; 20 BP.
XX
AC AAT36558;
XX
XX 10-FEB-1997 (first entry)
DT
XX Campylobacter fetus specific probe.
DE
XX c-gtp; guanosine 5'-triphosphatase; GTPase; enzyme; probe;
KW GTP-binding protein; primer; detection; differentiation; microorganism;
KW biological sample; thermophilic; veterinary; Campylobacter; jejuni; coli;
KW lari; upsaliensis; human; pathogen; diarrhoea; infection; fetus;
KW hyointestinalis; mucosalis; ss.
XX
OS Synthetic.
XX WO9613608-A2.
PN
XX 09-MAY-1996.
PD
XX 30-OCT-1995; 95WO-EP004264.
PF
XX 28-OCT-1994; 94EP-00870171.
PR
XX (INNO-) INNOGENETICS NV.
PA (DELF-) DELFT DIAGNOSTIC LAB BV.
XX
XX Giesendorf B, Quint W, Van Doorn L;
PI
XX WPI; 1996-239513/24.
DR
XX GTPase gene family sequences derived from Campylobacter species - for use
PT
```

PT in the detection and differentiation of thermophilic and veterinary
PT species of Campylobacter.
XX
PS Claim 21; Page 62; 104pp; English.
XX
CC The present sequence is a Campylobacter fetus c-gtp gene specific probe.
CC The c-gtp gene encodes a guanosine 5'-triphosphatase (GTPase) enzyme, or
CC GTP-binding protein. The gene can be used in the prepn. of probes and
CC primers, i.e. the present sequence, for the detection and differentiation
CC of microorganisms in biological samples. Thermophilic and veterinary
CC Campylobacter sp. can be detected with probes or primers derived from the
CC c-gtp-1 and c-gtp-2 gene families, respectively. Thermophilic
CC Campylobacter sp. include C. jejuni, C. coli, C. lari and C. upsaliensis,
CC which are human pathogens involved in diarrhoea causing infections.
CC Veterinary Campylobacter sp., encompass sp. which are important in
CC veterinary infections, e.g. C. fetus, C. hyointestinalis and C. mucosalis
XX
SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 TAGAATGCAGAAATCTGAA 949
Db ||| ||||| ||||| |||||
2 TAGCAATGCAGAAATCTGCA 20

RESULT 69
ADG37263
ID ADG37263 standard; DNA; 20 BP.
XX
AC ADG37263;
XX
DT 26-FEB-2004 (first entry)
XX
DE Fox specific PCR primer #2.
XX
KW fur textile; animal fur; ss; PCR; primer; fox.
XX
OS Canidae.
XX
PN JP2003204798-A.
XX
PD 22-JUL-2003.
XX
PF 31-OCT-2002; 2002JP-00317866.
PR 31-OCT-2001; 2001JP-00334739.
XX
PA (NIBO-) ZH NIPPON BOSEKI KENSA KYOKAI.
XX
DR WPI; 2003-819736/77.
XX
PT Identifying fur textiles involves amplifying DNA fragment specific for
PT each animal fur, and analyzing amplified DNA.
XX
PS Claim 1; SEQ ID NO 2; 9pp; Japanese.
XX
CC The invention relates to a method of identifying textiles of fur,
CC comprising amplifying DNA fragment specific for each animal fur, and
CC analysing amplified DNA. The method is useful for identifying fur
CC textiles. The method effectively distinguishes the origin of animal fur.
CC The present sequence represents a fox specific PCR primer.
XX
SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 791 GTGCTTGAGAGGCAGATA 809
||| || ||||| ||||| |||||

Db 2 GTGCATGAAGAGGCAGATA 20

RESULT 70
ADG86812
ID ADG86812 standard; DNA; 20 BP.
XX
AC ADG86812;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PPAR antisense oligonucleotide ISIS 136891.
XX
KW Human; ss; PPAR delta; peroxisome proliferative activated receptor delta;
KW antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer;
KW osteoporosis; diabetes; endocrine disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages and all cytidines are 5
FT -methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
XX
PN US2003224514-A1.
XX
PD 04-DEC-2003.
XX
PF 31-MAY-2002; 2002US-00160807.
XX
PR 31-MAY-2002; 2002US-00160807.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde W, Freier SM, Watt AT;
XX
DR WPI; 2004-022078/02.
XX
PT New antisense oligonucleotides of 8-80 nucleobases, useful for treating
PT cancer, diabetes, osteoporosis or various endocrine disorders.
XX
PS Claim 1; SEQ ID NO 48; 155pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising 8-80
CC nucleobases in length targeted to the coding region of a nucleic acid
CC molecule encoding PPAR-delta (peroxisome proliferative activated receptor
CC delta), where the antisense compound inhibits the expression of the PPAR-
CC delta and has any of the 66 sequences of 20 amino acids fully defined in
CC the specification. Also included are a compound of 8-80 nucleobases in
CC length that specifically hybridises with at least an 8-nucleobase portion
CC of a preferred target region on a nucleic acid molecule encoding PPAR-
CC delta and a composition comprising the antisense oligonucleotide and a
CC carrier. The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage (preferably a phosphorothioate linkage), at least
CC one sugar moiety (preferably 2'-O-methoxyethyl moiety) and at least one
CC modified nucleobase (which is a 5-methyl cytosine). The antisense
CC compounds are useful for treating cancer, osteoporosis, diabetes or
CC various endocrine disorders. The Human PPAR delta gene is located on
CC chromosome 6p21. The present sequence is an antisense oligonucleotide of
CC the invention targeting human PPAR delta.
XX
SQ Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGGATGCTTGGAGA 801
Db 1 TTGTAGATGCTTGGAGA 19
||| |||||||||

RESULT 71
ADG86960/c
ID ADG86960 standard; cDNA; 20 BP.
XX
AC ADG86960;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PPAR antisense oligonucleotide target sequence #22.
XX
KW Human; ss; PPAR delta; peroxisome proliferative activated receptor delta;
KW antisense gene therapy; cytostatic; osteopathic; antidiabetic; cancer;
KW osteoporosis; diabetes; endocrine disorder.
XX
OS Homo sapiens.
XX
PN US2003224514-A1.
XX
PD 04-DEC-2003.
XX
PF 31-MAY-2002; 2002US-00160807.
XX
PR 31-MAY-2002; 2002US-00160807.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde W, Freier SM, Watt AT;
XX
DR WPI; 2004-022078/02.
XX
PT New antisense oligonucleotides of 8-80 nucleobases, useful for treating
PT cancer, diabetes, osteoporosis or various endocrine disorders.
XX
PS Example 16; SEQ ID NO 196; 155pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising 8-80
CC nucleobases in length targeted to the coding region of a nucleic acid
CC molecule encoding PPAR-delta (peroxisome proliferative activated receptor
CC delta), where the antisense compound inhibits the expression of the PPAR-
CC delta and has any of the 66 sequences of 20 amino acids fully defined in
CC delta and has any of the 66 sequences of 20 amino acids fully defined in
CC the specification. Also included are a compound of 8-80 nucleobases in
CC length that specifically hybridises with at least an 8-nucleobase portion
CC of a preferred target region on a nucleic acid molecule encoding PPAR-
CC delta and a composition comprising the antisense oligonucleotide and a
CC carrier. The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage (preferably a phosphorothioate linkage), at least
CC one sugar moiety (preferably 2'-O-methoxyethyl moiety) and at least one
CC modified nucleobase (which is a 5-methyl cytosine). The antisense
CC compounds are useful for treating cancer, osteoporosis, diabetes or
CC various endocrine disorders. The Human PPAR delta gene is located on
CC chromosome 6p21. The present sequence is a human PPAR delta cDNA target
CC sequence for the antisense oligonucleotides of the invention.
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGGATGCTTGGAGA 801
Db 20 TTGTAGATGCTTGGAGA 2
||| |||||||||

RESULT 72
ADJ61530/c
ID ADJ61530 standard; DNA; 20 BP.
XX
AC ADJ61530;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to ILSR-X61176 #222.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCRL1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 2386; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 624 GAGTTTATTCTCAGCAAA 642
||| |||||||

Db 20 GACTTTATCCTCAGCAAA 2
||| |||||||

RESULT 73
ADJ24889
ID ADJ24889 standard; DNA; 20 BP.
XX
AC ADJ24889;

XX 20-MAY-2004 (first entry)
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 3287.
DE
XX Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
XX WO2004009541-A2.
PN
XX 29-JAN-2004.
PD
XX 18-JUL-2003; 2003WO-US022410.
PF
XX 19-JUL-2002; 2002US-0397106P.
PR
XX (PHAA) PHARMACIA CORP.
PA
XX Bhat BG;
PI
XX WPI; 2004-132912/13.
DR
XX New antisense oligonucleotide for modulating endothelial lipase
expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
high density lipoprotein or cardiovascular disorders.
PT
PS Claim 3; SEQ ID NO 3287; 1007pp; English.
XX The present invention relates to antisense oligonucleotides (ADJ21603-
ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
(ADJ25517), where the antisense oligonucleotide specifically hybridises
with and inhibits the expression of EL. The antisense oligonucleotides
are useful for modulating the expression of endothelial lipase in cells
or tissues to treat diseases associated with EL expression, such as
dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
disorder or metabolic syndrome X. In addition, the oligonucleotides are
used for diagnostics, prophylaxis, or as research reagents or kits.
CC
SQ Sequence 20 BP; 3 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 19 GCCCGGGCGGTGGCAGGAA 37
Db 2 GCCCGGGCGGTGGCAGGGA 20
RESULT 74
ADJ23864
ID ADJ23864 standard; DNA; 20 BP.
XX
AC ADJ23864;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2262.
XX Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW

KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
XX WO2004009541-A2.
PN
XX 29-JAN-2004.
PD
XX 18-JUL-2003; 2003WO-US022410.
PF
XX 19-JUL-2002; 2002US-0397106P.
PR
XX (PHAA) PHARMACIA CORP.
PA
XX Bhat BG;
PI
XX WPI; 2004-132912/13.
DR
XX New antisense oligonucleotide for modulating endothelial lipase
expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
high density lipoprotein or cardiovascular disorders.
PT
PS Claim 3; SEQ ID NO 2262; 1007pp; English.
XX The present invention relates to antisense oligonucleotides (ADJ21603-
ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
(ADJ25517), where the antisense oligonucleotide specifically hybridises
with and inhibits the expression of EL. The antisense oligonucleotides
are useful for modulating the expression of endothelial lipase in cells
or tissues to treat diseases associated with EL expression, such as
dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
disorder or metabolic syndrome X. In addition, the oligonucleotides are
used for diagnostics, prophylaxis, or as research reagents or kits.
CC
SQ Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 CCGGGCCGTGGCAGGAAGC 39
Db 1 CCGGGCCGTGGCAGGGAGC 19
RESULT 75
ADL34750
ID ADL34750 standard; DNA; 20 BP.
XX
AC ADL34750;
XX
DT 17-JUN-2004 (first entry)
XX
DE Antisense oligonucleotide ISIS 136891.
XX
KW antisense; PPAR-delta; human; hybridisation; inhibitor;
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
KW hyperproliferative disorder; cancer; cytostatic; gene therapy; ss;
KW primer.
XX
OS Synthetic.
XX

PN US2004063129-A1.
XX
XX
PD 01-APR-2004.
XX
XX
PF 05-SEP-2003; 2003US-00655847.
XX
XX
PR 31-MAY-2002; 2002US-00160807.
XX
XX
PA (GAAR/) GAARDE W.
PA (FREI/) FREIER S M.
PA (WATT/) WATT A T.
PI Gaarde W, Freier SM, Watt AT;
XX
XX
DR WPI; 2004-282460/26.
XX
XX
PT New antisense oligonucleotide, having a sequence targeted to a nucleic
PT acid encoding PPAR-delta, useful for preparing a composition for treating
PT hyperproliferative disorder, e.g., cancer.
XX
PS Example 15; SEQ ID NO 48; Opp; English.
XX
XX
CC This invention describes novel antisense oligonucleotides targeted to a
CC nucleic acid encoding PPAR-delta, which specifically hybridise to and
CC inhibit expression of PPAR-delta. The oligonucleotide specifically
CC hybridises with at least an 8-nucleobase portion of an active site on the
CC nucleic acid molecule encoding the PPAR-delta and comprises at least one
CC modified internucleoside linkage, which is a 2'-O-methoxyethyl sugar
CC least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar
CC moiety or at least one modified nucleobase, which is a 5-methylcytosine.
CC The antisense oligonucleotides are useful for preparing a composition for
CC treating hyperproliferative disorders, e.g., cancer. The oligonucleotides
CC of the invention have cytostatic activity and can be used for gene
CC therapy.
XX
SQ Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGGATGTGCTTGGAGA 801
DB 1 TTGTAGATGTGCTTGGAGA 19

RESULT 76
ADL34898/c
ID ADL34898 standard; DNA; 20 BP.
XX
AC ADL34898;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human PPAR-delta target site ID 50011.
XX
XX
KW antisense; PPAR-delta; human; hybridisation; inhibitor;
KW phosphorothioate linkage; 2'-O-methoxyethyl sugar; 5-methylcytosine;
KW hyperproliferative disorder; cancer; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX
PN US2004063129-A1.
XX
XX
PD 01-APR-2004.
XX
XX
PF 05-SEP-2003; 2003US-00655847.
XX
XX
PR 31-MAY-2002; 2002US-00160807.
XX
XX
PA (GAAR/) GAARDE W.
PA (FREI/) FREIER S M.
PA (WATT/) WATT A T.

XX Gaarde W, Freier SM, Watt AT;
PI
XX
XX
DR WPI; 2004-282460/26.
XX
XX
PT New antisense oligonucleotide, having a sequence targeted to a nucleic
PT acid encoding PPAR-delta, useful for preparing a composition for treating
PT hyperproliferative disorder, e.g., cancer.
XX
XX
PS Example 16; SEQ ID NO 196; Opp; English.
XX
XX
CC This invention describes novel antisense oligonucleotides targeted to a
CC nucleic acid encoding PPAR-delta, which specifically hybridise to and
CC inhibit expression of PPAR-delta. The oligonucleotide specifically
CC hybridises with at least an 8-nucleobase portion of an active site on the
CC nucleic acid molecule encoding the PPAR-delta and comprises at least one
CC modified internucleoside linkage, which is a phosphorothioate linkage, at
CC least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar
CC moiety or at least one modified nucleobase, which is a 5-methylcytosine.
CC The antisense oligonucleotides are useful for preparing a composition for
CC treating hyperproliferative disorders, e.g., cancer. The oligonucleotides
CC of the invention have cytostatic activity and can be used for gene
CC therapy.
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 783 TTGGGGATGTGCTTGGAGA 801
DB 20 TTGTAGATGTGCTTGGAGA 2

RESULT 77
ADO46920/c
ID ADO46920 standard; DNA; 20 BP.
XX
AC ADO46920;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #2286.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
XX
PN US2004049022-A1.
XX
XX
PD 11-MAR-2004.
XX
XX
PF 25-JUL-2003; 2003US-00627930.
XX
XX
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.

PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-293804/27.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Claim 2; SEQ ID NO 2386; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 624 GAGTTTATTCTCAGCAAA 642
Db 20 GACTTTTATCCTCAGCAAA 2

RESULT 78
ABV76832/c
ID ABV76832 standard; DNA; 21 BP.
XX
AC ABV76832;
XX
DT 12-FEB-2003 (first entry)
XX
DE Control PCR primer used to amplify a beta-actin cDNA fragment.
XX
KW Arthritic condition; CD21L; lymphotoxin-beta; chemoattractant; arthritis;
KW beta-actin; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200280010-A1.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-US008856.
XX
PR 23-MAR-2001; 2001US-00816814.
XX

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Goronzy JJ, Weyand CM;
XX
DR WPI; 2003-058450/05.
XX
PT Determining the severity of arthritic conditions, e.g. rheumatoid
PT arthritis, in a mammal or human by detecting whether a sample contains
PT elevated levels of marker(s), e.g. CD21L polypeptides or lymphotoxin-beta
PT polypeptides.
XX
PS Example 2; Page 12; 27pp; English.
XX
CC The specification describes a method for determining the severity of an
CC arthritic condition in a mammal. The method comprises determining whether
CC or not a sample from the mammal contains at least 1 marker (e.g. an
CC elevated level of a CD21L polypeptide, an elevated level of a lymphotoxin
CC -beta polypeptide, or an elevated level of a chemoattractant
CC polypeptide). The presence of the marker indicates that the arthritis
CC condition is severe. The method is useful for diagnosing the severity of
CC an arthritis condition (e.g. rheumatoid arthritis) in a mammal,
CC particularly a human. Control PCR primers ABV76832-33 were used to
CC amplify a beta-actin cDNA fragment from a synovial tissue sample. The
CC primers were used in the method of the invention
XX
SQ Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 99;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 GCCGGAAGCAGCCGCGCC 56
Db 21 GCTGGAAGCAGCCGTGGCC 3

RESULT 79
ADA73990/c
ID ADA73990 standard; DNA; 21 BP.
XX
AC ADA73990;
XX
DT 20-NOV-2003 (first entry)
XX
DE PCR primer #1 for DNA encoding human beta-actin.
XX
KW Rheumatoid arthritis condition; RA; cytokine; interleukin-1 beta;
KW IL-1beta; interleukin-4; IL-4; interleukin-10; IL-10; interferon-gamma;
KW IFN-gamma; tumour necrosis factor-alpha; TNF-alpha;
KW transforming growth factor-beta; TGF-beta; diffuse; follicular;
KW granulomatous; human; beta-actin; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US6555320-B1.
XX
PD 29-APR-2003.
XX
PF 01-SEP-1999; 99US-00387467.
XX
PR 01-SEP-1998; 98US-0098718P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Goronzy JJ, Weyand CM;
XX
DR WPI; 2003-687206/65.
XX
PT Evaluating rheumatoid arthritis condition in patient, by comparing
PT cytokine levels in sample from patient to reference levels to obtain
PT information about condition, and classifying condition based on the
PT information.
XX

Fri Aug 19 11:00:00 2005

PS Example 1; Col 9; 25pp; English.

XX The present invention relates to a method for evaluating rheumatoid

CC arthritis (RA) condition in a patient. The method involves determining

CC the level of cytokines (e.g. interleukin-1 (IL-1) beta, interleukin-4 (IL

CC -4), interleukin-10 (IL-10), interferon gamma, tumour necrosis factor-

CC alpha (TNF-alpha), and transforming growth factor-beta (TGF-beta)) within

CC the sample from a patient, comparing the level to reference levels to

CC obtain information about the RA condition, and classifying the RA

CC condition as being or not being diffuse, follicular or granulomatous

CC condition based on information. The method is useful for classifying a RA

CC condition as diffuse, follicular, or granulomatous, and for determining

CC if an individual suffering from a RA condition will develop severe

CC disease. The present sequence represents a PCR primer used in the

CC examples of the present invention.

XX

SQ Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 21;

Best Local Similarity 89.5%; Pred. No. 99;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 GCCGGAAGCAGCCGCGGCC 56

Db 21 GCTGGAAGCAGCCGTCGCC 3

RESULT 80

AAS23701/c

ID AAS23701 standard; DNA; 22 BP.

XX

AC AAS23701;

XX

DT 04-DEC-2001 (first entry)

XX

DE Primer A #15 used as probe for identifying C. albicans GRACE strain.

XX

XX Gene identification; essential gene; GRACE; pathogenic fungus;

KW gene replacement and conditional expression; fungal infection; probe; ss.

XX

OS Candida albicans.

OS Synthetic.

XX

PN WO200160975-A2.

XX

PD 23-AUG-2001.

XX

PF 20-FEB-2001; 2001WO-US005551.

XX

PR 18-FEB-2000; 2000US-0183534P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Roemer T, Jiang B, Boone C, Bussey H;

XX

XX WPI; 2001-489080/53.

DR

XX Identifying genes essential to fungal metabolisms and identifying

PT potential therapeutic agents that target these genes.

XX

PS Disclosure; Page 303; 324pp; English.

XX

CC The present invention relates to novel methods for constructing fungal

CC strains useful for identification and validation of gene products as

CC targets for therapeutic agents, for creating a collection of identified

CC essential genes, and screening assays for the discovery of new drugs. The

CC invention provides the GRACE (gene replacement and conditional

CC expression) method for the construction of mutant organisms referred to

CC as GRACE strains of the organism. The invention can be applied to any

CC organism, particularly a pathogenic fungus e.g. Candida albicans,

CC Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful

CC to identify agents that may be used in the treatment of fungal

CC infections. AAS23687-AAS23747 represent primers A #1-61 used as probes

CC for identifying C. albicans GRACE strains

XX

SQ Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;

Best Local Similarity 89.5%; Pred. No. 1e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 337 TCGTGTGGCTGTGATCAAA 355

Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 81

ABZ29880/c

ID ABZ29880 standard; DNA; 22 BP.

XX

AC ABZ29880;

XX

DT 30-JAN-2003 (first entry)

XX

DE Candida albicans GRACE strain PCR primer SEQ ID NO 4031.

XX

KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;

KW signal transduction; DNA replication; cell division; growth;

KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.

XX

OS Candida albicans.

XX

PN WO200253728-A2.

XX

PD 11-JUL-2002.

XX

PF 26-DEC-2001; 2001WO-US049486.

XX

PR 29-DEC-2000; 2000US-0259128P.

PR 20-FEB-2001; 2001US-00792024.

PR 22-AUG-2001; 2001US-0314050P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX

XX WPI; 2002-566694/60.

CC Constructing strains for identifying gene products as effective targets

CC for therapeutic intervention, by inactivating in the strain one allele of

CC a gene and placing other allele of the gene under conditional expression.

PS Claim 36; SEQ ID NO 4031; 167pp + Sequence Listing; English.

XX

CC The invention relates to constructing (M1) a strain of diploid fungal

CC cells in which both alleles of a gene are modified, comprising modifying

CC one allele by insertion or replacement by a cassette having an

CC expressible selectable marker and modifying other allele by

CC recombination, of a promoter replacement fragment with a heterologous

CC promoter, so that expression of the second allele is regulated by the

CC promoter. (M1) is useful for constructing a strain of diploid fungal

CC cells in which both alleles of a gene are modified. The diploid fungal

CC cells having both alleles modified are useful for identifying a gene that

CC is essential to the survival or growth of a fungus, a gene that

CC contributes to the virulence and/or pathogenicity of a fungus, a gene

CC that contributes to the resistance of a diploid fungus to an antifungal

CC agent, an antifungal agent that inhibits the growth of a diploid fungus

CC and for identifying a therapeutic agent for treatment of a mammalian

CC disease. (M1) is useful for identifying a compound which modulates the

CC activity of a gene product, preferably enzymatic activity, carbon

CC compound catabolism, biosynthetic, transporter, transcriptional,

CC translational, signal transduction, DNA replication and cell division

CC activity. The method is useful for identifying a compound having the

CC ability to inhibit growth or proliferation of C. albicans cells and for

CC treating infection by C. albicans. The present sequence is that of a PCR

CC primer used in the method of the invention. Note: The sequence data for

CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 22 BP; 9 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 337 TCGTGTGGCTGTGATCAAA 355
Db 19 TCGTGTGGCTGTCTCAAA 1

RESULT 82
AAV73536
ID AAV73536 standard; DNA; 20 BP.
XX
AC AAV73536;
XX
DT 22-MAR-2000 (first entry)
XX
DE H. pylori vacA probe P4S1 DNA.
XX
KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
KW S region; Sla; Slb; Slc; S2; M region; M1; M2; ss.
XX
OS Helicobacter pylori.
XX
PN WO9816658-A2.
XX
PD 23-APR-1998.
XX
PF 10-OCT-1997; 97WO-EP005614.
XX
PR 16-OCT-1996; 96EP-00870131.
PR 09-SEP-1997; 97EP-00870133.
XX
PA (INNO-) INNOGENETICS NV.
PA (DDL-) DDL BV.
XX
PI Quint W, Van Doorn L;
XX
DR WPI; 1998-251300/22.
XX
PT Method for detecting and/or typing Helicobacter pylori strains -
PT comprises use of primers and probes based on vacA and cagA gene.
XX
PS Claim 3; Page 46; 122pp; English.
XX
CC This invention describes a novel method for the detection and/or typing
CC of Helicobacter pylori strains present in a sample using PCR primers and
CC probes to detect regions of the vacuolating toxin (vacA) gene and other
CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
CC gene. The method allows the typing and allele-specific detection of a
CC strain according to the VDG alleles present in that particular H. pylori
CC strain. The virulence determinant genes are the genetic elements involved
CC in enabling, determining, and marking the infectivity and/or
CC pathogenicity of the H. pylori strain. The method provides a way of
CC detecting H. pylori strains in a sample with respect to the development
CC of chronic active gastritis, gastric and duodenal ulcers, gastric
CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
CC determining eradication therapy. AAV73508-V73546 represent PCR primers
CC and probes used in the detection of the H. pylori vacA and cagA genes.
CC The primers and probes are used especially to detect the vacA S regions
CC Sla/b/c and S2 and the M regions M1 and M2 which are represented in
CC AAV73547-V73785
XX
SQ Sequence 20 BP; 2 A; 1 C; 7 G; 8 T; 0 U; 2 Other;

Query Match 1.4%; Score 15.6; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 103 CTTCAGTGGGGCTATTGG 120
Db 2 CTTTAGTRGGGYTATTGG 19

RESULT 83
ADH42586
ID ADH42586 standard; DNA; 22 BP.
XX
AC ADH42586;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human nucleic acid NOVX gene probe Ag650 forward primer.
XX
KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003102159-A2.
XX
PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.
PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.
PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 07-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.

Fri Aug 19 11:00:00 2005

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PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 12-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 13-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VV, Herrmann JL, Ji W, Kekuda R;
PI Khrantsov NV, Larochele WJ, McQueeney K, Mezzick AJ, Miller CE;
PI Maclachlan T, Malyankar UM, McQueeney K, Peyman JA, Qian X, Rastelli L;
PI Millet I, Padigaru M, Patturajan M, Shimkets RA, Smithson G;
PI Rieger DK, Rothenberg ME, Shenoy SG, Vernet CAM, Voss EZ;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Zhong H;
PI Wolenc AR, Zhong M, Zhong H;
XX
XX WPI; 2004-053467/05.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 1139; 1503pp; English.
XX
XX The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the forward primer used to amplify a probe to isolate the
CC nucleic acid sequences of the invention.
XX
SQ Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 478 GATTACAGTGCATTGAATTCT 499
Db 1 GTTTTCATTGCATTGCATTCT 22

RESULT 84
ADS75784
ID ADS75784 standard; DNA; 22 BP.
XX
AC ADS75784;
```

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XX 16-DEC-2004 (first entry)
DT
XX DNA molecule preparation method oligonucleotide primer #95.
DE
XX ss; primer; DNA preparation; adaptor.
KW
XX Synthetic.
OS
XX WO2004081183-A2.
PN
XX 23-SEP-2004.
PD
XX 08-MAR-2004; 2004WO-US006982.
PF
XX 07-MAR-2003; 2003US-0453071P.
PR
XX (RUBI-) RUBICON GENOMICS INC.
PA
XX Pinter J, Kurihara T, Sleptsova I, Bruening E, Ziehler W;
PI Makarov VL;
XX
XX WPI; 2004-668947/65.
DR
XX
XX Preparing a DNA molecule comprises attaching an adaptor having at least
PT one known sequence and a nonblocked 3' end to the ends of the modified
PT DNA fragments to produce adaptor-linked fragments.
PT
XX Disclosure; SEQ ID NO 95; 205pp; English.
PS
XX The invention relates to a method of preparing a DNA molecule by
XX attaching an adaptor having at least one known sequence and a nonblocked
CC 3' end to the ends of the modified DNA fragments to produce adaptor-
CC linked fragments, where the 5' end of the modified DNA is attached to the
CC nonblocked 3' end of the adaptor, leaving a nick site between the
CC juxtaposed 3' end of the DNA and a 5' end of the adaptor. The method
CC comprises: (a) obtaining at least one DNA molecule; (b) randomly
CC fragmenting the DNA molecule to produce DNA fragments; (c) modifying the
CC ends of the DNA fragments to provide attachable ends; (d) attaching an
CC adaptor having at least one known sequence and a nonblocked 3' end to
CC the ends of the modified DNA fragments to produce adaptor-linked
CC fragments, where the 5' end of the modified DNA is attached to the
CC nonblocked 3' end of the adaptor, leaving a nick site between the
CC juxtaposed 3' end of the DNA and a 5' end of the adaptor; (e) extending
CC the 3' end of the modified DNA from the nick site; and (f) amplifying
CC the adaptor-linked fragments. This sequence corresponds to an
CC oligonucleotide used in the method of the invention.
XX
SQ Sequence 22 BP; 2 A; 2 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 297 GAATTGTTGTTCTGCTTTGG 318
Db 1 GAATTTTGGTTTCTTGCTTTGG 22

RESULT 85
ADS08410
ID ADS08410 standard; DNA; 22 BP.
XX
AC ADS08410;
XX
DT 16-DEC-2004 (first entry)
XX
DE STS marker secondary targeted amplification primer, SEQ ID 93.
XX
XX Primer; PCR; ss.
XX
OS Synthetic.
XX
```

PN WO2004081225-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US006983.
XX
PR 07-MAR-2003; 2003US-0453060P.
XX
PA (RUBI-) RUBICON GENOMICS INC.
XX
PI Kamberov E, Sun T, Bruening E, Pinter J, Sleptsova I, Kurihara T;
XX Makarov VL;
DR WPI; 2004-677550/66.
XX
PT Preparing and amplifying a genome or a transcriptome comprises subjecting
PT the molecule/primer mixture to a polymerase.
XX
PS Example 25; SEQ ID NO 93; 208pp; English.
XX
CC The present invention relates to a method for preparing and amplifying a
CC genome, a transcriptome, or both, or a nucleic acid, e.g. DNA or RNA
CC molecule or a DNA molecule generated from at least one mRNA molecule. The
CC method comprises subjecting the DNA molecule/primer mixture or the RNA
CC molecule/primer mixture or the ssDNA molecule/primer mixture to a
CC polymerase, under conditions where the subjecting steps generate
CC molecules including all or part of the constant region at each end. The
CC present sequence was used to illustrate the method of the invention.
XX
SQ Sequence 22 BP; 2 A; 2 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 297 GAATGTTGTTTCTGCTTTGG 318
||||| ||||| |||||
Db 1 GAATTTGGTTTCTTGCTTTGG 22

RESULT 86
ABK18401
ID ABK18401 standard; RNA; 17 BP.
XX
AC ABK18401;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 1048.
XX
KW Human; hammerhead ribozyme; cytosstatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 78; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 958 CTGGACCCAGGACATTT 974
|:||||| |||||:::
Db 1 CUGGACUCAGGACAUUU 17

RESULT 87
ABT38549/c
ID ABT38549 standard; DNA; 17 BP.
XX
AC ABT38549;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4186.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.

XX
PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX
PS Disclosure; Page 523; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 838 GAAGCGCGGGTGGATC 854
Db 17 GAAGGCTGGGTGGATC 1

RESULT 88
ADB42880/c
ID ADB42880 standard; DNA; 17 BP.
XX
AC ADB42880;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #3203.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX

PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 406; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 838 GAAGCGCGGGTGGATC 854
Db 17 GAAGGCTGGGTGGATC 1

RESULT 89
AAZ77304
ID AAZ77304 standard; DNA; 18 BP.
XX
AC AAZ77304;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11660.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
XX
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX

DR WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
PT
XX
PS Claim 9; Page 2716; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 4 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 TTCAGTGGGGCTATTGG 120
Db ||||| ||||| ||||| ||||| |||||
2 TTCAATGGGGCTATTGG 18

RESULT 90
ADD24780/c
ID ADD24780 standard; DNA; 18 BP.
XX
AC ADD24780;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human CYP2D6 C100T mutant probe H154.
XX
KW diagnostic; pharmaceutical tolerance; side effect; drug; human;
KW allelic variability; polymorphism; phase I; phase II;
KW detoxification mechanism; PCR; primer; probe; NAT2; CYP2D6; CYP1A2;
KW CYP3A4; mEH; TPMT; MTHFR; paraoxonase; CYP2C9; CYP2C19; CYP2E1; DPD; ss.
XX
OS Homo sapiens.
XX
PN WO2003018837-A2.
XX
PD 06-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-EP009386.
XX
PR 24-AUG-2001; 2001DE-01040651.
PR 30-APR-2002; 2002DE-01019373.
XX
PA (ADNA-) ADNAGEN AG.
XX
PI Waschuetza S, Schnakenberg E, Lustig M;
XX
DR WPI; 2003-290079/28.
XX
PT Diagnostic kit, useful for assessing a subject's tolerance of drugs,
PT comprises reagents for determining alleles of genes encoding
PT detoxification enzymes.
XX
PS Claim 6; Page 13; 156pp; German.
XX
CC This invention describes a novel diagnostic kit for determining tolerance

CC of pharmaceuticals in humans by determining allelic variability of at
CC least two polymorphisms of a human enzyme involved in phase I and/or II
CC of the detoxification mechanism in a blood, tissue or other human sample,
CC where tolerance is determined from presence or absence of alleles. The
CC kit comprises two pairs of oligonucleotide primers, in which each pair
CC amplifies, by PCR, part of a gene for a human detoxification mechanism-
CC associated enzyme. The kit may also contain two further pairs of
CC oligonucleotides, serving as probes for detection of amplified DNA
CC segments, especially where the probes are complementary to a single
CC strand of one allele of the target gene. The probes are labelled with
CC fluorophores (LC-Red640 or LC-Red705 for 5'-labelling or fluorescein for
CC 3'-labelling) which generate a different signal in the hybridized and non
CC -hybridized condition. The enzymes detected include NAT2, CYP2D6, CYP1A2,
CC CYP3A4, mEH, TPMT, MTHFR, paraoxonase, CYP2C9, CYP2C19, CYP2E1 or DPD.
CC The kit is used to determine an individual's tolerance of a particular
CC drug, to establish a suitable dose and/or to predict if a subject will
CC show side-effects to a drug. The kit provides minimally invasive, safe
CC and reliable determination of the metabolic capacity of phase I and/or II
CC enzymes at the molecular level. This sequence represents a probe used in
CC the kit of the invention.
XX
SQ Sequence 18 BP; 1 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GCCCGGGCCGTGGCAGG 35
Db ||||| ||||| ||||| ||||| |||||
17 GCCCGGGCAGTGGCAGG 1

RESULT 91
AAQ81302/c
ID AAQ81302 standard; mRNA; 19 BP.
XX
AC AAQ81302;
XX
DT 25-MAR-2003 (revised)
DT 07-SEP-1995 (first entry)
XX
DE Ribozyme target sequence in TGF-beta mRNA (bases 2447-2465).
XX
KW Target site; ribozyme; hammerhead; hairpin; hepatitis delta virus;
KW group 1 intron; RNaseP RNA motif; transforming growth factor-beta;
KW TGF-beta; fibrous; connective; tissue disease; TGF-alpha; inhibin;
KW epidermal growth factor; EGF; activin; amphiregulin; insulin;
KW bone morphogenic protein; fibroblast growth factor; relaxin; ss.
XX
OS Homo sapiens.
XX
PN WO9429452-A2.
XX
PD 22-DEC-1994.
XX
PF 02-JUN-1994; 94WO-US006331.
XX
PR 09-JUN-1993; 93US-00074343.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG;
XX
DR WPI; 1995-051612/07.
XX
PT Enzymatic RNA molecule with, e.g. a hammerhead or hairpin motif - cleaves
PT mRNA associated with fibrous or connective tissue disease, and is useful
PT for treatment or prophylaxis of such diseases.
XX
PS Claim 3; Page 5; 63pp; English.
XX
CC The sequences (AAQ81238-304) represent the target sites where a ribozyme
CC (hammerhead, hairpin, hepatitis delta virus, group 1 intron or RNaseP RNA

Fri Aug 19 11:00:00 2005

CC motif) cleaves the mRNA of the transforming growth factor-beta (TGF-beta)
CC gene. This sequence corresponds to bases 2447-2465 of the TGF-beta mRNA.
CC The ribozymes can also target the mRNAs of genes associated with the
CC development or maintenance of fibrous or connective tissue disease in
CC order to prevent or treat these diseases. Such genes include TGF-alpha or
CC beta, epidermal growth factor, inhibitors, activins, amphiregulin, bone
CC morphogenic proteins, fibroblast growth factors a and b, insulin growth
CC factor 1 or 2, insulin or relaxin. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 19 BP; 6 A; 3 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1077 CACTTAACCTCTCTGGG 1093
Db 18 CCCTTAACCTCTCTGGG 2

RESULT 92
AAA85723/c
ID AAA85723 standard; DNA; 19 BP.
XX
AC AAA85723;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin B1 ribozyme binding site #52.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX WO200032765-A2.
PN
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 96; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 5 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 790 TGTGCTGGAGGGCAG 806
Db 18 TGGGCTTGGAGGGCAG 2

RESULT 93
AAH60885/c
ID AAH60885 standard; DNA; 19 BP.
XX
AC AAH60885;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cyclin B1 ribozyme binding site SEQ ID NO:3309.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 312; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscikling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 5 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 790 TGTGCTGGAGGGCAG 806

Db 18 TGGCTTGGAGAGGCAG 2

RESULT 94
AAT50899/c
ID AAT50899 standard; DNA; 20 BP.
XX
AC AAT50899;
XX
DT 26-AUG-1997 (first entry)
XX
DE Probe #13 for interleukin-6 receptor.
XX
KW Probe; interleukin-6 receptor; IL-6R; cytokine; cellular proliferation;
KW transmembrane glycoprotein receptor; signal transducer; gp130; inhibitor;
KW IL-6; cancer; renal cell carcinoma; autoimmune disease; viral infection;
KW therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "optionally phosphorothioated"
XX
PN EP747386-A2.
XX
PD 11-DEC-1996.
XX
PF 07-JUN-1996; 96EP-00304315.
XX
PR 07-JUN-1995; 95US-00484666.
PR 07-JUN-1995; 95US-00486408.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Brown SJ, Dattagupta N, Naidu YM;
XX WPI; 1997-023093/03.
DR
XX Oligo:nucleotide(s) complementary to interleukin-6 receptor mRNA - for
PT treating proliferative diseases, e.g. cancer, auto-immune diseases or
PT viral infections.
XX
PS Claim 1; Page 16; 18pp; English.
XX
CC AAT50887-T50904 represent oligonucleotides of the invention. These
CC sequences are all probes for interleukin-6 receptor (IL-6R) mRNA. IL-6 is
CC one of the most well characterised of the cytokines. It functions through
CC interacting with at least two transmembrane glycoprotein receptor
CC molecules on the surface of target cells. The receptors are the IL-6R,
CC and the signal transducer gp130. Signal transduction by IL-6 involves the
CC concerted action of both IL-6R and gp130. IL-6 overproduction is
CC implicated in many different disease states, particularly in cellular
CC proliferation associated with these diseases. These sequences bind to the
CC IL-6R coding sequence, thereby inhibiting IL-6R production. The sequences
CC therefore inhibit the functioning of IL-6. These sequences can be used
CC for inhibiting disease-associated cellular proliferation. The
CC oligonucleotides are especially useful for treating cancer (e.g. renal
CC cell carcinoma), autoimmune diseases or viral infections. They can also
CC be used as probes for detecting IL-6 receptor mRNA, especially for
CC evaluating the effectiveness of drugs in reducing IL-6 receptor mRNA
CC levels
XX
SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 32 CAGGAAGCCGGAAGCAG 48

Db 18 CAGGAAGCCGGCAGCAG 2

RESULT 95
AAS97050
ID AAS97050 standard; DNA; 20 BP.
XX
AC AAS97050;
XX
DT 26-FEB-2002 (first entry)
XX
DE TRA-8 heavy and light chain RT-PCR primer H5SS2.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Crohn's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; PCR primer; chromosome 8p21-22;
KW TRA-8; ss.
XX
OS Synthetic.
XX WO200183560-A1.
XX
PN 08-NOV-2001.
XX
PD 02-MAY-2001; 2001WO-US014151.
XX
PF 02-MAY-2000; 2000US-0201344P.
PR
XX (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX WPI; 2002-049338/06.
DR
XX Novel antibody specific for tumor necrosis factor-related apoptosis-
PT inducing ligand, useful for inhibiting cell proliferation in cancer.
PT
XX Example 16; Page 72; 229pp; English.
PS
XX The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Crohn's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. This primer was used to isolate the mouse TRAIL TRA-8, a
CC ligand of the DR5 receptor and the TRAIL on which the humanised
CC antibodies of the invention are based
XX
SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 992 GTTGATGCACATGAA 1008

Db ||||||| |
 3 GTGTATGCACATGAGA 19

RESULT 96
AAL60465
ID AAL60465 standard; DNA; 20 BP.
XX
AC AAL60465;
XX
DT 27-AUG-2003 (first entry)
XX
DE Mouse anti-human DR5 antibody (TRA-8) cDNA cloning PCR primer, H5SS2.
XX
KW Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW Crohn's disease; diabetes mellitus; TRA-8 antibody; mouse; PCR; primer;
KW ss.
XX
OS Mus sp.
XX
PN WO2003037913-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035333.
XX
PR 01-NOV-2001; 2001US-0346402P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX
XX WPI; 2003-441350/41.
DR
XX
XX New purified antibody that specifically binds a TNF-related apoptosis-
PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT rheumatoid arthritis.
XX
PS Example 16; Page 77; 251pp; English.
XX
CC The invention relates to an antibody that specifically binds a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR4 or DR5. Antibodies of the invention are useful for selectively
CC inducing apoptosis in target cells expressing DR4, for inhibiting
CC proliferation of target cells expressing DR4 or for treating cancer,
CC inflammatory disease or autoimmune disease in a subject e.g. systemic
CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is a PCR primer used to clone
CC mouse anti-human DR5 antibody (TRA-8) cDNA
XX
SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
 1.4%; Score 15.4; DB 1; Length 20;
Query Match 94.1%; Pred. No. 1.1e+02;
Best Local Similarity 0; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 1; Indels 0; Gaps 0;

QY 992 GTGTATGCACATGAAA 1008
 ||||||| |
Db 3 GTGTATGCACATGAGA 19

RESULT 97
ADF87587/c
ID ADF87587 standard; DNA; 20 BP.
XX
AC ADF87587;

XX
DT 26-FEB-2004 (first entry)
XX
DE single nucleotide polymorphism detection primer, SEQ ID No 1170.
XX
KW human; single nucleotide polymorphism; microarray; side effect; ss;
KW primer; PCR.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2003235571-A.
XX
PD 26-AUG-2003.
XX
PF 12-FEB-2002; 2002JP-00034717.
XX
PR 12-FEB-2002; 2002JP-00034717.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2003-820454/77.
XX
XX Novel polynucleotide useful for detecting single nucleotide polymorphisms
PT in human gene.
XX
PS Claim 2; SEQ ID NO 1170; 704pp; Japanese.
XX
CC The invention relates to a novel polynucleotide isolated and purified
CC from a human gene having any one of 935 fully defined sequences as given
CC in specification, or a sequence having a base substitution. The invention
CC further relates to: an oligonucleotide containing single nucleotide
CC polymorphisms; a PCR primer set chosen from the combination of two DNA
CC fragments from any one of 1220 fully defined sequences as given in
CC specification; a labelling probe containing the SNP containing oligo; and
CC a microarray equipped with the SNP containing oligo. The isolated human
CC gene of the invention is useful for detecting the single nucleotide
CC polymorphisms in human gene. The isolated human gene is also useful for
CC diagnosis of disease and determination of side effect to a medical agent.
CC The isolated human gene is also effective in detecting single nucleotide
CC polymorphisms in a human gene. This polynucleotide sequence represents
CC one of the PCR primers used in the single nucleotide polymorphism
CC detection method of the invention.
XX
SQ Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 1.4%; Score 15.4; DB 1; Length 20;
Query Match 94.1%; Pred. No. 1.1e+02;
Best Local Similarity 0; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 1; Indels 0; Gaps 0;

QY 1018 GCATCATCATAGAGAAG 1034
 ||||||| |
Db 17 GCATCATCACAGAGAAG 1

RESULT 98
ADJ79773
ID ADJ79773 standard; DNA; 20 BP.
XX
AC ADJ79773;
XX
DT 06-MAY-2004 (first entry)
XX
DE TRA-8 antibody PCR primer #4.
XX
KW ss; primer; nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
KW antiallergic; antiinflammatory; antidiabetic; haemostatic;
KW neuroprotective; antiinfertility; immunosuppressive; dermatological;
KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
KW proliferation;
KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
KW TRAIL; synovial cell; lymphocyte; neutrophil;
KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;

KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
KW autoimmune hemolytic anemia; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anemia.
XX
OS Homo sapiens.
XX
XX
PN WO2003038043-A2.
XX
PD 08-MAY-2003.
XX
XX
PF 25-OCT-2002; 2002WO-US034420.
XX
PR 01-NOV-2001; 2001US-0346402P.
PR 24-JUN-2002; 2002US-0391478P.
XX
XX
PA (UABR-) UAB RES FOUND.
XX
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;
PI Lobuglio AF, Buchsbaum DJ;
XX
XX
DR WPI; 2003-421518/39.
XX
XX
PT Inducing apoptosis and inhibiting proliferation of target cells
PT expressing DR5, by contacting the target cell with an antibody that binds
PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
PT agents.
XX
PS Example 16; SEQ ID NO 9; 274pp; English.
XX
CC The invention relates to a method of selectively inducing apoptosis in
CC and inhibiting (M1) proliferation of target cells expressing DR5,
CC comprising contacting the cell with an antibody that specifically binds
CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC vitro apoptosis-inducing activity in the cell expressing DR5, and
CC contacting the cell with one or more therapeutic agents. M1 is useful for
CC inducing apoptosis in target cell and inhibiting proliferation of target
CC cell expressing DR5, where the target cell is an abnormally proliferating
CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC cell. M2 is useful for treating a subject having inflammatory and
CC autoimmune diseases. The inflammatory or autoimmune disease are selected
CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC primer used in the method of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 992 GTTGATGCACATGAAA 1008
Db 3 GTTGATGCACATGAGA 19

RESULT 99
ADJ25296
ID ADJ25296 standard; DNA; 20 BP.
XX
AC ADJ25296;
XX

DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3694.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX
PN WO2004009541-A2.
XX
XX
PD 29-JAN-2004.
XX
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Bhat BG;
XX
XX
DR WPI; 2004-132912/13.
XX
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 3694; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GCCCGGGCGGTGGCAGG 35
Db 4 GCCCGGGCGGTGGCAGG 20

RESULT 100
ADJ24880
ID ADJ24880 standard; DNA; 20 BP.
XX
XX
AC ADJ24880;
XX
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 3278.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;

KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
XX 29-JAN-2004.
XX
XX 18-JUL-2003; 2003WO-US022410.
XX
XX 19-JUL-2002; 2002US-0397106P.
XX (PHAA) PHARMACIA CORP.
PA
XX Bhat BG;
XX
XX WPI; 2004-132912/13.
DR
XX New antisense oligonucleotide for modulating endothelial lipase
XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
PT
XX
XX Claim 3; SEQ ID NO 3278; 1007pp; English.
PS
XX The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridizes
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
XX Sequence 20 BP; 2 A; 5 C; 12 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 19 GCCCGGGCGGTGCAGG 35
Db 3 GCCCGGGCGGTGCAGG 19
RESULT 101
ADP78840
ID ADP78840 standard; DNA; 20 BP.
XX
AC ADP78840;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2639.
XX
KW GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..4

FT /*tag= a
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT modified_base 17..20
FT /*tag= b
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
XX
PN WO2004035763-A2.
XX
XX 29-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US033332.
XX
XX 17-OCT-2002; 2002US-0419268P.
XX (PHAA) PHARMACIA CORP.
PA
XX Broschat KO, Crosby SD;
PI
XX WPI; 2004-348453/32.
DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
PT ischemia/reperfusion injury.
PT
XX
XX Claim 4; SEQ ID NO 2639; 175pp; English.
PS
XX The present invention relates to a compound which specifically hybridizes
CC with a nucleic acid molecule encoding GFAT, and inhibits the expression
CC of GFAT. Specifically claimed are antisense oligonucleotides capable of
CC modulating the expression of GFAT, and which comprise any of the 3063
CC sequences of 20 base pairs, given in the specification. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with GFAT, such as a disease or condition, e.g. diabetes, a
CC cardiovascular or neurological disorder, ischemia/reperfusion injury.
CC They are also useful in research and diagnostics for modulating the
CC expression of GFAT. The present sequence represents a chimeric
CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
CC oligonucleotides inhibit human GFAT expression.
XX
XX Sequence 20 BP; 5 A; 2 C; 5 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 553 TTAATATGCTGGGTTT 569
Db 1 TTAATAAGCTGGGTTT 17
RESULT 102
ADP78598
ID ADP78598 standard; DNA; 20 BP.
XX
AC ADP78598;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2397.
XX
KW GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..4
FT /*tag= a
FT /mod_base= other

```
FT modified_base /note= "2-methoxyethyl wing"
FT 17. .20
FT /*tag= b
FT /*mod_base= other
FT /*note= "2-methoxyethyl wing"
FT XX
FT PN WO2004035763-A2.
FT XX
FT PD 29-APR-2004.
FT XX
FT PF 02-OCT-2003; 2003WO-US033332.
FT XX
FT PR 17-OCT-2002; 2002US-0419268P.
FT XX
FT PA (PHAA ) PHARMACIA CORP.
FT XX
FT PI Broschat KO, Crosby SD;
FT XX
FT DR WPI; 2004-348453/32.
FT XX
FT DR New compounds, particularly antisense oligonucleotides targeted to a
FT XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
FT PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
FT PT ischemia/reperfusion injury.
FT XX
FT PS Claim 4; SEQ ID NO 2397; 175pp; English.
FT XX
FT CC The present invention relates to a compound which specifically hybridizes
FT CC with a nucleic acid molecule encoding GFAT, and inhibits the expression
FT CC of GFAT. Specifically claimed are antisense oligonucleotides capable of
FT CC modulating the expression of GFAT, and which comprise any of the 3063
FT CC sequences of 20 base pairs, given in the specification. The compound,
FT CC composition and methods are useful for treating a disease or condition
FT CC associated with GFAT, such as a disease or condition, e.g. diabetes, a
FT CC cardiovascular or neurological disorder, ischemia/reperfusion injury.
FT CC They are also useful in research and diagnostics for modulating the
FT CC expression of GFAT. The present sequence represents a chimeric
FT CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
FT CC oligonucleotides inhibit human GFAT expression.
FT XX
FT SQ Sequence 20 BP; 4 A; 2 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 553 TTAATATGCTGGGTTTT 569
Db 4 TTAATAAGCTGGGTTTT 20

RESULT 103
ADP78693
ID ADP78693 standard; DNA; 20 BP.
XX
AC ADP78693;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2492.
XX
KW GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .4
FT /*tag= a
FT /*mod_base= other
FT /*note= "2-methoxyethyl wing"
FT modified_base 17. .20
FT
```

```
FT /*tag= b
FT /*mod_base= other
FT /*note= "2-methoxyethyl wing"
FT XX
FT PN WO2004035763-A2.
FT XX
FT PD 29-APR-2004.
FT XX
FT PF 02-OCT-2003; 2003WO-US033332.
FT XX
FT PR 17-OCT-2002; 2002US-0419268P.
FT XX
FT PA (PHAA ) PHARMACIA CORP.
FT XX
FT PI Broschat KO, Crosby SD;
FT XX
FT DR WPI; 2004-348453/32.
FT XX
FT PT New compounds, particularly antisense oligonucleotides targeted to a
FT PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
FT PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
FT PT ischemia/reperfusion injury.
FT XX
FT PS Claim 4; SEQ ID NO 2492; 175pp; English.
FT XX
FT CC The present invention relates to a compound which specifically hybridizes
FT CC with a nucleic acid molecule encoding GFAT, and inhibits the expression
FT CC of GFAT. Specifically claimed are antisense oligonucleotides capable of
FT CC modulating the expression of GFAT, and which comprise any of the 3063
FT CC sequences of 20 base pairs, given in the specification. The compound,
FT CC composition and methods are useful for treating a disease or condition
FT CC associated with GFAT, such as a disease or condition, e.g. diabetes, a
FT CC cardiovascular or neurological disorder, ischemia/reperfusion injury.
FT CC They are also useful in research and diagnostics for modulating the
FT CC expression of GFAT. The present sequence represents a chimeric
FT CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
FT CC oligonucleotides inhibit human GFAT expression.
FT XX
FT SQ Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 553 TTAATATGCTGGGTTTT 569
Db 3 TTAATAAGCTGGGTTTT 19

RESULT 104
ADP78666
ID ADP78666 standard; DNA; 20 BP.
XX
AC ADP78666;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2465.
XX
KW GFAT; Antidiabetic; Cardiant;
KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW reperfusion; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .4
FT /*tag= a
FT /*mod_base= other
FT /*note= "2-methoxyethyl wing"
FT modified_base 17. .20
FT /*tag= b
FT /*mod_base= other
FT
```

FT /note= "2-methoxyethyl wing"

XX WO2004035763-A2.

PN 29-APR-2004.

PD 02-OCT-2003; 2003WO-US033332.

XX 17-OCT-2002; 2002US-0419268P.

PR (PHAA) PHARMACIA CORP.

XX Broschat KO, Crosby SD;

PI WPI; 2004-348453/32.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,

PT ischemia/reperfusion injury.

XX Claim 4; SEQ ID NO 2465; 175pp; English.

PS The present invention relates to a compound which specifically hybridizes

XX with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX Sequence 20 BP; 4 A; 3 C; 5 G; 8 T; 0 U; 0 Other;

SQ Query Match 1.4%; Score 15.4; DB 1; Length 20;

Best Local Similarity 94.1%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 553 TTAATAATGCTGGGTTT 569

Db 2 TTAATAAGCTGGGTTT 18

RESULT 105

ABK53793/c

ID ABK53793 standard; DNA; 21 BP.

XX ABK53793;

AC 05-JUN-2002 (first entry)

XX DMS:acceptor oxidoreductase, PCR primer #39.

DT DMS:acceptor oxidoreductase; dimethyl sulphide; sulphoxide;

DE prochiral organic sulphide; sulphoxide enantiomer; primer;

XX chiral drug production; optically-active functional drug; ss.

XX Rhodovulum sulfidophilum.

OS WO200216570-A1.

XX 28-FEB-2002.

PN 21-AUG-2001; 2001WO-AU001033.

PD 21-AUG-2000; 2000AU-00009559.

XX (UYQU) UNIV QUEENSLAND.

XX

PI Mcdevitt CA, Mcewan AG;

XX WPI; 2002-280922/32.

DR New recombinant dimethyl sulfide:acceptor oxidoreductase or its subunits,

XX useful for oxidizing prochiral organic sulfides to form sulfoxide

PT enantiomers for chiral drug synthesis.

PT Claim 15; Page 46; 66pp; English.

XX The invention relates to a recombinant dimethyl sulphide (DMS):acceptor

XX oxidoreductase (I) or its subunit selected from recombinant alpha, beta,

CC delta and gamma subunits. (I) is useful for oxidising prochiral organic

CC sulphides to form sulphoxide enantiomers for chiral drug synthesis. (I)

CC is expressed in a transformed bacterium. The enantiomer formed is useful

CC for producing a chiral drug. (I) is useful for synthesis of optically-

CC active functional groups of drug. DNA encoding (I) is useful for

CC producing a strain of DMS:acceptor oxidoreductase- deficient Rhodovulum

CC sulfidophilum, which is useful in whole-cell reaction, where DMS:acceptor

CC oxidoreductase activity is unwanted. ABK53751-ABK53805 represent R.

CC sulfidophilum DMS:acceptor oxidoreductase subunit coding sequences and

CC PCR primers of the invention

XX Sequence 21 BP; 3 A; 9 C; 8 G; 1 T; 0 U; 0 Other;

SQ Query Match 1.4%; Score 15.4; DB 1; Length 21;

Best Local Similarity 94.1%; Pred. No. 1.2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GGGCAGGCTGCCCGGC 26

Db 18 GGTGAGGCTGCCCGGC 2

RESULT 106

AAX96738/c

ID AAX96738 standard; DNA; 20 BP.

XX AAX96738;

AC 13-SEP-1999 (first entry)

DT PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

XX neutralising epitope; PCR primer; ss.

XX Synthetic.

OS Chlamydophila pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

PF 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.

XX Griffais R;

PI WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

PT Page 1849; Disclosure; 1912pp; English.

PS AAX91991-X97517 represent PCR primers used to amplify open reading frames

XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae

CC (see AAX91990). C. pneumoniae causes respiratory disease such as

CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 459 AGTGGTAGCAGTTTATTCG 478
DB 20 AGCGGTAGCAGTTTCTTCG 1

RESULT 107
AAC67691/c
ID AAC67691 standard; DNA; 20 BP.
XX
AC AAC67691;
XX
DT 16-FEB-2001 (first entry)
XX
DE Oligonucleotide #2 ISIS #116870.
XX
KW Antiinflammatory; cytostatic; antibacterial; methionine aminopeptidase 2;
KW inhibitor; MetAP2; eukaryotic initiation factor associated protein; p67;
KW eIF-2; protein synthesis; antisense oligonucleotide; infection; human;
KW inflammation; tumour; phosphorothioate; 2-methoxyethyl wing; ss.
XX
OS Homo sapiens.
XX
PN US6136604-A.
XX
PD 24-OCT-2000.
XX
PF 27-OCT-1999; 99US-00428584.
XX
PR 27-OCT-1999; 99US-00428584.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt J;
XX
DR WPI; 2001-030942/04.
XX
PT New antisense compounds which specifically hybridize with and inhibit
PT human methionine aminopeptidase 2 expression, useful for treating
PT methionine aminopeptidase 2 related disorders and preventing inflammation
PT or tumor formation.
XX
PS Claim 14; Col 39-40; 39pp; English.
XX
CC Methionine aminopeptidase 2 (also known as MetAP2 and eukaryotic
CC initiation factor [eIF-2] associated protein, p67) is a cellular
CC glycoprotein that promotes protein synthesis in the presence of active
CC eIF-2 kinases by protecting the eIF-2 alpha subunit from phosphorylation.
CC The present invention relates to antisense oligonucleotides (AAC67690-
CC C67767) which inhibit human methionine aminopeptidase 2 coding sequence
CC expression (see AAC67683). The present sequence is one such antisense
CC oligonucleotide. The present sequence may be used for treating a patient
CC suspected of having or being prone to a disease or condition associated
CC with expression of MetAP2. In addition, the present sequence can also be
CC used as research reagents, diagnostics and to distinguish between
CC functions of various members of a biological pathway. The antisense
CC oligonucleotide may further be used prophylactically, e.g. to prevent or
CC delay infection, inflammation or tumour formation. Note: the present
CC sequence may have a phosphorothioate backbone and 2-methoxyethyl (2'-MOE)

CC wings
XX
SQ Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 TCGGGAGACATGGCGGCGT 81
DB 20 TCGGGCAACATGGCGGGTGT 1

RESULT 108
AAF23345
ID AAF23345 standard; DNA; 20 BP.
XX
AC AAF23345;
XX
DT 19-MAR-2001 (first entry)
XX
DE Oligonucleotide for detection of Mycobacterium diernhoferi.
XX
KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
XX
OS Mycobacterium diernhoferi.
XX
PN WO200073436-A1.
XX
PD 07-DEC-2000.
XX
PF 16-MAY-2000; 2000WO-KR000477.
XX
PR 29-MAY-1999; 99KR-00019631.
PR 29-MAY-1999; 99KR-00019632.
PR 29-MAY-1999; 99KR-00019633.
PR 29-MAY-1999; 99KR-00019634.
PR 29-MAY-1999; 99KR-00019635.
PR 07-APR-2000; 2000KR-00018189.
XX
PA (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
PI Kim CM, Park HK, Jang HJ;
XX
DR WPI; 2001-061527/07.
XX
PT Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
PS Claim 36; Page 82; 89pp; English.
XX
CC The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC diernhoferi genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made

Fri Aug 19 11:00:00 2005

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CC from ITS of mycobacteria, it is possible to detect mycobacteria,
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
SQ Sequence 20 BP; 9 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match      1.4%; Score 15.2; DB 1; Length 20;
  Best Local Similarity 85.0%; Pred. No. 1.2e+02;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 998 TGCACATGAAAGTTTGAGAA 1017
Db 1 TGCACACACAAACTTTGAGAA 20

RESULT 109
AAD20131
ID AAD20131 standard; DNA; 20 BP.
XX
AC AAD20131;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human histone deacetylase antisense oligonucleotide, HDAC8 AS2.
XX
KW Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
KW protozoal disease; fungal disease; infection; ss.
XX
OS Homo sapiens.
XX
PN WO200170675-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-IB000683.
XX
PR 24-MAR-2000; 2000US-0192151P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Woo SH, Vaisburg A;
XX
XX WPI; 2001-639108/73.
DR
XX
XX An inhibitor of histone deacetylase for the treatment of cell
PT proliferation diseases and conditions such as cancer, restenosis or
PT psoriasis or preventing protozoal or fungal disease or infections.
XX
XX Disclosure; Page 54; 241pp; English.
XX
XX The present invention relates to compounds and methods for inhibiting
CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
CC are used for the treatment of cell proliferative diseases and conditions
CC such as cancer, restenosis or psoriasis. They are also used for treating
CC or preventing protozoal or fungal disease or infections. The present
CC sequence is antisense oligonucleotide, HDAC8 AS2 which is targetted to
CC the 3' untranslated region (UTR) of human HDAC8 to inhibit its enzymatic
CC activity
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match      1.4%; Score 15.2; DB 1; Length 20;
  Best Local Similarity 85.0%; Pred. No. 1.2e+02;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 110
AAF92365
```

```
ID AAF92365 standard; DNA; 20 BP.
XX
AC AAF92365;
XX
DT 16-MAY-2001 (first entry)
XX
DE PCR primer specific for human CYP3A4 DNA SEQ ID 10.
XX
KW Human; cytochrome P450; Cyp3A; PCR primer; transgenic mouse;
KW immortalised cell; ss.
XX
OS Homo sapiens.
XX
PN WO200111951-A1.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-JP005424.
XX
PR 13-AUG-1999; 99JP-00229094.
XX
PA (KIRI ) KIRIN BEER KK.
XX
PI Ishida I, Tomizuka K, Kuroiwa Y, Ohshima T, Suzuki M, Itoh K;
XX
XX WPI; 2001-202806/20.
DR
XX Mouse having completely humanized human cytochrome P450 gene for use in
PT studying drug efficacy, metabolism and toxicity with ease.
PT
XX
XX Example 5; Page 43; 137pp; Japanese.
PS
XX This invention relates to a mouse containing the human cytochrome P450
CC gene (from the CYP3A family). PCR primers AAF92356 - AAF92441 are used in
CC examples illustrating the construction of vectors used in the production
CC of the transgenic mouse of the invention. The mouse can be used for
CC studying human drug efficacy, metabolism and toxicity, including the
CC application of immortalised cell and tissue cultures
XX
SQ Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 U; 0 Other;

  Query Match      1.4%; Score 15.2; DB 1; Length 20;
  Best Local Similarity 85.0%; Pred. No. 1.2e+02;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 105 TCAGTGGGGCTATTGGACTG 124
Db 1 TCAGTGAGGCTGTGGATTG 20

RESULT 111
ABV73091
ID ABV73091 standard; DNA; 20 BP.
XX
AC ABV73091;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human HDAC-8 mRNA inhibiting antisense oligo HDAC8 AS2.
XX
KW Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation;
KW HDAC-8; human; cancer; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200269947-A2.
XX
PD 12-SEP-2002.
XX
PF 14-JAN-2002; 2002WO-IB002002.
XX
PR 12-JAN-2001; 2001US-0261522P.
```

PR 12-JAN-2001; 2001US-0261674P.
XX (METH-) METHYLGENE INC.
PA
XX
PI Besterman JM, Bonfils C, Woo SH, Vaisburg A, Delorme D;
PI Fournel M, Lavoie R, Li Z;
XX
XX WPI; 2002-750436/81.
XX
XX Inhibition of HDAC-4 activity in a cell useful for treating e.g. cancer
PT involves contacting the cell with an antisense oligonucleotide or a small
PT molecule inhibitor of HDAC-4.
XX
PS Disclosure; Page 33; 124pp; English.
XX
CC The invention relates to inhibition of histone deacetylase (HDAC)-4
CC activity in a cell that involves contacting the cell with an antisense
CC oligonucleotide complementary to a region of RNA encoding a portion of
CC HDAC-4 or a small molecule inhibitor of HDAC-4. The method is useful for
CC inhibiting neoplastic cell proliferation in an animal (preferably human)
CC and for treating cancer. Sequences ABV73073-3091 represent HDAC isotype-
CC specific antisense and mismatch oligonucleotides
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 112
ABI93053/c
ID ABI93053 standard; DNA; 20 BP.
XX
AC ABI93053;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#140 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
XX WPI; 2002-034366/04.
DR
XX Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
PT
XX Example 5; Fig 29; 300pp; English.
PS
XX The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary

CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 767 CATCGAAACCTTTTGCTTGG 786
Db 20 CATCGACACCGTTTGCTTCG 1

RESULT 113
ABK87739
ID ABK87739 standard; DNA; 20 BP.
XX
AC ABK87739;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human histone deacetylase isoform 8 antisense oligonucleotide AS2.
XX
KW Human; ss; histone deacetylase; HDAC-8; cancer; cytostatic; antisense;
KW tumour suppressor; cell proliferation; tumour; programmed cell death;
KW necrotic cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1. .4
FT /*tag= b
FT /mod_base= OTHER
FT /note= "These nucleotides have 2'-O-methyl groups
FT attached to their sugar residues"
FT modified_base 17. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "These nucleotides have 2'-O-methyl groups
FT attached to their sugar residues"
XX
PN US2002061860-A1.
XX
XX 23-MAY-2002.
PD
XX
PF 06-AUG-2001; 2001US-00817913.
XX
PR 24-MAR-2000; 2000US-0192157P.

XX (LIZZ/) LI Z.
PA (BONF/) BONFILS C.
PA (BEST/) BESTERMAN J.
XX
PI Li Z, Bonfils C, Besterman J;
XX
DR WPI; 2002-507650/54.
XX
XX Agent that specifically inhibits an isoform of histone deacetylase,
PT useful for treating cancer and other cell proliferative diseases,
PT preferably comprises an antisense oligonucleotide.
XX
PS Claim 25; Page 6; 60pp; English.
XX
CC The invention relates to an agent that inhibits an isoform of histone
CC deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense
CC oligonucleotide. Also included are inhibiting an HDAC isoform in a cell
CC by treatment with the agent, identifying an HDAC isoform that is required
CC for induction of cell proliferation or differentiation and inhibiting
CC cell proliferation by treatment with two antisense oligonucleotides or
CC small molecules that inhibit a specific HDAC isoform, or antisense
CC oligonucleotide or small molecules that inhibit DNA methyltransferase.
CC The agent therefore acts as a tumour suppressor. The agents are used to
CC treat diseases of cell proliferation and differentiation (e.g cancer and
CC tumours), by inducing growth retardation, growth arrest or
CC programmed/necrotic cell death, specifically neoplastic cell
CC proliferation in humans. The agents are selective for particular
CC isoforms, compared to known inhibitors which are not selective. The
CC present sequence is an antisense oligonucleotide of the invention
CC targeting the polynucleotide which encodes the HDAC-8 isoform
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 743 AGGAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 114
ABV74507/C
ID ABV74507 standard; DNA; 20 BP.
XX
AC ABV74507;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human alphainterferon-21, IFNalpha-21 sense PCR primer A.
XX
KW Human; alphainterferon-21; cancer; leukaemia; cardiovascular disease;
KW metabolic disease; infection; hepatitis B; hepatitis C; AIDS; depression;
KW associated Kaposi sarcoma; pneumonia; ulcerative colitis; osteoporosis;
KW central nervous system disease; schizophrenia; Alzheimer's disease;
KW Parkinson's disease; graft rejection; wound; anaemia; allergy; asthma;
KW multiple sclerosis; psoriasis; rheumatoid arthritis; Crohn's disease;
KW autoimmune disorder; gastro-intestinal disease; chemotherapy; cytostatic;
KW anorectic; virucide; anti-HIV; antiinflammatory; hepatotropic; antiulcer;
KW neuroleptic; wart; immunosuppressive; vulnerable; antianaemic; nootropic;
KW antiallergic; antiasthmatic; neuroprotective; osteopathic; antipsoriatic;
KW antiarthritic; antirheumatic; dermatological; antiemetic; antidepressant;
KW antiparkinsonian; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN FR2822845-A1.
XX
PD 04-OCT-2002.
XX
PF 30-MAR-2001; 2001FR-00004404.

XX 30-MAR-2001; 2001FR-00004404.
PR
XX (GENO-) GENODYSSEE SA.
PA
XX Escary JL;
PI
XX WPI; 2003-021472/02.
DR
XX New nucleic acid, useful for treatment or diagnosis of e.g. cancer,
PT encodes mutant forms of human interferon-alpha21, also derived
PT polypeptides and antibodies.
PT
XX Example 2; Page 45; 100pp; French.
PS
XX The present invention relates to human alphainterferon-21. The coding
CC sequence (see ABV74504) for this protein can contain at least one of the
CC following single nucleotide polymorphisms (SNP): C973A, G1011C, T1049A,
CC T1155A and A1204G. alphainterferon-21 and its coding sequence are useful
CC for treatment or prevention of a wide range of cancers (solid or
CC leukaemia); cardiovascular diseases; metabolic diseases not associated
CC with the immune system such as obesity; infections (particularly by
CC viruses such as hepatitis B or C; or AIDS and associated Kaposi sarcoma);
CC pneumonia; ulcerative colitis; central nervous system diseases (e.g.
CC schizophrenia; depression; Alzheimer's and Parkinson's diseases); graft
CC rejection; wounds; anaemia; allergy; asthma; multiple sclerosis;
CC osteoporosis; psoriasis; rheumatoid arthritis; Crohn's diseases;
CC autoimmune disorders; genital or venereal warts; Gastro-intestinal
CC disease and diseases associated with chemotherapy. The present sequence
CC is a PCR primer, used in an example from the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 608 TTCATAAGTAGGAGATGAGT 627
Db 20 TTCCCAAGTAGCAGATGAGT 1
||| ||||| ||||| |||||

RESULT 115
ADC21719
ID ADC21719 standard; DNA; 20 BP.
XX
AC ADC21719;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human HDAC-8 antisense oligonucleotide AS2.
XX
KW Human; histone deacetylase; isoform; HDAC-1; HDAC-2; HDAC-3; HDAC-4;
KW HDAC-5; HDAC-6; HDAC-7; HDAC-8; antisense gene therapy;
KW cell proliferation; programmed cell death; necrotic cell death;
KW neoplastic cell proliferation; cell differentiation; neoplasm; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methyl residues"
FT modified_base 17..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methyl residues"
XX

PN US2002137162-A1.
XX
PD 26-SEP-2002.
XX
XX
PF 26-MAR-2001; 2001US-00817538.
XX
XX
PR 24-MAR-2000; 2000US-0192157P.
PR 12-JAN-2001; 2001US-0261522P.
XX
PA (LIZZ/) LI Z.
PA (BONF/) BONFILS C.
PA (BEST/) BESTERMAN J M.
XX
PI Li Z, Bonfils C, Besterman JM;
XX WPI; 2003-786641/74.
XX
PT New antisense oligonucleotide that inhibits one or more specific histone
PT deacetylase isoforms, is useful in modulating cell proliferation
PT especially neoplasia.
XX
PS Claim 21; SEQ ID NO 33; 52pp; English.
XX
CC The invention relates to an antisense oligonucleotide comprising a
CC nucleotide sequence of 13 to 15 nucleotides that inhibits one or more
CC specific histone deacetylase isoforms (HDAC-1 to HDAC-8), where the
CC oligonucleotide is complementary to a region of RNA or double stranded
CC DNA. The oligonucleotide is useful in inhibiting one or more histone
CC deacetylases isoforms in a cell comprising contacting the cell with the
CC oligonucleotide. Cell proliferation is inhibited in the contacted cell
CC which undergoes growth retardation and growth arrest. The contacted cell
CC undergoes programmed and necrotic cell death. The oligonucleotide is also
CC useful in inhibiting neoplastic cell proliferation in an animal,
CC preferably a human. The oligonucleotide is also useful in identifying a
CC histone deacetylase isoform that is required for the induction of cell
CC proliferation comprising contacting the histone deacetylase isoform with
CC the oligonucleotide where a decrease in induction of cell proliferation
CC indicates that the isoform is required for the induction of cell
CC proliferation. The above method is also applicable to identifying
CC isoforms required for cell proliferation. The oligonucleotide is useful
CC in identifying an isoform required for the induction of cell
CC differentiation, where an induction of cell differentiation indicates
CC that the isoform is required for differentiation. Also useful in
CC modulating cell proliferation especially neoplasia. The present sequence
CC an antisense oligonucleotide directed against an HDAC isoform containing
CC mismatched bases.
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20

RESULT 116
ADC79289
ID ADC79289 standard; DNA; 20 BP.
XX
AC ADC79289;
XX
DT 01-JAN-2004 (first entry)
XX
DE 5'-RACE primer for amplifying fluorescent protein cDNA #SEQ ID 18.
XX
KW Fluorescent protein; label; protein function; protein distribution;
KW fungal; PCR; primer; ss; 5'RACE.
XX
OS Fungia sp.
XX

PN WO2003054191-A1.
XX
PD 03-JUL-2003.
XX
XX
PF 20-DEC-2002; 2002WO-JP013363.
XX
XX
PR 20-DEC-2001; 2001JP-00387510.
XX
PA (RIKE) RIKEN KK.
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Miyawaki A, Karasawa S;
XX WPI; 2003-541818/51.
DR
XX
XX
PT Fluorescent proteins from Fungia species and DNA encoding them for
PT analysis of function and distribution of proteins in living systems.
XX
XX
PS Example 1; Page 21; 59pp; Japanese.
XX
CC The invention relates to 4 fluorescent proteins originating from Fungia
CC species. Also disclosed are DNA sequences encoding the novel fluorescent
CC proteins, expression vectors containing this DNA, hosts transformed by
CC this vector, fluorescent fusion proteins containing the novel fluorescent
CC proteins fused to another protein, and a method for analysis of function
CC and distribution of another protein using the fluorescent fusion protein.
CC Novel proteins of the invention are useful for analysis of the
CC intracellular activity, function and localisation of proteins of the
CC biological interest, using the fluorescent protein as a fluorescence
CC label. The fluorescent proteins have desirable fluorescence properties
CC and a low sensitivity to pH. The current sequence represents a 5'-RACE
CC (rapid amplification of cDNA ends) primer used to recover fungal
CC fluorescent protein terminal sequence from extracted cDNA.
XX
SQ Sequence 20 BP; 5 A; 6 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 497 TCTTAGAACTCATCTATCT 516
Db 1 TCTTCGAACTCAAACTTTCT 20

RESULT 117
ABZ76492
ID ABZ76492 standard; DNA; 20 BP.
XX
AC ABZ76492;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human HDAC8 mRNA targeting antisense oligo HDAC8 AS2.
XX
KW HDAC; histone deacetylase; cytostatic; vasotropic; antipsoriatic;
KW antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003024448-A2.
PN
XX
PD 27-MAR-2003.
XX
XX
PF 12-SEP-2002; 2002WO-US029017.
XX
XX
PR 14-SEP-2001; 2001US-0322402P.
PR 26-JUN-2002; 2002US-0391728P.
XX
XX (METH-) METHYLGENE INC.
PA
XX
PI Delorme D, Woo SH, Vaisburg A, Moradel O, Leit S, Raeppe S;

Fri Aug 19 11:00:00 2005

PI Frechette S, Bouchain G;
XX WPI; 2003-342612/32.
DR
XX New histone deacetylase inhibitors, useful for treatment of proliferative
PT diseases or conditions e.g. cancer.
PT
XX
XX Disclosure; Page 72; 347pp; English.
XX
XX The invention relates to histone deacetylase inhibitors of specified
CC formulae and their salts. The compounds inhibit histone deacetylase
CC (HDAC) enzymatic activity. They can be used for treating cell
CC proliferative diseases or condition (e.g. cancer, restenosis and
CC psoriasis). Sequences ABZ76476-492 represent antisense and mismatch
CC oligonucleotides targeting the 5'- UTR (untranslated region) and 3'-UTRs
CC of the human HDAC1-8 genes
XX
XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20
RESULT 118
ADH50696
ID ADH50696 standard; DNA; 20 BP.
XX
AC ADH50696;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human IRAK-1 DNA target sequence #18.
XX
XX Antisense therapy; human; interleukin-1 receptor-associated kinase-1;
KW IL-1 receptor-associated kinase-1; IRAK-1;
KW hyperproliferative disorder e.g.; cancer; autoimmune disorder;
KW altered bone metabolism or inflammation; cytostatic; immunosuppressive;
KW osteopathic; antiinflammatory; ds.
XX
OS Homo sapiens.
XX
XX US2003228690-A1.
XX
PD 11-DEC-2003.
XX
PF 10-JUN-2002; 2002US-00167034.
XX
PR 10-JUN-2002; 2002US-00167034.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Freier SM, Dobie KW;
PI
XX WPI; 2004-052028/05.
DR
XX New compound having a sequence targeted to a nucleic acid encoding IL-1
PT receptor-associated kinase-1, useful for preparing a composition for
PT treating hyperproliferative or autoimmune disorder or inflammation.
XX
XX Example 15; SEQ ID NO 103; 66pp; English.
PS
XX The present invention relates to antisense compounds targeted to a
CC nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-1
CC (IRAK-1). The antisense compound comprises an antisense oligonucleotide
CC that specifically hybridises with the nucleic acid and inhibits the
CC expression of IRAK-1. The antisense oligonucleotide is a chimeric
CC oligonucleotide. The antisense oligonucleotide comprises at least one
CC modified internucleoside linkage, preferably a phosphorothioate linkage.

CC It also comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC autoimmune disorders, altered bone metabolism, and inflammation. The
CC present sequence represents a human IRAK-1 DNA target sequence for an
CC antisense oligonucleotide.
XX
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 817 AGCAGGCCTCTCATGACCCA 836
Db 1 AGGAGGCCTCCTATGACCCA 20
RESULT 119
ADH50625/C
ID ADH50625 standard; DNA; 20 BP.
XX
AC ADH50625;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human IRAK-1 DNA, antisense oligonucleotide #19.
XX
XX Antisense therapy; human; interleukin-1 receptor-associated kinase-1;
KW IL-1 receptor-associated kinase-1; IRAK-1;
KW hyperproliferative disorder e.g.; cancer; autoimmune disorder;
KW altered bone metabolism or inflammation; cytostatic; immunosuppressive;
KW osteopathic; antiinflammatory; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 5 nucleotides in length at each
FT end. All cytidine residues are 5-methylcytidines"
XX
XX US2003228690-A1.
XX
PD 11-DEC-2003.
XX
PF 10-JUN-2002; 2002US-00167034.
XX
PR 10-JUN-2002; 2002US-00167034.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Freier SM, Dobie KW;
PI
XX WPI; 2004-052028/05.
DR
XX New compound having a sequence targeted to a nucleic acid encoding IL-1
PT receptor-associated kinase-1, useful for preparing a composition for
PT treating hyperproliferative or autoimmune disorder or inflammation.
XX
XX Example 15; SEQ ID NO 32; 66pp; English.
PS
XX The present invention relates to antisense compounds targeted to a
CC nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-1
CC (IRAK-1). The antisense compound comprises an antisense oligonucleotide
CC that specifically hybridises with the nucleic acid and inhibits the
CC expression of IRAK-1. The antisense oligonucleotide is a chimeric
CC oligonucleotide. The antisense oligonucleotide comprises at least one
CC modified internucleoside linkage, preferably a phosphorothioate linkage.

CC modified internucleoside linkage, preferably a phosphorothioate linkage.
CC It also comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC autoimmune disorders, altered bone metabolism, and inflammation. The
CC present sequence represents an antisense oligonucleotide used in the
CC examples of the present invention.

XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 817 AGCAGGCCTCTCATGACCCA 836
Db 20 AGGAGGCCTCCTATGACCCA 1

RESULT 120
ADJ45254/c
ID ADJ45254 standard; DNA; 20 BP.

XX AC ADJ45254;

XX DT 06-MAY-2004 (first entry)

XX DE Hepatoma-derived growth factor antisense oligo seqid 24.

XX KW cytostatic; endocrine; hepatoma-derived growth factor inhibitor;
KW hepatoma-derived growth factor; metabolic disorder; hyperproliferative;
KW human; ss; antisense oligonucleotide.

OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

PN US2004023379-A1.
XX
PD 05-FEB-2004.
XX
PF 31-JUL-2002; 2002US-00210429.
XX
PR 31-JUL-2002; 2002US-00210429.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX
DR WPI; 2004-142660/14.

XX
PT New compound, particularly an antisense oligonucleotide targeted to a
PT nucleic acid encoding a hepatoma-derived growth factor, useful for
PT treating a hyperproliferative disorder e.g. cancer, or a metabolic
PT disorder.
XX
PS Example 15; SEQ ID NO 24; 6lpp; English.

CC The invention describes a compound 8-80 nucleobases in length targeted
CC to, and which specifically hybridises with a nucleic acid molecule
CC encoding hepatoma-derived growth factor, and inhibits the expression of
CC hepatoma-derived growth factor. The compound, composition and methods are
CC useful for treating a disease or condition associated with hepatoma-
CC derived growth factor, such as a metabolic disorder, or a
CC hyperproliferative disorder, e.g. cancer, which is selected from
CC hepatoma, leiomyoma, esophageal cancer or ovarian cancer. They are also
CC useful in research and diagnostics for modulating the expression of
CC hepatoma-derived growth factor. This sequence represents a human hepatoma
CC -derived growth factor antisense oligonucleotide.

XX
SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 801 AGGCAGATAACGCTGAAGCA 820
Db 20 AGGCAGAAACCCCTGAAGGA 1

RESULT 121
ADJ45325

ID ADJ45325 standard; DNA; 20 BP.

XX AC ADJ45325;

XX DT 06-MAY-2004 (first entry)

XX DE Hepatoma-derived growth factor antisense oligo seqid 95.

XX KW cytostatic; endocrine; hepatoma-derived growth factor inhibitor;
KW hepatoma-derived growth factor; metabolic disorder; hyperproliferative;
KW human; ss; antisense oligonucleotide.

OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

PN US2004023379-A1.
XX
PD 05-FEB-2004.
XX
PF 31-JUL-2002; 2002US-00210429.
XX
PR 31-JUL-2002; 2002US-00210429.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX

XX
PT New compound, particularly an antisense oligonucleotide targeted to a
PT nucleic acid encoding a hepatoma-derived growth factor, useful for
PT treating a hyperproliferative disorder e.g. cancer, or a metabolic
PT disorder.
XX
PS Example 15; SEQ ID NO 24; 6lpp; English.

PS Example 15; SEQ ID NO 95; 61pp; English.

XX The invention describes a compound 8-80 nucleobases in length targeted to, and which specifically hybridises with a nucleic acid molecule encoding hepatoma-derived growth factor, and inhibits the expression of hepatoma-derived growth factor. The compound, composition and methods are useful for treating a disease or condition associated with hepatoma-derived growth factor, such as a metabolic disorder, or a hyperproliferative disorder, e.g. cancer, which is selected from hepatoma, leiomyoma, esophageal cancer or ovarian cancer. They are also useful in research and diagnostics for modulating the expression of hepatoma-derived growth factor. This sequence represents a human hepatoma -derived growth factor antisense oligonucleotide.

XX

SQ Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 801 AGGCAGATAACGCTGAAGCA 820
||||||| ||| ||||| |

Db 1 AGGCAGAAACCCCTGAAGGA 20

RESULT 122

ADI34745

ID ADI34745 standard; DNA; 20 BP.

XX

AC ADI34745;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human HDAC8-specific oligo HDAC8AS2.

XX

KW HDAC; histone deacetylase; HDAC-7; HDAC-8; cell proliferation; growth retardation; cytostatic; antisense therapy; apoptosis;

KW p21 transcription; antisense; ss.

XX

OS Synthetic.

XX

PN WO2004005513-A2.

XX

PD 15-JAN-2004.

XX

PF 12-JUN-2003; 2003WO-IB003052.

XX

PR 03-JUL-2002; 2002US-00189818.

XX

PA (METH-) METHYLGENE INC.

XX

PI Besterman JM, Li Z, Delorme D, Bonfils C;

XX

DR WPI; 2004-099393/10.

XX

PT Inhibiting neoplastic cell proliferation in animals by administering an antisense oligonucleotide complementary to region of RNA encoding portion of histone deacetylase-7 (HDAC-7) or HDAC-8, or small molecule inhibitor of HDAC-7 or HDAC-8.

XX

PS Disclosure; Page 25; 98pp; English.

XX

CC The invention relates to inhibiting neoplastic cell proliferation in an animal by administering to the animal having at least one neoplastic cell present in its body: an antisense oligonucleotide complementary to a region of RNA that encodes a portion of histone deacetylase-7 (HDAC-7) or HDAC-8; and/or a small molecule inhibitor of HDAC-7 or HDAC-8. Inhibition of HDAC-7 or HDAC-8 activity in the contacted cell further leads to an inhibition of cell proliferation, growth retardation and to necrotic cell death, growth arrest, or programmed cell death of the contacted cell. The method is useful for inhibiting neoplastic cell proliferation in an animal, preferably human. The method further comprises administering an antisense oligonucleotide complementary to a region of RNA that encodes a

CC portion of HDAC-1, preferably chimeric or hybrid HDAC-1 antisense oligonucleotide. Sequences ADI34722-ADI34746 represent HDAC isotype-specific antisense and mismatch oligonucleotides.

XX

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 3 T; 1 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCTTATGC 762
||| ||||| ||||| | :||

Db 1 AGCCAGCTGCCACTTGAUGC 20

RESULT 123

ADJ96374

ID ADJ96374 standard; DNA; 20 BP.

XX

AC ADJ96374;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human breast cancer-1 antisense oligonucleotide #159144.

XX

KW Breast cancer-1; diagnosis; hyperproliferative disorder; cancer; antisense therapy; human; antisense; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..20 /*tag= b

FT /*mod_base= OTHER

FT /*note= "Phosphorothioate backbone where all cytidines are 5' - methylcytidines"

FT modified_base 1..5 /*tag= a

FT /*mod_base= OTHER

FT /*note= "2' - methoxyethyl (2' -MOE) nucleotides"

FT modified_base 16..20 /*tag= c

FT /*mod_base= OTHER

FT /*note= "2' - methoxyethyl (2' -MOE) nucleotides"

XX

PN US2004014051-A1.

XX

PD 22-JAN-2004.

XX

PF 18-JUL-2002; 2002US-00199676.

XX

PR 18-JUL-2002; 2002US-00199676.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Brown-Driver VL, Dobie KW;

XX

DR WPI; 2004-121557/12.

XX

PT New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating conditions with aberrant activity of breast cancer-1, such as breast, ovary, prostate and/or peritoneum cancers.

PT

XX Example 15; Page 31; 175pp; English.

XX

CC The present invention is directed to novel antisense compounds targeted to breast cancer-1 proteins and their encoding nucleic acids. The invention is useful for the diagnosis, prevention and/or treatment of diseases and conditions associated with aberrant expression and activity of breast cancer-1 such as a hyperproliferative disorder in particular breast, ovary, prostate and peritoneum cancers. The invention is also used in antisense therapy. The present sequence is human breast cancer-1

CC antisense oligonucleotide. Note: This sequence given in example 15 of the
CC specification differs from that given in the sequence listing.
XX
SQ Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 224 GCCAAAAGAGTCACCTATGA 243
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGCAGAGAGTCACTTATGA 20

RESULT 124
ADJ96440/c
ID ADJ96440 standard; DNA; 20 BP.
XX
AC ADJ96440;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human breast cancer-1 target, oligonucleotide #25.
XX
KW Breast cancer-1; diagnosis; hyperproliferative disorder; cancer;
KW antisense therapy; human; ss.
XX
OS Homo sapiens.
XX US2004014051-A1.
XX
PD 22-JAN-2004.
XX
PF 18-JUL-2002; 2002US-00199676.
XX
PR 18-JUL-2002; 2002US-00199676.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Brown-Driver VL, Dobie KW;
XX
DR WPI; 2004-121557/12.
XX
PT New antisense oligonucleotide compounds, useful for diagnosing,
PT preventing and/or treating conditions with aberrant activity of breast
PT cancer-1, such as breast, ovary, prostate and/or peritoneum cancers.
XX
PS Example 15; Page 32; 175pp; English.
XX
CC The present invention is directed to novel antisense compounds targetted
CC to breast cancer-1 proteins and their encoding nucleic acids. The
CC invention is useful for the diagnosis, prevention and/or treatment of
CC diseases and conditions associated with aberrant expression and activity
CC of breast cancer-1 such as a hyperproliferative disorder in particular
CC breast, ovary, prostate and peritoneum cancers. The invention is also
CC used in antisense therapy. The present sequence is human breast cancer-1
CC target oligonucleotide.
XX
SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 224 GCCAAAAGAGTCACCTATGA 243
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGCAGAGAGTCACTTATGA 1

RESULT 125
ADJ23397
ID ADJ23397 standard; DNA; 20 BP.
XX

AC ADJ23397;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 1795.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Bhat BG;
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 1795; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 865 TTGTAGTCCATGCTATTAA 884
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTGTAGCCAATGCTATTACA 20

RESULT 126
ADJ23964
ID ADJ23964 standard; DNA; 20 BP.
XX
AC ADJ23964;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2362.
XX

KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Bhat BG;
XX
DR WPI; 2004-132912/13.
XX
XX New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
PT
XX
PS Claim 3; SEQ ID NO 2362; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 866 TGTAGTCCATGCTATTAAAA 885
Db 1 TGTAGCCAATGCTATTACAA 20
RESULT 127
ADO07539
ID ADO07539 standard; DNA; 20 BP.
XX
AC ADO07539;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human histone deacetylase coding sequence antisense oligonucleotide #17.
XX histone deacetylase; HDAC; enzyme; benzamide derivative;
KW cell proliferation; antisense; ss.
KW
XX Homo sapiens.
OS
XX
PN WO2004035525-A1.

XX 29-APR-2004.
PD
XX 16-OCT-2003; 2003WO-CA001557.
PF
XX 17-OCT-2002; 2002US-0419688P.
PR
XX (METH-) METHYLGENE INC.
PA
XX Raeppeel S, Gaudette F, Paquin I, Vaisburg A, Delorme D;
PI
XX WPI; 2004-365141/34.
DR
XX New benzamide derivatives, useful to treat cell proliferative disease or
PT conditions, are histone deacetylase inhibitors.
PT
XX
PS Disclosure; Page 27; 73pp; English.
XX
CC The present invention relates to benzamide derivatives capable of
CC inhibiting histone deacetylase (HDAC) enzymes. These are useful in the
CC treatment of a cell proliferative disease or condition in a mammal
CC (preferably human). The present sequence is an antisense oligonucleotide
CC for use against a human histone deacetylase gene.
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTTATGC 762
Db 1 AGCCAGCTGCCACTTGATGC 20
RESULT 128
ADR20736
ID ADR20736 standard; DNA; 20 BP.
XX
AC ADR20736;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human histone deacetylase (HDAC8) gene-specific antisense oligo #2.
XX
KW histone deacetylase inhibitor; HDAC inhibitor; antisense oligonucleotide;
KW proliferative disease; proliferative condition; ss; HDAC8.
XX
OS Homo sapiens.
XX
PN WO2004069823-A1.
XX
PD 19-AUG-2004.
XX
PF 04-FEB-2004; 2004WO-CA000139.
XX
PR 04-FEB-2003; 2003US-00358556.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Zhou Z;
XX
DR WPI; 2004-615556/59.
XX
PT New N-(2-Aminophenyl)-4-((4-pyridin-3-yl-pyrimidin-2-ylamino)-methyl)-
PT benzamideis histone deacetylase inhibitor useful to treat cell
PT proliferative diseases.
XX
PS Disclosure; Page 77; 335pp; English.
XX
CC The invention comprises histone deacetylase (HDAC) inhibitors of the
CC formula: N-(2-Amino-phenyl)-4-[(4-pyridin-3-yl-pyrimidin-2-ylamino)-
CC methyl]-benzamide. The invention also comprises a method of inhibiting

AAF96968/c
ID AAF96968 standard; DNA; 21 BP.
XX
AC AAF96968;
XX
DT 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1729.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT variation 11
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX
DR WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 163; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
CC
CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a captial V
XX
SQ Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CTGGCTTGGGCAGGCTGCC 22
||| || ||||| ||||| ||
Db 21 CTGCCTGGGCGAGGCTGTCC 2

RESULT 132
ABK82248
ID ABK82248 standard; DNA; 21 BP.
XX
AC ABK82248;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human ATP-binding cassette (ABC) transporter probe #86.
XX
KW Human; ATP-binding cassette transporter; ABC transporter;
KW expression rate; drug development; biochemical kinetic; anthelmintic;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN JP2002112775-A.
XX
PD 16-APR-2002.
XX
PF 03-OCT-2000; 2000JP-00303404.
XX
PR 03-OCT-2000; 2000JP-00303404.
XX
PA (SAKA) OTSUKA SEIYAKU KOGYO KK.
XX
DR WPI; 2002-458864/49.
XX
PT Probes for determination of human ATP-binding cassette (ABC) transporters
PT capable of hybridization with 33 regions of genes.
XX
PS Claim 8; Page 29; 36pp; Japanese.
XX
CC The invention describes new probes for identification of human ATP-
CC binding cassette (ABC) transporters capable of hybridisation with 33
CC regions of genes. Elucidation of expression rate of ABC transporters is
CC useful for development of drugs and their biochemical kinetics. This
CC sequence represents a probe used to detect human ATP-binding cassette
CC (ABC) transporters
XX
SQ Sequence 21 BP; 2 A; 4 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 295 TGGAAATTGTTGTTTCTGCCT 314
||||| ||| ||||| ||||| |||||
Db 1 TGGAGTTCTTGTGTGCTGCCT 20
RESULT 133
ABS98518/c
ID ABS98518 standard; DNA; 21 BP.
XX
AC ABS98518;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human acetyl choline muscarinic receptor 2 polymorphic sequence #1.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

Best Local Similarity 85.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 3; Gaps 0; Matches 17; Conservative 0;

QY 221 ATTGCCAAAGAGTACCTA 240
Db 1 ATTGGCAAAAGATTCTCCTA 20

RESULT 135
ADR68090
ID ADR68090 standard; DNA; 21 BP.
XX AC ADR68090;
XX 18-NOV-2004 (first entry)
XX BAFF siRNA sense strand DNA, SEQ ID 101.
KW Antiarthritic; Antirheumatic; Muscular; Neuroprotective;
KW Antiinflammatory; Antipsoriatic; Gastrointestinal; Antiallergic;
KW Dermatological; Antulcer; Vasotropic; Antiasthmatic; Immunosuppressive;
KW Antidiabetic; cancer; B cell activation factor; BAFF;
KW small interfering RNA; siRNA; systemic anaphylaxis;
KW hypersensitivity response; allergy; multiple sclerosis;
KW systemic lupus erythematosus; diabetes; graft rejection; ds.
XX Synthetic.
OS WO2004074511-A1.
PN 02-SEP-2004.
PD 20-FEB-2004; 2004WO-AU000215.
XX PF 21-FEB-2003; 2003US-0449037P.
XX PR (GARV-) GARVAN INST MEDICAL RES.
XX PA Mackay F, Mackay C, Batten M;
XX PI WPI; 2004-652968/63.
XX DR Determining cancer cell or predisposition to developing cancer in subject
XX PT candidate for anti- tumor necrosis factor therapy, by determining level
XX PT of expression of B cell activation factor gene in sample of subject.
XX PS Claim 66; SEQ ID NO 101; 148pp; English.
XX The present invention relates to a method for determining predisposition
CC to developing cancer in subject, particularly for a subject having anti-
CC tumour necrosis factor (TNF) therapy. The method comprises determining
CC the expression level of B cell activation factor (BAFF) gene in a sample,
CC where elevated expression of BAFF gene relative to its level of
CC expression in healthy subject is indicative of predisposition to
CC developing cancer. Also claimed are small interfering RNA (siRNA)
CC molecules (ADR67998-ADR68129) which antagonizes the expression of a BAFF
CC gene. The siRNAs are useful in a method for preventing or delaying the
CC development of a cancer in a subject. The invention is also useful for
CC treating or preventing diseases such as systemic anaphylaxis or
CC hypersensitivity responses, drug allergies (e.g. to penicillin,
CC cephalosporins), insect sting allergies, inflammatory dermatoses (e.g.
CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis),
CC vasculitis (e.g. necrotizing, cutaneous and hypersensitivity vasculitis),
CC respiratory allergic diseases (e.g. asthma, allergic rhinitis,
CC interstitial lung diseases), multiple sclerosis, systemic lupus
CC erythematosus, diabetes, graft rejection, etc.
XX Sequence 21 BP; 6 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 139 GGGATGTGCTTAGAGGATT 158
Db 2 GGGAGTGCCTTAGAAGATT 21

RESULT 136
AAX79744/c
ID AAX79744 standard; DNA; 20 BP.
XX AC AAX79744;
XX 17-AUG-1999 (first entry)
XX PCR primer H5528 for mitochondrial DNA analysis.
XX PCR primer; human; mitochondrial DNA; genetic diagnosis;
KW adult disease contraction; ss.
XX Synthetic.
OS Homo sapiens.
XX JP11113597-A.
XX 27-APR-1999.
XX 13-OCT-1997; 97JP-00279127.
XX 13-OCT-1997; 97JP-00279127.
XX (TANA/) TANAKA M.
XX WPI; 1999-320841/27.
XX Genetic diagnosis using human mitochondrial DNA - comprises detecting
PT base replacements.
XX Example 2; Page 5; 15pp; Japanese.
XX This sequence represents a PCR primer that can be used in the method of
CC the invention. The method is for genetic diagnosis using human
CC mitochondrial DNA where there is at least one base replacement from among
CC the following five replacements: the 3010th base is changed from guanine
CC to adenine; the 4883rd base from cytosine to thymine; the 5178th base
CC from cytosine to adenine; the 8414th base from cytosine to thymine; and
CC the 14668th base from cytosine to thymine. The method can be used for
CC diagnosing the probability of contracting adult diseases. A confirmation
CC of base replacement can give a diagnosis of the level of probability of
CC contraction of adult diseases
XX Sequence 20 BP; 3 A; 3 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 ACAGACCAAGAGCCT 909
Db 19 ACAGACCAAGAGCCT 5

RESULT 137
ADJ33553/c
ID ADJ33553 standard; DNA; 20 BP.
XX ADJ33553;
XX 18-NOV-2004 (first entry)
XX Human LAR chimeric phosphorothioate oligonucleotide SEQ ID NO:82.
XX LAR; leukocyte antigen related protein; LAR inhibitor;
KW antisense oligonucleotide; cytostatic; gene therapy; metabolic disorder;
KW hyperproliferative disorder; cancer; human; phosphorothioate;

KW 2'-O-methoxyethyl; ss.
XX
OS Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004010956-A2.
XX
PD 05-FEB-2004.
XX
PF 31-JUL-2003; 2003WO-US023994.
XX
PR 31-JUL-2002; 2002US-00210838.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Bhanot S, Dobie KW, Freier SM;
XX
XX WPI; 2004-143728/14.
DR
XX
XX New compound comprises a sequence targeted to a nucleic acid encoding
PT Leukocyte Antigen Related protein (LAR), useful for preparing a
PT composition for treating metabolic or hyperproliferative disorders, e.g.
PT cancer.
XX
PS Example 15; SEQ ID NO 82; 197pp; English.
XX
XX The present invention describes a compound (I) comprising a sequence
CC comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding LAR
CC (leukocyte antigen related protein), where (I) specifically hybridises
CC with the nucleic acid and inhibits expression of LAR. Also described: (1)
CC a composition comprising the compound (I) and a carrier or diluent; (2)
CC inhibiting the expression of LAR in cells or tissues; (3) treating an
CC animal having or suspected of having a disease or condition associated
CC with LAR; and (4) screening for an antisense compound. (I) has cytostatic
CC activity, and can be used in gene therapy. The antisense oligonucleotide
CC compound (I) can be used for preparing a composition for treating
CC metabolic or hyperproliferative disorders, particularly cancer. The
CC present sequence represents a human LAR chimeric phosphorothioate
CC antisense oligonucleotide, which is used in an example from the present
CC invention.
XX
SQ Sequence 20 BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1079 CTTAACTCTCTGGG 1093
DB 20 CTTAACTCTCTGGG 6

RESULT 138
AAH73748
ID AAH73748 standard; DNA; 18 BP.
XX
AC AAH73748;
XX
DT 28-SEP-2001 (first entry)

XX PCR primer used to amplify murine Tspy pseudogene fragment.
DE
XX Sex determination; ratio; offspring; transgenic animal; PCR primer; tsy;
KW testis specific protein Y-linked; ss.
KW
XX Mus sp.
OS
XX WO200147353-A1.
PN
XX 05-JUL-2001.
PD
XX 27-DEC-2000; 2000WO-US035275.
PF
XX 27-DEC-1999; 99US-0173096P.
PR
XX (LIUC/) LIU C.
PA
XX Liu C, Costantini F, Wang J;
PI
XX WPI; 2001-425551/45.
DR
XX
XX Producing transgenic animals, involves creating transgene whose
PT expression interfere with sperm's ability to undergo fertilization, and
PT placing it under post-meiotic spermatogenesis-specific promoter control.
PT
XX Disclosure; Page 8; 20pp; English.
PS
XX This invention relates to a method for controlling the sex ratio of
CC offspring. The invention involves producing transgenic animals with
CC somatic/germ cells which contain a transgene whose expression can
CC interfere with sperm's ability to undergo fertilisation. The transgene is
CC placed under control of post-meiotic spermatogenesis-specific promoters,
CC and is inserted on to one of the sex chromosomes. The present sequence
CC represents a PCR primer used to amplify a fragment of murine tsy
CC pseudogene (testis specific protein Y-linked). The DNA fragment is used
CC in an example illustrating the method of the invention where the
CC transgene is targeted to the tsy locus on the Y chromosome. The method
CC is useful for producing transgenic animals having somatic/germ cells
CC containing one or more transgenes whose expression results in alteration
CC of the sex ratio of the offspring of the animals
XX
SQ Sequence 18 BP; 9 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 934 AAATGCAGAAATCTGAAGC 951
DB 1 AAATGCACAAATCTAAAGC 18

RESULT 139
ADE29652/c
ID ADE29652 standard; RNA; 19 BP.
XX
AC ADE29652;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:274.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.

ngs.res

Fri Aug 19 11:00:00 2005

inflammatory disease; asthma; septic shock; rheumatoid arthritis; psoriasis; inflammatory bowel disease; drug screening; genetic engineering; pharmacogenomic; gene mapping; ss.

Synthetic.

WO2003072590-A1.

04-SEP-2003.

28-JAN-2003; 2003WO-US002510.

20-FEB-2002; 2002US-0358580P.

11-MAR-2002; 2002US-0363124P.

06-JUN-2002; 2002US-0386782P.

29-AUG-2002; 2002US-0406784P.

05-SEP-2002; 2002US-0408378P.

09-SEP-2002; 2002US-0409293P.

15-JAN-2003; 2003US-0440129P.

(SIRN-) SIRNA THERAPEUTICS INC.

Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;

WPI; 2003-689980/65.

New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated protein kinase genes.

Example 3; SEQ ID NO 111; 164pp; English.

The present invention describes a short interfering nucleic acid (siNA) that downregulates expression of a mitogen-activated protein kinase (MAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or organisms by introduction of siNA; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that express siNA and cells containing these vectors. MAPK siNAs have cytostatic, anorectic, antidiabetic, antiinflammatory, antiasthmatic, immunosuppressive, antibacterial, antirheumatic, antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK siNAs can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obesity; diabetes types I and II; a wide range of tumours, and inflammatory diseases (asthma, septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target identification and validation; genetic engineering; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents a MAPK siNA which is used in the exemplification of the present invention.

Sequence 19 BP; 7 A; 2 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 382 AGGCAATGCAGTCATTTT 399
|||:|||||:|:|:
Db 2 AGAAAUGCAGUCAUUUU 19

RESULT 141
ADQ27277

ID ADQ27277 standard; DNA; 19 BP.

XX ADQ27277;

XX 26-AUG-2004 (first entry)

DT RNA interference target sequence #185.

XX

XX WO2003072590-A1.

PD 04-SEP-2003.

PF 28-JAN-2003; 2003WO-US002510.

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;

DR WPI; 2003-689980/65.

XX New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated protein kinase genes.

XX Example 3; SEQ ID NO 274; 164pp; English.

The present invention describes a short interfering nucleic acid (siNA) that downregulates expression of a mitogen-activated protein kinase (MAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or organisms by introduction of siNA; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that express siNA and cells containing these vectors. MAPK siNAs have cytostatic, anorectic, antidiabetic, antiinflammatory, antiasthmatic, immunosuppressive, antibacterial, antirheumatic, antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK siNAs can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obesity; diabetes types I and II; a wide range of tumours, and inflammatory diseases (asthma, septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target identification and validation; genetic engineering; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents a MAPK siNA which is used in the exemplification of the present invention.

XX Sequence 19 BP; 7 A; 3 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 382 AGGCAATGCAGTCATTTT 399
|||:|||||:|:|:
Db 18 AGAAAATGCAGTCATTTT 1

RESULT 140
ADE29489

ID ADE29489 standard; RNA; 19 BP.

XX ADE29489;

XX 29-JAN-2004 (first entry)

DT Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:111.

XX

XX short interfering nucleic acid; siNA; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour;

KW ss; detection; RNA interference; siRNA; gene silencing; gene expression;
KW cytotoxicity.
XX
OS Homo sapiens.
XX
PN WO2004048566-A1.
XX
PD 10-JUN-2004.
XX
XX 21-NOV-2003; 2003WO-JP014893.
PF
XX 22-NOV-2002; 2002JP-00340053.
PR
XX (NATO/) NATORI Y.
PA (SAIG/) SAIGO K.
PA (TEIK/) TEI K.
PA (NAIT/) NAITO Y.
XX
PI Saigo K, Tei K, Naito Y;
XX
DR WPI; 2004-487423/46.
XX
PT Detecting sequence of RNA interference useful for synthesizing siRNA, by
PT detecting regions in sequence fulfilling specific criteria such as base
PT at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
PT guanine or cytosine.
XX
PS Disclosure; SEQ ID NO 199; 325pp; Japanese.
XX
CC The invention relates to a method of detecting the base sequence for RNA
CC interference by detecting the regions in the DNA sequence fulfilling the
CC following requirements such as: (i) the base at 3' terminal is adenine,
CC thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine;
CC (iii) the seven base sequence at 3' terminal is rich in adenine, thymine
CC and uracil, and; (iv) there are bases in a such a number that it causes
CC RNA interference without showing cytotoxicity. The method is used for
CC designing and synthesizing siRNA causing RNA interference. This sequence
CC corresponds to an RNA interference target sequence of the invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 744 GGCAGCTGCCACCTTATG 761
Db | ||||| |||||
1 GACAGCTGCGACCTTATG 18

RESULT 142
ADR27528
ID ADR27528 standard; DNA; 19 BP.
XX
AC ADR27528;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human single nucleotide polymorphism detection primer #618.
XX
KW ss; primer; single nucleotide polymorphism; SNP; diagnosis;
KW disease association; linkage analysis; autoimmune disease;
KW rheumatoid arthritis; diabetes; multiple sclerosis;
KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
KW glomerulonephritis; Graves' disease; myocarditis; Sjogren disease;
KW primary systemic vasculitis; genotyping; gene therapy; PCR primer.
XX
OS Homo sapiens.
XX
PN WO2004067779-A2.
XX
PD 12-AUG-2004.

XX 30-JAN-2004; 2004WO-US002652.
PF
XX
PR 30-JAN-2003; 2003US-0443566P.
PR 18-MAR-2003; 2003US-0455444P.
PR 25-APR-2003; 2003US-0465241P.
PR 15-AUG-2003; 2003US-0495115P.
PR 13-NOV-2003; 2003US-0519270P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Begovich AB, Carlton VE, Schrodi SJ, Alexander HC;
XX
DR WPI; 2004-594223/57.
XX
PT New single nucleotide polymorphisms (SNPs) associated with rheumatoid
PT arthritis (RA), useful in identification of individuals at risk of
PT developing RA or other autoimmune disease, and in development of
PT therapeutic agents.
XX
PS Claim 21; SEQ ID NO 50200; 141pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising at
CC least 8 contiguous nucleotides where one of the nucleotides is a single
CC nucleotide polymorphism (SNP) selected from any one of the nucleotide
CC sequences of SEQ ID NOS:1-669 and 1339-49582, or their complements. The
CC SNPs are useful as targets for the design of diagnostic reagents and the
CC development of therapeutic agents, as well as for disease association and
CC linkage analysis. In particular, the SNPs are useful for identifying an
CC individual who is at an increased or decreased risk for developing an
CC autoimmune disease such as rheumatoid arthritis, type 1 diabetes,
CC multiple sclerosis, systemic lupus erythematosus, inflammatory bowel
CC diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia,
CC asthma, vitiligo, glomerulonephritis, Graves' disease, myocarditis,
CC Sjogren disease, or primary systemic vasculitis. Methods associated with
CC the SNPs are useful for early detection of the disease, for providing
CC clinically important information for the prevention and/or treatment of
CC the autoimmune diseases particularly rheumatoid arthritis, and for
CC screening and selecting therapeutic agents. The SNPs are useful for human
CC identification applications. The genes containing the SNPs are useful for
CC treating the diseases defined above. The nucleic acid molecules are
CC useful as hybridization probes for genotyping SNPs in messenger RNA,
CC cDNA, genomic DNA, and genomic clones. The nucleic acid molecules are
CC useful for constructing host cells expressing a part or all of the
CC nucleic acid molecules and variant peptides, for constructing transgenic
CC animals, for assaying or screening drugs that modulate nucleic acid
CC expression, or for gene therapy in patients whose cells have aberrant
CC gene expression. This sequence corresponds to a PCR primer which
CC hybridises to the nucleic acids of the invention to amplify the SNP
CC containing region. (Note: SEQ ID NOS 1-49582 are claimed and stated as
CC being provided in the specification, however these sequences are not
CC provided in the printed specification).
XX
SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1064 CCAGTGGCTAAACCACTT 1081
Db ||||| |||||
2 CCAGTGGCTCAACAACCTT 19

RESULT 143
AAT36153/c
ID AAT36153 standard; DNA; 20 BP.
XX
AC AAT36153;
XX
DT 15-MAY-1997 (first entry)
XX
DE PCR primer for detecting mutations in human Int6 gene homologue.

XX MMTV; mouse mammary tumour virus; Int6; breast cancer; neoplasia;
KW diagnosis; treatment; immunotherapy; vaccine; probe; primer;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN WO9624672-A1.
XX
XX 15-AUG-1996.
PD
XX 09-FEB-1996; 96WO-US001884.
PF
XX
XX 09-FEB-1995; 95US-00385998.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Marchetti A, Buttitta F, Smith GH, Callahan R;
PI
XX WPI; 1996-384444/38.
DR
XX
XX DNA encoding Int6 tumour associated protein - and use of reagents derived
PT from them in cancer gene therapy, vaccines, diagnosis and immunotherapy.
PT
XX
XX Claim 16; Page 22; 93pp; English.
PS
XX AAT36149-T36174 are PCR primers derived from intronic sequences of human
XX homologue of the murine Int6 gene located at chromosome 15 of a mouse
CC genome. The primers are used for detecting mutations within the human
CC Int6 gene. The Int6 gene is associated with MMTV (mouse mammary tumour
CC virus) integration into a host genome during tumourigenesis. Primers and
CC probes can be used in assays to diagnose MMTV infection, or any other
CC Int6 gene integration. Antibodies against the Int6 protein can be used in
CC the same way
XX
XX Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 926 CTTATTAGAAATGCAGAA 943
Db || |||| |||||
20 CTAATTAAAAAATGCAGAA 3
RESULT 144
AAI72504/C
ID AAI72504 standard; DNA; 20 BP.
XX
XX AAI72504;
AC
XX 21-MAY-2002 (first entry)
DT
XX Human Int6 exon 3 primer #1.
DE
XX PCR; murine; human; Int6; integration site; deregulation; neoplasia;
KW mouse mammary tumour virus; MMTV; cancer; immunotherapy; gene therapy;
KW prenatal screening; foetus; vaccine; primer; polymerase chain reaction;
KW amplify; ss.
XX
XX Homo sapiens.
OS
XX US6342392-B1.
PN
XX 29-JAN-2002.
PD
XX 23-AUG-1999; 99US-00378842.
PF
XX 09-FEB-1995; 95US-00385998.
PR
XX 09-FEB-1996; 96WO-US001884.
PR
XX 25-SEP-1997; 97US-00875847.
PR
XX

(USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Marchetti A, Buttitta F, Smith GH, Callahan R;
PI
XX WPI; 1996-384444/38.
DR
XX
XX DNA encoding Int6 tumour associated protein - and use of reagents derived
PT from them in cancer gene therapy, vaccines, diagnosis and immunotherapy.
PT
XX
XX Claim 11; Col 14; 45pp; English.
PS
XX The sequences given in AAI72500-23 are primers which were used to amplify
CC the human Int6 coding sequence. The primers were derived from the
CC intronic sequences which border the 5' and 3' ends of each exon of the
CC human Int6 gene. Human Int6 is organised into 13 exons as is the murine
CC Int6 gene, and contains a CA-repeat in the 7th intron. Human Int6 has
CC been localised to chromosome 8, more specifically to 8q22-q24. Int6 is an
CC integration site for mouse mammary tumour virus (MMTV), which causes
CC deregulation of expression of cellular genes adjacent to the site of MMTV
CC integration in mammary tumours. The Int6 protein has been found to be
CC highly conserved across species, with Drosophila Int6 being 60% identical
CC to human/mouse Int6. This indicates that Int6 is serving a basic life
CC function. The method of the invention comprises assaying a sample to
CC detect a human Int6 nucleic acid sequence, or its fragment, by contacting
CC the sample with a sequence of at least 15 consecutive nucleotides of
CC human Int6 cDNA or a conservative variant of it, where a disrupted
CC expression or loss of expression of the variant is associated with
CC neoplasia. The method is useful for prenatal screening of a foetus or to
CC pre-symptomatically screen a subject at risk of having cancer. Detecting
CC mutations in the Int6 gene can provide diagnostic and prognostic
CC information. The nucleic acids and proteins are useful in immunotherapy,
CC gene therapy or as vaccines for treating or preventing cancer. The
CC nucleic acids are useful as probes for isolating homologues of Int6 gene
CC or for detecting mutations in the Int6 gene
XX
XX Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 926 CTTATTAGAAATGCAGAA 943
Db || |||| |||||
20 CTAATTAAAAAATGCAGAA 3
RESULT 145
AAZ03074
ID AAZ03074 standard; DNA; 20 BP.
XX
XX AAZ03074;
AC
XX 07-OCT-1999 (first entry)
DT
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
DE
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
OS
XX Chlamydia trachomatis.
OS
XX WO9928475-A2.
PN
XX 10-JUN-1999.
PD
XX 27-NOV-1998; 98WO-IB001939.
PF
XX 28-NOV-1997; 97FR-00015041.
PR
XX 17-DEC-1997; 97FR-00016034.
PR
XX 04-NOV-1998; 98US-0107077P.
PR

XX (GEST) GENSET.
PA Griffais R;
XX WPI; 1999-371125/31.
XX Genome sequence of Chlamydia trachomatis.
PT Disclosure; Page 1577; 1755pp; English.
XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 230 AGAGTCACCTATGACTCA 247
Db 3 AGAGGTACCTATGACTCA 20

RESULT 146
AAC73799
ID AAC73799 standard; DNA; 20 BP.
XX AAC73799;
AC
XX 02-FEB-2001 (first entry)
XX Mouse IL-5R antisense oligonucleotide ISIS #23238.
DE Mouse; interleukin-5; IL-5; signal transduction;
XX antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;
KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;
KW inflammation; cancer; ss.
XX Mus musculus.
OS Synthetic.
OS WO200058512-A1.
XX 05-OCT-2000.
PD 17-MAR-2000; 2000WO-US007318.
PF 26-MAR-1999; 99US-00280799.
XX (ISIS-) ISIS PHARM INC.
PA Dean NM, Karras JG, McKay R;
XX WPI; 2000-594648/56.
XX Antisense oligonucleotide compound used to treat asthma and eosinophilic
PT syndrome in humans modulates interleukin-5 signal transduction.
PT Example 25; Page 77; 156pp; English.
XX The present sequence is an oligonucleotide used for antisense modulation

CC of interleukin-5 (IL-5) signal transduction. Oligonucleotides were
CC designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha.
CC The antisense oligonucleotides may be used for the treatment of diseases
CC associated with IL-5 signal transduction, IL-5 expression or IL-5
CC receptor-alpha expression. Such diseases include asthma and eosinophilic
CC syndrome. The oligonucleotides are also useful for research uses and to
CC prevent or delay infection, inflammation or tumour formation
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCTCG 19

RESULT 147
AAS15166
ID AAS15166 standard; DNA; 20 BP.
XX AAS15166;
AC
XX 16-JAN-2002 (first entry)
XX Mouse interleukin-5 receptor antisense oligonucleotide ISIS 23238.
DE Mouse; antisense oligonucleotide; IL-5R; interleukin-5 receptor; ss;
KW antiinfection; antiinflammatory; cytostatic; inflammation; infection;
KW tumour; ISIS 23238; probe.
XX Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..20 /*tag= b
FT /mod_base= OTHER
FT /note= "2' methoxyethoxy residues. All cytosines in this
FT region are also 5-methyl-cytosine"
XX WO200172765-A1.
XX 04-OCT-2001.
XX 28-MAR-2000; 2000WO-US008174.
XX 28-MAR-2000; 2000WO-US008174.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Crooke ST, Manoharan M, Wyatt JR, Baker BF, Monia BP;
PI Freier SM, McKay R, Karras JG;
XX WPI; 2001-626250/72.
XX Controlling cell behavior, useful e.g. for treatment of tumors, by
PT modulating processing, e.g. splicing, of specific mRNA sequences with non
PT -cleaving antisense agents.
XX Example 8; Page 70; 121pp; English.
PS The invention relates to controlling cell behaviour by modulating the
XX processing of a selected wild-type mRNA target in the cell, is new. The
CC mRNA is bound to a specific-binding antisense compound that does not
CC cleave bound mRNA. The antisense oligonucleotides are useful as research
CC reagents, diagnostic agents (in hybridisation assays), and for treatment

CC or prevention of diseases, e.g. to prevent or delay infections,
CC inflammation and tumours. The present sequence is an antisense
CC oligonucleotide which targets exon 9 of mouse interleukin-5 receptor,
CC with mismatched bases
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 148
ABV73625
ID ABV73625 standard; DNA; 20 BP.
XX
AC ABV73625;
XX
XX 06-JAN-2003 (first entry)
XX
XX Mouse IL-5R antisense oligonucleotide uniform 2'MOE #SEQ ID 16.
XX
XX Antisense therapy; antisense oligonucleotide; apoptosis; mitosis;
KW differentiation; stress; hormone; cytokine; signalling molecule;
KW mRNA modulation; mRNA cleavage; therapeutic; mouse; IL-5R;
KW interleukin 5 receptor; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "all nucleotides are 2'-methoxyethoxy (2'MOE); all
FT C nucleotides are 5-methyl-cytosines; all linkages are
FT phosphorothioate"
XX
XX US2002049173-A1.
XX
XX 25-APR-2002.
PD
XX
XX 12-DEC-2000; 2000US-00734847.
PF
XX
XX 26-MAR-1999; 99US-00277020.
PR
XX
XX (BENN/) BENNETT C F.
PA (CROO/) CROOKE S T.
PA (MANO/) MANOHARAN M.
PA (WYAT/) WYATT J.
PA (BAKE/) BAKER B F.
PA (MONI/) MONIA B P.
PA (MCKA/) MCKAY R.
PA (KARR/) KARRAS J G.
XX
XX Bennett CF, Crooke ST, Manoharan M, Wyatt J, Baker BF, Monia BP;
PI Mckay R, Karras JG;
XX
XX WPI; 2002-415043/44.
DR
XX Controlling cell behavior by modulating mRNA modification, useful in
XX therapeutics and as research tool, comprises using antisense
PT oligonucleotide which hybridize to mRNA and block modification regions
PT such as splice acceptor sites.
PT
XX Example 8; Page 23; 50pp; English.
PS
XX The invention relates to the control of cell behaviour by modulating the
CC processing of a wild-type mRNA target, comprising binding to the target
CC an antisense compound which specifically hybridises to the target and

CC does not elicit cleavage of the mRNA upon binding. The method of the
CC invention can be used in therapeutics (i.e antisense therapy), including
CC prophylaxis, and as a research tool. It is used for controlling the
CC behaviour of a cell (especially responses such as apoptosis, mitosis,
CC differentiation and quiescence to stimuli such as stress, hormones,
CC cytokines and other signalling molecules), tissue or organism through
CC antisense modulation of mRNA processing. The current sequence represents
CC a mouse IL-5R (interleukin-5 receptor) antisense oligonucleotide uniform
CC 2'MOE assigned SEQ ID 16, designed to target exon 9 and intron/exon
XX boundaries
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCAG 1067
Db 2 ACTTCCTTACCTTTCCTG 19

RESULT 149
ABL45391
ID ABL45391 standard; DNA; 20 BP.
XX
AC ABL45391;
XX
XX 11-APR-2002 (first entry)
DT
XX Human chromosome 21q22.1 PCR primer SEQ ID NO:2435.
DE
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX JP2001321190-A.
PN
XX 20-NOV-2001.
PD
XX
XX 12-MAR-2001; 2001JP-00068285.
PF
XX
XX 10-MAR-2000; 2000JP-00066716.
PR
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
DR
XX
XX Arraying genome clones.
PT
XX
XX Claim 6; Page 53; 528pp; Japanese.
PS
XX
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634

CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1010 TTTGAGAAGCATCATCAT 1027
Db 1 TTTGAAAAGCATCAGCAT 18
RESULT 150
AAL42513/c
ID AAL42513 standard; DNA; 20 BP.
XX
AC AAL42513;
XX 28-JUN-2002 (first entry)
XX Alpha-V integrin-specific inhibitory antisense nucleic acid 2.
DE Antisense nucleic acid; ss; alpha-V integrin chain; antisense inhibition;
XX cell adhesion modulation; platelet aggregation; immune function;
KW tissue repair; cell proliferation; tumour invasion; cancer; gingivitis;
KW chronic inflammatory disease; Chron's disease; rheumatoid arthritis;
KW ocular neovascular disease; diabetic retinopathy; osteoporosis;
KW excessive bone resorption; inflammatory skin disorder; psoriasis.
XX Unidentified.
OS EP1197553-A1.
XX PN 17-APR-2002.
XX PD 12-OCT-2000; 2000EP-00121394.
XX PF 12-OCT-2000; 2000EP-00121394.
XX PR (ATHR-) A3D GMBH ANTISENSE DESIGN & DRUG DEV.
XX PA Kronenwett R, Graef T, Haas R, Nedbal W;
XX PI WPI; 2002-364499/40.
XX DR Antisense nucleic acid against alpha V integrin for use in pharmaceutical
XX PT compositions for the specific inhibition of the expression of alpha
XX PT integrins in mammalian cells useful.
XX PS Claim 8; Page 3; 17pp; English.
XX CC The invention comprises antisense nucleic acids that are capable of
CC binding to the transcription product of the gene coding for the alpha-V
CC integrin chain, thereby inhibiting the expression of alpha-V integrins in
CC mammalian cells. The antisense nucleic acids of the invention are useful
CC for the treatment of pathological disorders by the modulation of cell
CC adhesion which affects platelet aggregation, immune functions, tissue
CC repair, cell proliferation, tumour invasion, inflammation and inherited
CC diseases. Disorders which can be treated include: cancer; restenosis
CC after angioplasty; stenosis to vein bypass; chronic inflammatory diseases
CC (e.g. Chron's disease and rheumatoid arthritis); ocular neovascular
CC diseases (e.g. diabetic retinopathy); disorders associated with excessive
CC bone resorption (e.g. osteoporosis); disorders of mammalian oral cavity
CC (e.g. gingivitis); and inflammatory skin disorders (e.g. psoriasis). The
CC present DNA sequence represents an antisense nucleic acid of the
CC invention used to inhibit alpha-V integrin expression
XX SQ Sequence 20 BP; 10 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 417 TTTTCCTTATATTGGAA 434
Db 18 TTTTCCTTATATTCCAA 1
RESULT 151
ABT05772/c
ID ABT05772 standard; DNA; 20 BP.
XX
AC ABT05772;
XX 16-OCT-2002 (first entry)
DT Nod2 related oligonucleotide SEQ ID No 52.
XX Intracellular signaling polypeptide; Nod2; Crohn's disease; mutation;
KW cytosine residue insertion; nuclear factor; NF-B activation; NF-kappa B;
KW RICK signaling; gene therapy; transgenic plant; plant; ds.
XX Unidentified.
OS WO200244426-A2.
XX PN 06-JUN-2002.
XX PD 26-OCT-2001; 2001WO-US051068.
XX PF 30-OCT-2000; 2000US-0244266P.
XX PR 25-APR-2001; 2001US-0286316P.
XX PR 26-OCT-2001; 2001US-00286316.
XX (UNMI) UNIV MICHIGAN.
PA (UYCH-) UNIV CHICAGO.
XX
PI Nunez G, Inohara N, Ogura Y, Cho J, Nicolae DL, Bonen D;
XX WPI; 2002-547704/58.
XX New isolated intracellular signaling polypeptide, termed Nod2, useful for
XX PT producing an antibody that recognizes Nod2, and as a target for screening
XX PT drugs.
XX Example 9; Page 231; 316pp; English.
XX The invention relates to an isolated intracellular signaling polypeptide,
XX termed Nod2, comprising a sequence of 1007 or 1040 amino acids, given in
XX the specification. The nucleic acid encoding the isolated protein is
XX useful for identifying subjects at risk of developing Crohn's disease by
XX providing a nucleic acid from the subject, where the nucleic acid
XX comprises a Nod2 gene, and detecting the presence or absence of one or
XX more variations in the Nod2 gene. Detecting comprises comparing the
XX sequence of the nucleic acid to the sequence of a wild-type Nod2 nucleic
XX acid. Detection is accomplished by hybridisation analysis. The method
XX further comprises determining if the subject is at risk of developing
XX Crohn's disease based on the presence or absence of the variations, and
XX determining a genotype relative risk or a population attributable risk
XX for the subject. The variation is a polymorphism or a mutation,
XX preferably a cytosine residue insertion, where the mutation causes a
XX deletion of a Leu-Arg-Arg repeat of Nod2. The variation results in
XX increased nucleic acid (NF)-B activation. The variation is selected
XX from the sequences of the Nod2 gene. The isolated protein is useful as a
XX target for screening drugs that can alter, for example, RICK signaling,
XX and thus the physiological effects of NF-kappa B. The Nod2 gene is useful
XX for producing the isolated protein by recombinant techniques, as starting
XX nucleic acids for directed evolution, for gene therapy, or to decrease
XX the level of Nod2 protein or mRNA in transgenic plants, plant tissues, or
XX plant cells as compared to wild-type plants, plant tissues or plant
XX cells. This polynucleotide represents a Nod2 gene related DNA sequence of
XX the invention
XX SQ Sequence 20 BP; 5 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 784 TGGGGATGTGCTTGGAGA 801
DB 18 TGGGGATGTGCTTGAAGA 1

RESULT 152
ABX04453
ID ABX04453 standard; DNA; 20 BP.
XX AC ABX04453;
DT 13-JAN-2003 (first entry)
XX Mouse Interleukin 5 receptor antisense oligonucleotide ISIS 23238.
DE Mouse; ss; antisense; interleukin 5; IL-5; IL-5 receptor; antiasthmatic;
KW immunosuppressant; eosinophilic syndrome; asthma.
KW
XX Mus musculus.
OS Synthetic.
XX US2002128216-A1.
PN 12-SEP-2002.
XX 07-MAR-2001; 2001US-00800629.
PF 26-MAR-1999; 99US-00280799.
XX 17-MAR-2000; 2000WO-US007318.
PR (DEAN/) DEAN N M.
XX (KARR/) KARRAS J G.
PA (MCKA/) MCKAY R.
PA (MANO/) MANOHARAN M.
XX Dean NM, Karras JG, Mckay R, Manoharan M;
PI WPI; 2003-039602/03.
DR Novel antisense compound for treating disease/condition e.g. eosinophilic
XX syndrome or asthma associated with interleukin-5 or IL-5 receptor
PT expression or IL-5 signal transduction, modulates IL-5 signal
PT transduction.
PT
XX
PS Example 25; Page 24; 77pp; English.
XX The invention relates to an antisense compound of 8-30 nucleobases in
CC length, which modulates interleukin (IL)-5 signal transduction. Also
CC include are a pharmaceutical composition comprising the antisense
CC oligonucleotide and a pharmaceutically acceptable carrier or diluent, and
CC a diagnostic kit for detecting the expression level of the membrane form
CC versus soluble form of IL-5 receptor a. The antisense compound is useful
CC for modulating IL-5 signal transduction, modulating expression of
CC mammalian IL-5 or modulating the expression of mammalian IL-5 receptor a,
CC in cells or tissues, for altering the ratio of the isoforms of mammalian
CC IL-5 receptor a in mammalian cells or tissues, treating a mammalian
CC having a disease or condition associated with IL-5 signal transduction,
CC IL-5 expression or IL-5 receptor a expression, where the disease or
CC condition include eosinophilic syndrome or asthma. An antisense compound
CC which alters splicing of an RNA encoding IL-5 receptor a is also useful
CC for treating a mammal having a disease or condition. The present sequence
CC is an antisense oligonucleotide targeting mouse IL-5 receptor
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTTCCAG 1067
DB 2 ACTTCCTTACCTTTCTG 19

RESULT 153
ABZ81557
ID ABZ81557 standard; DNA; 20 BP.
XX AC ABZ81557;
DT 26-AUG-2003 (first entry)
XX PKA regulatory subunit RII beta antisense oligonucleotide ISIS #114487.
DE Human; cytostatic; antidiabetic; antisense therapy; phosphorothioate;
XX protein kinase inhibitor; protein kinase A; PKA;
KW regulatory subunit RII beta; cAMP-dependent protein kinase; diabetes;
KW cancer; infection; inflammation; tumour; ss.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Oligonucleotide has phosphorothioate backbone and
FT all cytidine nucleotides are 5-methylcytidine. Optionally
FT some nucleotides with 2'-methoxyethyl (2'-MOE wings)
FT modification"
XX
XX WO2003010283-A2.
PN 06-FEB-2003.
XX 15-JUL-2002; 2002WO-US022629.
PF 25-JUL-2001; 2001US-00915485.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
PI WPI; 2003-239434/23.
DR New antisense oligonucleotides targeted to nucleic acid encoding protein
XX kinase A regulatory subunit RII beta, useful in treating diseases e.g.
PT cancer associated with the aberrant expression of the protein kinase.
PT
XX
PS Claim 3; Page 74; 98pp; English.
XX The present invention relates to novel antisense oligonucleotides
CC (ABZ81522-ABZ81593) which are targeted to human protein kinase A (PKA)
CC regulatory subunit RII beta nucleotide sequence (ABZ81513), and which
CC specifically hybridise with and inhibit the expression of the PKA
CC regulatory subunit RII beta (PKA is also known as cAMP-dependent protein
CC kinase). The antisense oligonucleotides are useful for modulating the
CC expression of PKA regulatory subunit RII beta and for treating diseases
CC or conditions associated with aberrant expression of PKA regulatory
CC subunit RII beta, e.g. diabetes or cancer. The antisense compounds are
CC also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent
CC or delay infection, inflammation or tumour formation, as research
CC reagents and kits, and in distinguishing between functions of various
CC members of a biological pathway
XX
SQ Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 663 TATGTTACTCAAAATTATG 680

```
Db          ||||| ||||| ||||| |||||
            3 TATGTTACTGACATTATG 20

RESULT 154
AAD57723/c
ID  AAD57723 standard; DNA; 20 BP.
XX
AC  AAD57723;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human PLSCR4 antisense oligonucleotide, ISIS #196336.
XX
KW  Human; phospholipid scramblase 4; autoimmune disorder; gene therapy;
KW  neurodegenerative disease; hyperproliferative disorder; HuPLSCR4;
KW  MuPLSCR4; PLSCR4; LOC57088; antisense; phosphorothioate; ss.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  modified_base 1..20
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "Phosphorothioate backbone; All cytidine residues
FT  are 5-methylcytidines"
FT  modified_base 1..5
FT  /*tag= b
FT  /mod_base= OTHER
FT  /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT  modified_base 16..20
FT  /*tag= c
FT  /mod_base= OTHER
FT  /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN  WO2003048331-A2.
XX
PD  12-JUN-2003.
XX
PF  04-DEC-2002; 2002WO-US038619.
XX
PR  04-DEC-2001; 2001US-00012984.
XX
PA  (ISIS-) ISIS PHARM INC.
XX
PI  Dobie K;
XX
DR  WPI; 2003-569054/53.
XX
PT  New compound, useful for preparing a composition for treating
PT  hyperproliferative or autoimmune disorders, comprises a sequence targeted
PT  to a nucleic acid encoding human phospholipid scramblase 4.
XX
PS  Example 15; Page 78; 166pp; English.
XX
CC  The invention relates to novel antisense compounds targetted to a nucleic
CC  acid encoding human phospholipid scramblase 4 (also known as PLSCR4,
CC  HuPLSCR4, MuPLSCR4 and LOC57088) to inhibit its expression. Antisense
CC  compounds of the invention are useful for preparing compositions for
CC  treating neurodegenerative diseases, e.g. hyperproliferative or
CC  autoimmune disorders. The invention is also useful in gene therapy. The
CC  present sequence is an antisense oligo targetted to human PLSCR4 DNA
XX
SQ  Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 418 TTTCCTTATATTTGGAAG 435
    ||||| ||||| ||||| |||||
Db 18 TTGCCTTATATTTGAAAG 1
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```
RESULT 155
ADE25541/c
ID  ADE25541 standard; DNA; 20 BP.
XX
AC  ADE25541;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Human TLR1 related PCR primer SEQ ID NO 7.
XX
KW  Human; TLR1; cancer; cytostatic; primer; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
PN  WO2003061697-A1.
XX
PD  31-JUL-2003.
XX
PF  26-DEC-2002; 2002WO-JP013642.
XX
PR  27-DEC-2001; 2001JP-00398165.
XX
PA  (TAKE ) TAKEDA CHEM IND LTD.
XX
PI  Hikichi Y, Katsuyama R, Kakoi Y, Nishizawa S;
XX
DR  WPI; 2003-598709/56.
XX
PT  Treatment and prevention for cancer of the e.g. digestive system, liver
PT  and lung.
XX
PS  Example 2; Page 89; 98pp; Japanese.
XX
CC  The invention relates to the treatment and prevention of cancer
CC  comprising a compound that inhibits the activity of protein or peptide
CC  fragment of a fully defined amino acid sequence TLR1 given as SEQ ID NO
CC  1. TLR1 is useful in the treatment and prevention of cancers of the large
CC  intestine, mammary glands, lung, prostate, digestive tract, stomach and
CC  liver. TLR1 gene expression is detected in breast cancer tissue. The
CC  present sequence is that of a human TLR1 related PCR primer used in
CC  examples of the invention.
XX
SQ  Sequence 20 BP; 10 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 305 GTTTCCTGCCTTTGGATT 322
    ||||| ||||| ||||| |||||
Db 19 GTTCCTGCATTTGGATT 2

RESULT 156
ABZ93663
ID  ABZ93663 standard; DNA; 20 BP.
XX
AC  ABZ93663;
XX
DT  17-OCT-2003 (first entry)
XX
DE  Human oligonucleotide sequence.
XX
KW  Human; antisense; lung dysfunction; nasal airway dysfunction;
KW  antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW  antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW  antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW  adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW  lung inflammation; respiratory disease; ds.
XX
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Fri Aug 19 11:00:00 2005

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OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 8905; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 8 A; 6 C; 2 G; 2 T; 0 U; 2 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 936 ATGCAGAATCTGAAGCCCCA 955
Db ||| ||||| || |||||
1 ATGNAGAATCNAAACCCCCA 20
RESULT 157
ABD29893
ID ABD29893 standard; DNA; 20 BP.
XX
AC ABD29893;
XX
DT 29-JUL-2004 (first entry)
XX
DE T74688-derived oligonucleotide SEQ ID 8905.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
```

```
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 8905; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 8 A; 6 C; 2 G; 2 T; 0 U; 2 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 936 ATGCAGAATCTGAAGCCCCA 955
Db ||| ||||| || |||||
1 ATGNAGAATCNAAACCCCCA 20
RESULT 158
ADJ86050
ID ADJ86050 standard; DNA; 20 BP.
XX
AC ADJ86050;
```


XX 06-MAY-2004 (first entry)
DT Nucleic acid analysis-related Tag probe SeqID1118.
XX
DE
XX
KW restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
KW T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
KW assay development; product development; product validation;
KW quality control; probe; ss.
XX
OS Synthetic.
OS Unidentified.
XX
XX WO2004007684-A2.
PN
XX
PD 22-JAN-2004.
XX
XX 14-JUL-2003; 2003WO-US021990.
PF
XX
XX 12-JUL-2002; 2002US-0395530P.
PR
XX (AFFY-) AFFYMETRIX INC.
PA
XX Christians FC;
PI
XX WPI; 2004-122923/12.
DR
XX New DNA molecules made by annealing and extending overlapping 60mer
PT oligonucleotides, useful in producing synthetic tag genes useful as assay
PT controls, in assay development, product development and for quality
PT control.
XX
PS Disclosure; SEQ ID NO 1118; 91pp; English.
XX
XX This invention relates to a novel DNA molecule which comprises a DNA
CC molecule made up of the following elements in a 5' to 3' direction: a
CC first restriction endonuclease site; a T3 promoter site; at least one Tag
CC gene comprising at least 5 20mer Tag sequences; a Poly A site having at
CC least 21 consecutive A residues; a second restriction endonuclease site
CC which may be the same or different than the first restriction
CC endonuclease site; or a T7 Promoter on the opposite strand as the T3
CC promoter. The invention may be useful in nucleic acid analysis, in
CC particular to synthetic Tag genes useful as assay controls, in assay
CC development, product development and validation and for quality control.
CC The present sequence is that of a Tag oligonucleotide probe which may be
CC used during the creation of the novel DNA molecule of the invention.
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 697 TCATGTAGTCACGGTGCT 714
Db 2 TCATGTAGTGACAGTGCT 19

RESULT 159
ADJ54494/c
ID ADJ54494 standard; DNA; 20 BP.
XX
AC ADJ54494;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human B7-2 DNA antisense oligonucleotide #109.
XX
KW Airway hyperresponsiveness; pulmonary inflammation;
KW antisense oligonucleotide; human; B7 protein; B7-2; asthma;
KW antiasthmatic; antiinflammatory; ss.
XX
OS Homo sapiens.

XX 06-MAY-2004 (first entry)
DT Nucleic acid analysis-related Tag probe SeqID1118.
XX
DE
XX
KW restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
KW T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
KW assay development; product development; product validation;
KW quality control; probe; ss.
XX
OS Synthetic.
OS Unidentified.
XX
XX WO2004007684-A2.
PN
XX
PD 22-JAN-2004.
XX
XX 14-JUL-2003; 2003WO-US021990.
PF
XX
XX 12-JUL-2002; 2002US-0395530P.
PR
XX (AFFY-) AFFYMETRIX INC.
PA
XX Christians FC;
PI
XX WPI; 2004-122923/12.
DR
XX New DNA molecules made by annealing and extending overlapping 60mer
PT oligonucleotides, useful in producing synthetic tag genes useful as assay
PT controls, in assay development, product development and for quality
PT control.
XX
PS Disclosure; SEQ ID NO 1118; 91pp; English.
XX
XX This invention relates to a novel DNA molecule which comprises a DNA
CC molecule made up of the following elements in a 5' to 3' direction: a
CC first restriction endonuclease site; a T3 promoter site; at least one Tag
CC gene comprising at least 5 20mer Tag sequences; a Poly A site having at
CC least 21 consecutive A residues; a second restriction endonuclease site
CC which may be the same or different than the first restriction
CC endonuclease site; or a T7 Promoter on the opposite strand as the T3
CC promoter. The invention may be useful in nucleic acid analysis, in
CC particular to synthetic Tag genes useful as assay controls, in assay
CC development, product development and validation and for quality control.
CC The present sequence is that of a Tag oligonucleotide probe which may be
CC used during the creation of the novel DNA molecule of the invention.
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 697 TCATGTAGTCACGGTGCT 714
Db 2 TCATGTAGTGACAGTGCT 19

RESULT 159
ADJ54494/c
ID ADJ54494 standard; DNA; 20 BP.
XX
AC ADJ54494;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human B7-2 DNA antisense oligonucleotide #109.
XX
KW Airway hyperresponsiveness; pulmonary inflammation;
KW antisense oligonucleotide; human; B7 protein; B7-2; asthma;
KW antiasthmatic; antiinflammatory; ss.
XX
OS Homo sapiens.

XX US2004023917-A1.
PN
XX 05-FEB-2004.
PD
XX 23-MAY-2003; 2003US-00444206.
PF
XX 31-DEC-1996; 96US-00777266.
PR 04-JUN-1999; 99US-00326186.
PR 25-MAY-2000; 2000WO-US014471.
PR 09-MAY-2001; 2001US-00851871.
XX
XX (BENN/) BENNETT C F.
PA (VICK/) VICKERS T A.
PA (KARR/) KARRAS J G.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX WPI; 2004-132608/13.
DR
XX Treating airway hyperresponsiveness or pulmonary inflammation comprises
PT administering an antisense compound targeted to a nucleic acid molecule
PT encoding a human B7 protein to the individual.
PT
XX Example 27; SEQ ID NO 314; 182pp; English.
PS
XX The invention relates to a method for treating airway hyperresponsiveness
CC or pulmonary inflammation in an individual comprising administering an
CC antisense compound targeted to a nucleic acid molecule encoding a human
CC B7 protein. The invention also relates to a method of inhibiting
CC expression of a nucleic acid molecule encoding B7-1 or B7-2. The
CC antisense compound is an antisense oligonucleotide which has a modified
CC sugar moiety and nucleobase. The human B7 protein is human B7-1 or B7-2
CC protein or both. The compound is useful for treating airway
CC hyperresponsiveness or pulmonary inflammation, which is associated with
CC asthma, by inhibiting expression of human B7 protein. This sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 1 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 AAATAGACCTGTCAATT 657
Db 20 AAATAGACCTCTCAATT 3

RESULT 160
ADJ23824
ID ADJ23824 standard; DNA; 20 BP.
XX
AC ADJ23824;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2222.
XX
KW Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key... Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2-'methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all


```
FT      cytidine residues are 5-methylcytidines"
XX
PN      WO2004009541-A2.
XX
PD      29-JAN-2004.
XX
PF      18-JUL-2003; 2003WO-US022410.
XX
PR      19-JUL-2002; 2002US-0397106P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Bhat BG;
XX
DR      WPI; 2004-132912/13.
XX
PT      New antisense oligonucleotide for modulating endothelial lipase
PT      expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT      high density lipoprotein or cardiovascular disorders.
XX
PS      Claim 3; SEQ ID NO 2222; 1007pp; English.
XX
CC      The present invention relates to antisense oligonucleotides (ADJ21603-
CC      ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC      (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC      with and inhibits the expression of EL. The antisense oligonucleotides
CC      are useful for modulating the expression of endothelial lipase in cells
CC      or tissues to treat diseases associated with EL expression, such as
CC      dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC      disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC      used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ      Sequence 20 BP; 3 A; 4 C; 12 G; 1 T; 0 U; 0 Other;
      Query Match      1.3%; Score 14.8; DB 1; Length 20;
      Best Local Similarity 88.9%; Pred. No. 1.4e+02;
      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      22 CGGGCCGTGGCAGGAAC 39
Db      1 CGGGCGGTGGCAGGAGC 18

RESULT 161
ADJ22770
ID      ADJ22770 standard; DNA; 20 BP.
XX
AC      ADJ22770;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human endothelial lipase antisense oligonucleotide, SEQ ID 1168.
XX
KW      Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW      Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW      cardiovascular disorder; metabolic syndrome X; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "This oligonucleotide has a phosphorothioate
FT      backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT      and 3' ends, which are 4 nucleotides in length. Also all
FT      cytidine residues are 5-methylcytidines"
XX
PN      WO2004009541-A2.
XX
PD      29-JAN-2004.
XX
```

```
PF      18-JUL-2003; 2003WO-US022410.
XX
PR      19-JUL-2002; 2002US-0397106P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Bhat BG;
XX
DR      WPI; 2004-132912/13.
XX
PT      New antisense oligonucleotide for modulating endothelial lipase
PT      expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT      high density lipoprotein or cardiovascular disorders.
XX
PS      Claim 3; SEQ ID NO 1168; 1007pp; English.
XX
CC      The present invention relates to antisense oligonucleotides (ADJ21603-
CC      ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC      (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC      with and inhibits the expression of EL. The antisense oligonucleotides
CC      are useful for modulating the expression of endothelial lipase in cells
CC      or tissues to treat diseases associated with EL expression, such as
CC      dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC      disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC      used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ      Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
      Query Match      1.3%; Score 14.8; DB 1; Length 20;
      Best Local Similarity 88.9%; Pred. No. 1.4e+02;
      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      865 TTGTAGTCCATGCTATTA 882
Db      3 TTGTAGCCAATGCTATTA 20

RESULT 162
ADJ23294
ID      ADJ23294 standard; DNA; 20 BP.
XX
AC      ADJ23294;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human endothelial lipase antisense oligonucleotide, SEQ ID 1692.
XX
KW      Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW      Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW      cardiovascular disorder; metabolic syndrome X; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "This oligonucleotide has a phosphorothioate
FT      backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT      and 3' ends, which are 4 nucleotides in length. Also all
FT      cytidine residues are 5-methylcytidines"
XX
PN      WO2004009541-A2.
XX
PD      29-JAN-2004.
XX
PF      18-JUL-2003; 2003WO-US022410.
XX
PR      19-JUL-2002; 2002US-0397106P.
PA      (PHAA ) PHARMACIA CORP.
XX
```

PI Bhat BG;
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 1692; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 865 TTGTAGTCCATGCTATTATTA 882
Db 2 TTGTAGCCAATGCTATTATTA 19

RESULT 163
ADK19749/c
ID ADK19749 standard; DNA; 20 BP.
XX
AC ADK19749;
XX
DT 03-JUN-2004 (first entry)
XX
DE Mouse cDNA clone C630041L24 RT-PCR primer #2.
XX
KW Mouse; ss; PCR; cancer; prostate cancer; neuroblastoma; leukaemia;
KW inflammation; arthritis; inflammatory skin disorder;
KW insulin dependent diabetes; adult respiratory distress syndrome;
KW cell death-related disorder; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis; AIDS; septic shock; stroke; osteoporosis; ischaemia;
KW reperfusion injury; myocardial infarction; appetite; immune response;
KW antigen; anaphylaxis; primer; RT-PCR; reverse transcriptase PCR.
XX
OS Mus musculus.
XX
PN US2004053306-A1.
XX
PD 18-MAR-2004.
XX
PF 17-JUN-2003; 2003US-00462691.
XX
PR 17-JUN-2002; 2002US-0389145P.
XX
PA (HAYA/) HAYASHIZAKI Y.
PA (KAMI/) KAMIYA M.
XX
PI Hayashizaki Y, Kamiya M;
XX
DR WPI; 2004-247724/23.
XX
PT New polynucleotides encoding short polypeptides, for preventing and
PT treating disease conditions associated with the activity of the
PT polypeptide, e.g. inflammation, cancer, arthritis, insulin-dependent
PT diabetes or osteoporosis.
XX
PS Example 1; SEQ ID NO 67; 122pp; English.
XX

CC The invention relates to an isolated mouse polynucleotide having a
CC nucleotide sequence of a clone consisting of 1110005117, 1700007F22,
CC 1700011J22, 1700056N09, 2310014H11, 2310031C01, 4930563B01, 9130004I05,
CC 9230110A19, 9230111O07, A030004E11, A430045L05, A530065I17, A830010B16,
CC B230114O10, B230352O20, C230071E12, C630041L24 or D630020P16, is new. The
CC clones 1110005117, 1700007F22, 1700011J22, 1700056N09, 2310014H11,
CC 2310031C01, 4930563B01, 9130004I05, 9230110A19, 9230111O07, A030004E11,
CC A430045L05, A530065I17, A830010B16, B230114O10, B230352O20, C230071E12,
CC C630041L24 and D630020P16, appearing as ADK19683-ADK19701 encoding the
CC proteins appearing as ADK19702-ADK19720. The polynucleotides and
CC polypeptides are useful in research, diagnostic and therapeutic agent
CC screening applications, and prevention and treatment of disease
CC conditions associated with the activity of the polypeptide, e.g.
CC inflammation, cancer (e.g. prostate cancer, neuroblastoma and leukaemia),
CC multiple sclerosis, arthritis, chronic inflammatory conditions of the
CC skin, insulin-dependent diabetes, adult respiratory distress syndrome, or
CC disorders relating cell death, such as Alzheimer's disease, Parkinson's
CC disease, septic shock, stroke, osteoporosis, ischaemia, reperfusion
CC injury, AIDS or myocardial infarction. The polypeptides are also useful
CC in modulating appetite and modulating an immune response, including
CC increasing antibody production in response to an antigen, inhibiting
CC anaphylaxis, and reducing inflammation. The present sequence is a reverse
CC transcriptase PCR (RT)-PCR primer used to isolate a mouse polynucleotide
CC of the invention.
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 56 CCCAGTTCGGGAGACATG 73
Db 18 CCCAGTTTGGGAGACAGG 1

RESULT 164
ADO56167/c
ID ADO56167 standard; DNA; 20 BP.
XX
AC ADO56167;
XX
DT 29-JUL-2004 (first entry)
XX
DE Cyclin-dependent kinase 6, antisense oligonucleotide #231.
XX
KW antisense therapy; cyclin-dependent kinase 6;
KW hyperproliferative disorder; cancer; bacterial infection;
KW viral infection; apoptosis; ss; probe; human.
XX
OS Homo sapiens.
XX
PN US2004087523-A1.
XX
PD 06-MAY-2004.
XX
PF 31-JUL-2002; 2002US-00210802.
XX
PR 31-JUL-2002; 2002US-00210802.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Freier SM, Dobie KW;
XX
DR WPI; 2004-356241/33.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding cyclin-dependent kinase 6, useful for treating
PT cancer, bacterial/viral infection or conditions involving aberrant
PT apoptosis.
XX
PS Example 15; Page 34; 68pp; English.
XX

Fri Aug 19 11:00:00 2005

CC The invention relates to antisense oligonucleotides targeted to cyclin-
CC dependent kinase 6, and which inhibit the expression of cyclin-dependent
CC kinase 6. The antisense oligonucleotides are useful for treating a
CC disease or condition associated with cyclin-dependent kinase 6, such as a
CC hyperproliferative disorder (e.g. cancer), or conditions arising from
CC bacterial or viral infections, or involving aberrant apoptosis. They are
CC also useful in research and diagnostics for modulating the expression of
CC cyclin-dependent kinase 6. The present sequence represents a cyclin-
CC dependent kinase 6 antisense oligonucleotide. Note: Seqid 15-134 are also
CC used in the sequence listing but these sequences do not match seqid 15-
CC 134 displayed in Tables 1 and 2 (page 30-34).
XX
SQ Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 602 AAAGACTTCATAAGTAGG 619
Db ||| ||||| ||||| |||||
18 AAACACTTCAGAGTAGG 1

RESULT 165
ADO56108
ID ADO56108 standard; DNA; 20 BP.
XX
AC ADO56108;
XX
DT 29-JUL-2004 (first entry)
XX
DE Cyclin-dependent kinase 6, antisense oligonucleotide #172.
XX
DE antisense therapy; cyclin-dependent kinase 6;
KW hyperproliferative disorder; cancer; bacterial infection;
KW viral infection; apoptosis; ss; probe; human.
KW
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone. All cytidines are 5-
FT methylcytidines."
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN US2004087523-A1.
XX
XX
PD 06-MAY-2004.
XX
XX
PF 31-JUL-2002; 2002US-00210802.
XX
PR 31-JUL-2002; 2002US-00210802.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Freier SM, Dobie KW;
PI
XX
XX WPI; 2004-356241/33.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding cyclin-dependent kinase 6, useful for treating
PT cancer, bacterial/viral infection or conditions involving aberrant
PT apoptosis.
PT
XX

PS Example 15; Page 32; 68pp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to cyclin-
CC dependent kinase 6, and which inhibit the expression of cyclin-dependent
CC kinase 6. The antisense oligonucleotides are useful for treating a
CC disease or condition associated with cyclin-dependent kinase 6, such as a
CC hyperproliferative disorder (e.g. cancer), or conditions arising from
CC bacterial or viral infections, or involving aberrant apoptosis. They are
CC also useful in research and diagnostics for modulating the expression of
CC cyclin-dependent kinase 6. The present sequence represents a cyclin-
CC dependent kinase 6 antisense oligonucleotide. Note: Seqid 15-134 are also
CC used in the sequence listing but these sequences do not match seqid 15-
CC 134 displayed in Tables 1 and 2 (page 30-34).
XX
SQ Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 602 AAAGACTTCATAAGTAGG 619
Db ||| ||||| ||||| |||||
3 AAACACTTCAGAGTAGG 20

RESULT 166
ADN31001/c
ID ADN31001 standard; DNA; 20 BP.
XX
AC ADN31001;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human Int6 cDNA PCR primer #5.
XX
XX Human; Int6; PCR; ss; mammary epithelial cellular growth; cancer;
KW cytostatic; primer.
KW
XX Homo sapiens.
OS
XX
XX US6737251-B2.
PN
XX 18-MAY-2004.
PD
XX 14-MAY-2001; 2001US-00858152.
PF
XX 09-FEB-1995; 95US-00385998.
PR 09-FEB-1996; 96US-00875847.
PR 09-FEB-1996; 96WO-US001884.
PR 23-AUG-1999; 99US-00378842.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Marchetti A, Buttitta F, Smith GH, Callahan R;
XX
XX WPI; 2004-387097/36.
DR
XX
XX Novel tumor Int6 recombinant protein that deregulates mammary epithelial
PT cellular growth, useful for treating cancer.
PT
XX
XX Example 13; SEQ ID NO 9; 44pp; English.
PS
XX
CC The invention relates to the Int6 protein and the cDNA encoding it. The
CC Int6 protein deregulates mammary epithelial cellular growth. The cDNA and
CC protein are useful as vaccines for treating cancer. This sequence
CC represents a PCR primer used to amplify cDNA encoding the human Int6
CC protein of the invention.
CC
XX
XX Sequence 20 BP; 4 A; 3 C; 2 G; 11 T; 0 U; 0 Other;
SQ

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 748 GCTGCCACCTTATGCAGT 765
|||||
Db 1 GCTGCCACCTGCTGCAGT 18

RESULT 169
ADRI12130
ID ADRI12130 standard; DNA; 20 BP.

XX ADRI12130;

XX 23-SEP-2004 (first entry)

XX Murine interleukin-5 (IL-5) receptor a DNA antisense oligonucleotide #72.

XX Mouse; interleukin-5; IL-5; ss; antisense oligonucleotide;
KW IL-5 receptor a; phosphorothioate; 2'-O-methoxyethyl sugar moiety;
KW 5-methylcytosine; IL-5 signal transduction; apoptosis;
KW eosinophilic syndrome; asthma; antiasthmatic; cytostatic.

XX Mus musculus.

OS US20041121376-A1.

XX 24-JUN-2004.

XX 06-OCT-2003; 2003US-00679532.

XX 26-MAR-1999; 99US-00280799.

PR 17-MAR-2000; 2000WO-US007318.

PR 07-MAR-2001; 2001US-00800629.

XX (DEAN/) DEAN N M.
PA (KARR/) KARRAS J G.
PA (MCKA/) MCKAY R.
PA (MANO/) MANOHARAN M.

XX Dean NM, Karras JG, Mckay R, Manoharan M;

PI WPI; 2004-479669/45.

XX New antisense compound modulating interleukin-5 signal transduction, useful in promoting apoptosis and in treating eosinophilic syndrome or asthma.

PS Example 25; SEQ ID NO 152; 77pp; English.

XX The invention relates to an antisense compound that modulates interleukin-5 (IL-5) signal transduction. The antisense compound is an antisense oligonucleotide targeted to a nucleic acid molecule encoding a mammalian IL-5 or IL-5 receptor a, where the antisense compound modulates the expression of mammalian IL-5 or IL-5 receptor a. The antisense oligonucleotide comprises at least one modified internucleoside linkage, i.e. a phosphorothioate linkage, or a peptide nucleic acid, at least one modified sugar moiety, i.e. a 2'-O-methoxyethyl sugar moiety, and at least one modified nucleobase, i.e. 5-methylcytosine. Altering the ratio of the isoforms of mammalian IL-5 receptor a in mammalian cells or tissues comprises contacting the cells or tissues with an antisense compound so that the ratio of the mammalian IL-5 receptor a isoforms is altered. Treating a mammal having a disease or condition associated with IL-5 signal transduction or IL-5 or IL-5 receptor a expression, or a disease or condition characterised by a reduction in apoptosis comprises administering to the mammal a therapeutic or prophylactic amount of an antisense compound so that IL-5 signal transduction, IL-5 or IL-5 receptor a expression, or IL-5 receptor a is modulated, the ratio of IL-5 receptor a isoforms is altered, or expression of membrane IL-5 receptor a is modulated. The antisense compounds, methods and compositions are useful in promoting apoptosis and in treating eosinophilic syndrome and

CC asthma. This sequence represents a murine IL-5 receptor a DNA antisense oligonucleotide of the invention.

XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

SQ Query Match 1.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ACTTCCTTATCTTCCAG 1067
|||||
Db 2 ACTTCCTTACCTTCCTG 19

RESULT 170
AAQ52344

ID AAQ52344 standard; DNA; 21 BP.

XX AAQ52344;

XX 25-MAR-2003 (revised)

DT 23-JUN-1994 (first entry)

XX Sequence of synthetic forward primer for the manual sequencing of human Y1 receptor cDNA clone hY1-5.

XX Y1 receptor; Y-evoked vasoconstriction; primer; ss.

XX Synthetic.

XX WO9324515-A1.

XX 09-DEC-1993.

XX 27-MAY-1993; 93WO-US005039.

XX 29-MAY-1992; 92US-00891453.

XX (CORR) CORNELL RES FOUND INC.

XX Wahlestedt C;

XX WPI; 1993-405721/50.

XX DNA encoding human neuro-peptide Y-peptide YY Y1 receptor - is used to develop drugs for treating e.g. hypertension, depression or obesity.

XX Example; Page 13; 50pp; English.

XX The lambda ZAPII cDNA library was mde from mRNA of a human female fetal (17-18 week gestation) brain, using both oligo (dT) and random- sequence primers. A 500-bp PCR product, corresp. to part of the coding region (547-1047) of the rat orphan receptor was used to screen the human fetal brain cDNA library. PCR was performed using the fetal brain cDNA library as template and a 23-mer forward primer posns 547-569 (AAQ52340) and a 25-mer reverse primer posns 1023-1047 (AAQ52341). Six positive plaques were isolated and sequenced. The DNA was amplified using two oligo primers, JS1 and JS2 (AAQ52342, AAQ52343). They corresp. to the sequences juxtaposed to the linker of the PUC plasmid and its derivs., making it possible to do PCR amplification of a DNA cloned in the plasmid's linker. The longest clone (hY1-5) was selected for sequencing analysis. 4 specific synthetic primers (3 forward primers (AAQ52344-Q52346) and one reverse primer (AAQ52347) were used for manual sequencing of the hY1-5 clones and its deletion constructs. Three oligos necessary to study the inhibition of the contractile effect of neuropeptide Y on human blood vessels were prepd: (1) an antisense oligo hY1-AS corresp. to the human Y1 receptor amino terminus (AAQ52328); (2) a corresp. sense oligo hY1-S (AAQ52329); and (3) a 3-base mismatched antisense oligo hY1MM (AAQ52330). (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 1 Other;

SQ Query Match 1.3%; Score 14.8; DB 1; Length 21;

```
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 331 TCCTGCTCGTGTGGCTGTGA 350
Db 2 TCCTGCTTATGGRGCTGTGA 21

RESULT 171
ABS66964
ID ABS66964 standard; DNA; 21 BP.
XX
AC ABS66964;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #229.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PF 25-JAN-2002; 2002WO-EP0000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 2; Page 82; 198pp; English.
XX
PF 25-JAN-2002; 2002WO-EP0000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 2; Page 82; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTCAACCTCTCTG 21

RESULT 172
ABS66965/c
ID ABS66965 standard; DNA; 21 BP.
XX
AC ABS66965;
XX
DT 29-NOV-2002 (first entry)
XX
```

```
DE Human MRP-1 polymorphic DNA region #230.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP0000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 2; Page 82; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTCAACCTCTCTG 1

RESULT 173
ABS66968
ID ABS66968 standard; DNA; 21 BP.
XX
AC ABS66968;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #233.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP0000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
```

XX Brinkmann U, Hoffmeyer S, Mornhinweg E;
PI WPI; 2002-657475/70.
XX Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX Claim 1; Page 82; 198pp; English.
PS
XX The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTAAACCTCTCTG 21

RESULT 174
ABS66966
ID ABS66966 standard; DNA; 21 BP.
XX
AC ABS66966;
XX
XX 29-NOV-2002 (first entry)
XX Human MRP-1 polymorphic DNA region #231.
XX Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
XX renal cancer; cytostatic; single nucleotide polymorphism.
OS Homo sapiens.
XX
XX WO200259142-A2.
XX
PD 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-EP000796.
XX
XX 26-JAN-2001; 2001EP-00101651.
XX (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX WPI; 2002-657475/70.
XX
XX Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 2; Page 82; 198pp; English.
XX The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1 or for identifying and obtaining an inhibitor

CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTMAACCTCTCTG 21

RESULT 175
ABS66967/c
ID ABS66967 standard; DNA; 21 BP.
XX
AC ABS66967;
XX
XX 29-NOV-2002 (first entry)
DT Human MRP-1 polymorphic DNA region #232.
XX Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
DE renal cancer; cytostatic; single nucleotide polymorphism.
XX Homo sapiens.
XX
XX WO200259142-A2.
XX
PD 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-EP000796.
XX
XX 26-JAN-2001; 2001EP-00101651.
XX (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX WPI; 2002-657475/70.
XX
XX Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 2; Page 82; 198pp; English.
XX The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
DB 18 AATCACTMAACCTCTCTG 1

RESULT 176
ABS66969/C
ID ABS66969 standard; DNA; 21 BP.
XX
AC ABS66969;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #234.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Claim 1; Page 82; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTAAACCTCTCTG 1

RESULT 177
ACF62467/C
ID ACF62467 standard; DNA; 21 BP.
XX
AC ACF62467;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:296.
XX
KW Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX
OS Synthetic.

XX WO2003013534-A2.
PN
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002WO-EP008219.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-268144/26.
XX
PT New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
PS Disclosure; Page 40; 86pp; English.
XX
CC The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTMAACCTCTCTG 1

RESULT 178
ACF62464
ID ACF62464 standard; DNA; 21 BP.
XX
AC ACF62464;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:293.
XX
KW Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO2003013534-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008219.
PR
XX 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; Page 40; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTAAACCTCTCTG 21

RESULT 179
ACF62465/C
ID ACF62465 standard; DNA; 21 BP.
XX
XX ACF62465;
AC
XX 08-OCT-2003 (first entry)
DT
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:294.
DE
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO2003013534-A2.
XX
XX 20-FEB-2003.
PD
XX 23-JUL-2002; 2002WO-EP008219.
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,

PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; Page 40; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTAAACCTCTCTG 1

RESULT 180
ACF62466
ID ACF62466 standard; DNA; 21 BP.
XX
XX ACF62466;
AC
XX 08-OCT-2003 (first entry)
DT
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:295.
DE
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO2003013534-A2.
XX
XX 20-FEB-2003.
PD
XX 23-JUL-2002; 2002WO-EP008219.
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; Page 40; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention

CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACP62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention

SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTMAACCTCTCTG 21

RESULT 181
ADB21135
ID ADB21135 standard; DNA; 21 BP.
XX ADB21135;
AC ADB21135;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:293.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.
XX

OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-354397/33.
XX
PT Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
PS Claim 8; Page 49; 100pp; English.
XX

CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.

SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
DB 4 AATCACTAAACCTCTCTG 21

RESULT 182
ADB21136/c
ID ADB21136 standard; DNA; 21 BP.
XX
AC ADB21136;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:294.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.
XX

OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-354397/33.
XX

PT Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.

PS Claim 8; Page 49; 100pp; English.

XX
CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.

SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
DB 18 AATCACTAAACCTCTCTG 1

Fri Aug 19 11:00:00 2005

```
RESULT 183
ADB21138/c
ID  ADB21138 standard; DNA; 21 BP.
XX
AC  ADB21138;
XX
DT  20-NOV-2003 (first entry)
XX
DE  MRP1 based cancer related nucleic acid SEQ ID NO:296.
XX
KW  irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW  lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW  variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW  ds.
XX
OS  Unidentified.
XX
PN  WO2003013533-A2.
XX
PD  20-FEB-2003.
XX
PF  23-JUL-2002; 2002WO-EP008200.
XX
KW  irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW  lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW  variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW  ds.
XX
OS  Unidentified.
XX
PN  WO2003013533-A2.
XX
PD  20-FEB-2003.
XX
PF  23-JUL-2002; 2002WO-EP008200.
XX
PR  23-JUL-2001; 2001EP-00117608.
PR  24-MAY-2002; 2002EP-00011710.
XX
PA  (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI  Heinrich G, Kerb R;
XX
WPI; 2003-354397/33.
XX
Use of irinotecan or its derivative for preparation of a pharmaceutical
composition for treating cancer in a subject having a genome with a
variant allele comprising a multidrug resistance protein 1
polynucleotide.
XX
PS  Disclosure; Page 49; 100pp; English.
XX
The present invention describes a method for the use of irinotecan (I) or
its derivative for the preparation of a pharmaceutical composition for
treating colorectal, cervical, gastric, lung, ovarian or pancreatic
cancer, or malignant glioma in a subject having a genome with a variant
allele which comprises a multidrug resistance protein 1 (MRP1)
polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
can be used for the preparation of a pharmaceutical composition for
treating colorectal, cervical, gastric, lung, ovarian or pancreatic
cancer, or malignant glioma in a subject, where the subject is a human
(preferably African or Asian) or a mouse. The present sequence represents
a sequence which is used in the exemplification of the present invention.
XX
SQ  Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTMAACCTCTCTG 1

RESULT 184
ADB21137
ID  ADB21137 standard; DNA; 21 BP.
XX
AC  ADB21137;
XX
DT  20-NOV-2003 (first entry)
XX
DE  MRP1 based cancer related nucleic acid SEQ ID NO:295.
XX
KW  irinotecan; colorectal cancer; cervical cancer; gastric cancer;
```

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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
ds.
XX
OS  Unidentified.
XX
PN  WO2003013533-A2.
XX
PD  20-FEB-2003.
XX
PF  23-JUL-2002; 2002WO-EP008200.
XX
PR  23-JUL-2001; 2001EP-00117608.
PR  24-MAY-2002; 2002EP-00011710.
XX
PA  (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI  Heinrich G, Kerb R;
XX
WPI; 2003-354397/33.
XX
Use of irinotecan or its derivative for preparation of a pharmaceutical
composition for treating cancer in a subject having a genome with a
variant allele comprising a multidrug resistance protein 1
polynucleotide.
XX
PS  Disclosure; Page 49; 100pp; English.
XX
The present invention describes a method for the use of irinotecan (I) or
its derivative for the preparation of a pharmaceutical composition for
treating colorectal, cervical, gastric, lung, ovarian or pancreatic
cancer, or malignant glioma in a subject having a genome with a variant
allele which comprises a multidrug resistance protein 1 (MRP1)
polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
can be used for the preparation of a pharmaceutical composition for
treating colorectal, cervical, gastric, lung, ovarian or pancreatic
cancer, or malignant glioma in a subject, where the subject is a human
(preferably African or Asian) or a mouse. The present sequence represents
a sequence which is used in the exemplification of the present invention.
XX
SQ  Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTMAACCTCTCTG 21

RESULT 185
ADB88225/c
ID  ADB88225 standard; DNA; 21 BP.
XX
AC  ADB88225;
XX
DT  04-DEC-2003 (first entry)
XX
DE  Human UGT1A1 variant allele sequence fragment SEQ ID NO:266.
XX
KW  ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW  colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW  ovarian cancer; pancreatic cancer; malignant glioma;
KW  uridine diphosphate glycosyltransferasel member A1.
XX
OS  Homo sapiens.
XX
PN  WO2003013536-A2.
XX
PD  20-FEB-2003.
XX
PF  23-JUL-2002; 2002WO-EP008217.
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XX 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX Heinrich G, Kerb R;
XX WPI; 2003-289896/28.
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX Disclosure; Page 53; 107pp; English.
XX The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTAAACCTCTCTG 1
RESULT 186
ADB88227/c
ID ADB88227 standard; DNA; 21 BP.
XX ADB88227;
AC ADB88227;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:268.
XX
KW ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW ovarian cancer; pancreatic cancer; malignant glioma;
KW uridine diphosphate glycosyltransferase1 member A1.
XX
OS Homo sapiens.
XX
PN WO2003013536-A2.
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:268.
XX
KW ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW ovarian cancer; pancreatic cancer; malignant glioma;
KW uridine diphosphate glycosyltransferase1 member A1.
XX
OS Homo sapiens.
XX
PN WO2003013536-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008217.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-289896/28.
XX
XX Use of irinotecan to treat cancer patient by determining if patient has

PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX Disclosure; Page 53; 107pp; English.
XX The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
SQ
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTMAACCTCTCTG 1
RESULT 187
ADB88224
ID ADB88224 standard; DNA; 21 BP.
XX ADB88224;
AC ADB88224;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:265.
XX
KW ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW ovarian cancer; pancreatic cancer; malignant glioma;
KW uridine diphosphate glycosyltransferase1 member A1.
XX
OS Homo sapiens.
XX
PN WO2003013536-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008217.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-289896/28.
XX
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
PS Disclosure; Page 53; 107pp; English.
XX
CC The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
SQ

Fri Aug 19 11:00:00 2005

CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTAAACCTCTCTG 21

RESULT 188
ADB88226
ID ADB88226 standard; DNA; 21 BP.
XX
AC ADB88226;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:267.
XX
KW ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KW ovarian cancer; pancreatic cancer; malignant glioma;
KW uridine diphosphate glycosyltransferasel member A1.
XX
OS Homo sapiens.
XX
PN WO2003013536-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008217.
PF 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-289896/28.
DR
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
PS Disclosure; Page 53; 107pp; English.
XX
CC The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTMAACCTCTCTG 21

RESULT 189
ADB97207
ID ADB97207 standard; DNA; 21 BP.
XX
AC ADB97207;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:293.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
KW TOP1.
XX
OS Homo sapiens.
XX
PN WO2003013537-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
PF 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-268145/26.
DR
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Claim 2; Page 77; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTAAACCTCTCTG 21

RESULT 190
ADB97210/C
ID ADB97210 standard; DNA; 21 BP.
XX
AC ADB97210;

XX 04-DEC-2003 (first entry)
DT Human MRP1 variant allele sequence fragment SEQ ID NO:296.
DE
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
KW TOP1.
XX Homo sapiens.
OS
XX WO2003013537-A2.
PN
XX 20-FEB-2003.
PD
XX 23-JUL-2002; 2002WO-EP008218.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
PR
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 77; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;
XX
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1074 AACCACTTAACCTCTCTG 1091
Db 18 AATCACTMAACCTCTCTG 1
RESULT 191
ADB97209
ID ADB97209 standard; DNA; 21 BP.
XX
AC ADB97209;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:295.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
KW TOP1.
XX
OS Homo sapiens.
XX

PN WO2003013537-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX WPI; 2003-268145/26.
DR
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 77; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;
XX
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1074 AACCACTTAACCTCTCTG 1091
Db 4 AATCACTMAACCTCTCTG 21
RESULT 192
ADB97208/C
ID ADB97208 standard; DNA; 21 BP.
XX
AC ADB97208;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:294.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; ds; Cyp3A5; MRP1; MDR1;
KW TOP1.
XX
OS Homo sapiens.
XX
XX WO2003013537-A2.
PN
XX 20-FEB-2003.
PD
XX 23-JUL-2002; 2002WO-EP008218.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
PI

XX WPI; 2003-268145/26.

DR New use of irinotecan for preparation of pharmaceutical compositions for

XX treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

PT Claim 2; Page 77; 130pp; English.

XX The invention relates to the novel use of irinotecan or its derivative

CC for the preparation of pharmaceutical compositions for treating

CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or

CC malignant glioma in a subject having a genome with a variant allele which

CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition

CC of the invention has cytostatic activity. The invention is useful for the

CC preparation of pharmaceutical compositions for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject (preferably human, more preferably African or Asian)

CC or a mouse. The present sequence is used in the exemplification of the

CC invention.

XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091

Db 18 AATCACTAAACCTCTCTG 1

RESULT 193

ADB92401/c

ID ADB92401 standard; DNA; 21 BP.

XX

AC ADB92401;

XX

XX 04-DEC-2003 (first entry)

XX Human MRP1 variant allele sequence fragment SEQ ID NO:296.

DE

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

KW multidrug resistance 1; MDR1; cytostatic; ds; human; UGT1A1; MRP1; TOP1.

XX

OS Homo sapiens.

XX WO2003013535-A2.

XX

PD 20-FEB-2003.

XX

XX 23-JUL-2002; 2002WO-EP008220.

XX

XX 23-JUL-2001; 2001EP-00117608.

PR 24-MAY-2002; 2002EP-00011710.

XX

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

XX Heinrich G, Kerb R;

XX WPI; 2003-342400/32.

XX

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; Page 48; 104pp; English.

XX

XX The invention relates ro a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the

CC invention has cytostatic activity. The present sequence is used in the

CC exemplification of the invention.

XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

PI

XX WPI; 2003-342400/32.

DR

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; Page 48; 104pp; English.

XX

XX The invention relates ro a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the

CC invention has cytostatic activity. The present sequence is used in the

CC exemplification of the invention.

XX Sequence 21 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 1 Other;

SQ

Query Match 1.3%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091

Db 18 AATCACTMAACCTCTCTG 1

RESULT 194

ADB92399/c

ID ADB92399 standard; DNA; 21 BP.

XX

AC ADB92399;

XX

XX 04-DEC-2003 (first entry)

XX Human MRP1 variant allele sequence fragment SEQ ID NO:294.

DE

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

KW multidrug resistance 1; MDR1; cytostatic; ds; human; UGT1A1; MRP1; TOP1.

XX

OS Homo sapiens.

XX WO2003013535-A2.

XX

PD 20-FEB-2003.

XX

XX 23-JUL-2002; 2002WO-EP008220.

XX

XX 23-JUL-2001; 2001EP-00117608.

PR 24-MAY-2002; 2002EP-00011710.

XX

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

XX Heinrich G, Kerb R;

XX WPI; 2003-342400/32.

XX

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; Page 48; 104pp; English.

XX

XX The invention relates ro a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the

CC invention has cytostatic activity. The present sequence is used in the

CC exemplification of the invention.

XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

PI

XX WPI; 2003-342400/32.

DR

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; Page 48; 104pp; English.

XX

XX The invention relates ro a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

ID ADB92398 standard; DNA; 21 BP.
XX
AC ADB92398;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:293.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytosstatic; ds; human; UGT1A1; MRP1; TOP1.
XX
OS Homo sapiens.
XX
PN WO2003013535-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008220.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-342400/32.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 48; 104pp; English.
XX
CC The invention relates ro a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-342400/32.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 48; 104pp; English.
XX
CC The invention relates ro a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db ||||| ||||| ||||| |||||
4 AATCACTAAACCTCTCTG 21

RESULT 196
ADB92400
ID ADB92400 standard; DNA; 21 BP.
XX
AC ADB92400;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:295.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytosstatic; ds; human; UGT1A1; MRP1; TOP1.
XX
OS Homo sapiens.
XX
PN WO2003013535-A2.
XX
PD 20-FEB-2003.

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db ||||| ||||| ||||| |||||
4 AATCACTAAACCTCTCTG 21

RESULT 196
ADB92400
ID ADB92400 standard; DNA; 21 BP.
XX
AC ADB92400;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MRP1 variant allele sequence fragment SEQ ID NO:295.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytosstatic; ds; human; UGT1A1; MRP1; TOP1.
XX
OS Homo sapiens.
XX
PN WO2003013535-A2.
XX
PD 20-FEB-2003.

XX 23-JUL-2002; 2002WO-EP008220.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
PR 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-342400/32.
DR
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 48; 104pp; English.
XX
CC The invention relates ro a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1074 AACCACTTAACCTCTCTG 1091
Db ||||| ||||| ||||| |||||
4 AATCACTMAACCTCTCTG 21

RESULT 197
ADF87704/C
ID ADF87704 standard; DNA; 21 BP.
XX
AC ADF87704;
XX
DT 26-FEB-2004 (first entry)
XX
DE Single nucleotide polymorphism detection primer, SEQ ID NO 1287.
XX
KW human; single nucleotide polymorphism; microarray; side effect; ss;
KW primer; PCR.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP2003235571-A.
XX
PD 26-AUG-2003.
XX
PF 12-FEB-2002; 2002JP-00034717.
XX
PR 12-FEB-2002; 2002JP-00034717.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2003-820454/77.
XX
PT Novel polynucleotide useful for detecting single nucleotide polymorphisms
PT in human gene.
XX
PS Claim 2; SEQ ID NO 1287; 704pp; Japanese.
XX
CC The invention relates to a novel polynucleotide isolated and purified
CC from a human gene having any one of 935 fully defined sequences as given
CC in specification, or a sequence having a base substitution. The invention

CC further relates to: an oligonucleotide containing single nucleotide
CC polymorphisms; a PCR primer set chosen from the combination of two DNA
CC fragments from any one of 1220 fully defined sequences as given in
CC specification; a labelling probe containing the SNP containing oligo; and
CC a microarray equipped with the SNP containing oligo. The isolated human
CC gene of the invention is useful for detecting the single nucleotide
CC polymorphisms in human gene. The isolated human gene is also useful for
CC diagnosis of disease and determination of side effect to a medical agent.
CC The isolated human gene is also effective in detecting single nucleotide
CC polymorphisms in a human gene. This polynucleotide sequence represents
CC one of the PCR primers used in the single nucleotide polymorphism
CC detection method of the invention.

XX
SQ Sequence 21 BP; 3 A; 4 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 899 ACCAAGAGCCTCAACATT 916
Db 19 ACCAAGGACTCAACATT 2

RESULT 198
ADP46739/C
ID ADP46739 standard; DNA; 21 BP.
XX
AC ADP46739;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human c-Cbl siRNA sense strand, SEQ ID 75.
XX
KW Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour;
KW fat deposition; metabolic rate; lean muscle mass; body fat; Cbl;
KW multi-adaptor protein; feeding disorder; glucose uptake disorder;
KW metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl;
KW siRNA; short interfering RNA; ds; RNA interference; gene silencing.

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004055181-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-AU001676.
XX
PR 16-DEC-2002; 2002AU-00953393.
PR 14-NOV-2003; 2003AU-00906285.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Molero JC, James D;
XX
XW WPI; 2004-488065/46.

XX
PT Identifying compounds capable of modulating feeding behavior, fat
PT deposition, metabolic rate, or the ratio of lean muscle mass to body fat
PT by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity
PT and hypolipidemia.

XX
PS Claim 86; SEQ ID NO 75; 213pp; English.
XX
CC The present invention relates to a method for identifying a compound that
CC is capable of modulating feeding behaviour, fat deposition, metabolic
CC rate, or the ratio of lean muscle mass to body fat in a subject. The
CC method comprises performing an assay to measure a metabolism-associated
CC phenotype that has been determined for a genetically modified non-human
CC animal that comprises a genetic modification within an allele of its Cbl
CC locus, and determining the effect of the compound on the phenotype. The
CC genetic modification reduces or prevents expression of a functional

CC endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
CC protein that is involved in ligand-induced down regulation of receptor
CC tyrosine kinases. The method of the invention is useful in the treatment
CC of feeding disorders or disorders of glucose uptake and metabolism, such
CC as diabetes, obesity and hyperlipidaemia. The present sequence is the
CC sense strand for a human c-Cbl siRNA. The siRNA is useful in modulating a
CC metabolism-associated phenotype in a cell, tissue or animal subject.

XX
SQ Sequence 21 BP; 0 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 AGGAAGCCCGAAGCAGCC 50
Db 18 AGGAGCCAGAGCAGCC 1

RESULT 199
ADP46857
ID ADP46857 standard; DNA; 21 BP.
XX
AC ADP46857;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human c-Cbl siRNA antisense strand, SEQ ID 193.
XX
KW Antidiabetic; Anorectic; Eating-Disorder; feeding behaviour;
KW fat deposition; metabolic rate; lean muscle mass; body fat; Cbl;
KW multi-adaptor protein; feeding disorder; glucose uptake disorder;
KW metabolism disorder; diabetes; obesity; hyperlipidaemia; human; c-Cbl;
KW siRNA; short interfering RNA; ds; RNA interference; gene silencing.

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004055181-A1.

XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-AU001676.
XX
PR 16-DEC-2002; 2002AU-00953393.
PR 14-NOV-2003; 2003AU-00906285.

XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Molero JC, James D;
XX
XW WPI; 2004-488065/46.

XX
PT Identifying compounds capable of modulating feeding behavior, fat
PT deposition, metabolic rate, or the ratio of lean muscle mass to body fat
PT by detecting a proto-oncogene Cbl in disorders such as diabetes, obesity
PT and hypolipidemia.

XX
PS Claim 86; SEQ ID NO 193; 213pp; English.

XX
CC The present invention relates to a method for identifying a compound that
CC is capable of modulating feeding behaviour, fat deposition, metabolic
CC rate, or the ratio of lean muscle mass to body fat in a subject. The
CC method comprises performing an assay to measure a metabolism-associated
CC phenotype that has been determined for a genetically modified non-human
CC animal that comprises a genetic modification within an allele of its Cbl
CC locus, and determining the effect of the compound on the phenotype. The
CC genetic modification reduces or prevents expression of a functional
CC endogenous Cbl in the animal. The c-Cbl protein is a multi-adaptor
CC protein that is involved in ligand-induced down regulation of receptor
CC tyrosine kinases. The method of the invention is useful in the treatment
CC of feeding disorders or disorders of glucose uptake and metabolism, such
CC as diabetes, obesity and hyperlipidaemia. The present sequence is the

CC antisense strand for a human c-Cbl siRNA. The siRNA is useful in
CC modulating a metabolism-associated phenotype in a cell, tissue or animal
CC subject.
XX
SQ Sequence 21 BP; 7 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 33 AGGAAGCCGGAAGCAGCC 50
Db 2 AGGAGCCAGAAGCAGCC 19
RESULT 200
ADR18488
ID ADR18488 standard; DNA; 21 BP.
XX
AC ADR18488;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human GOBLIN siRNA antisense strand oligonucleotide SEQ ID NO:269.
XX
KW cancer; GOBLIN; micrometastasis; metastasis; cytostatic; gene therapy;
KW squamous cell carcinoma; hepatocellular carcinoma; melanoma;
KW head and neck cancer; adenocarcinoma; gastrointestinal cancer;
KW renal cell cancer; bladder cancer; prostate cancer;
KW non-squamous carcinoma; glioblastoma; medullablastoma; ovarian cancer;
KW basal cell carcinoma; clear cell carcinoma; endometrioid ovarian cancer;
KW mucinous ovarian cancer; breast cancer; lobular lesion; stromal lesion;
KW ductal carcinoma; ductal adenocarcinoma;
KW proliferative fibrocystic change; epitheliosis; intraductal papilloma;
KW atypical ductal hyperplasia; hyperproliferative disease; human;
KW small interfering RNA; siRNA; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .19 /*tag= a
FT misc_feature 20. .21 /note= "human GOBLIN mRNA target sequence"
FT /*tag= b
FT /note= "3'-extension dinucleotide TT overhang"
XX
PN WO2004072285-A1.
XX
PD 26-AUG-2004.
XX
PF 12-FEB-2004; 2004WO-AU000169.
XX
PR 14-FEB-2003; 2003US-0447697P.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Stanford P, Harris J, Ormandy C;
XX
DR WPI; 2004-625877/60.
XX
PT Detecting a cancer, e.g. breast or ovarian cancer, in a subject comprises
PT determining the level of expression of a GOBLIN gene in a sample.
XX
PS Claim 93; SEQ ID NO 269; 217pp; English.
XX
CC The present invention describes a method for detecting a cancer cell in a
CC subject. The method comprises determining the level of expression of a
CC GOBLIN gene in a sample of the subject where elevated expression of the
CC gene is indicative of a primary cancer or its micrometastasis or
CC metastasis. Also described: (1) an isolated GOBLIN nucleic acid molecule;
CC (2) a vector comprising the isolated nucleic acid of (1); (3) a

CC monoclonal or polyclonal antibody that binds specifically to a GOBLIN
CC polypeptide; (4) an isolated GOBLIN polypeptide, or its immunogenic
CC epitope; (5) a fusion protein comprising the isolated polypeptide of (4);
CC (6) a method of identifying a compound that reduces or antagonises
CC expression of a GOBLIN gene; (7) a process for identifying or determining
CC and producing a compound; (8) an isolated nucleic acid that antagonises
CC expression of a GOBLIN gene, where the nucleic acid comprises a
CC nucleotide sequence comprising any of the 21 bp sequences of SEQ ID
CC NOS:46-353; (9) an isolated antisense nucleic acid that antagonises
CC expression of a GOBLIN gene, where the nucleic acid comprises a
CC nucleotide sequence capable of selectively hybridising to mRNA encoded by
CC the isolated nucleic acid of (1); and (10) a process for monitoring the
CC efficacy of treatment of a cancer in a subject. GOBLIN sequences have
CC cytostatic activity, and can be used in gene therapy. An isolated GOBLIN
CC nucleic acid molecule can be used for detecting a cancer cell. An
CC isolated GOBLIN polypeptide can be used for producing an antibody. The
CC method, nucleic acid molecules and the encoded polypeptides, and
CC antibodies can be used for detecting a cancer, e.g. squamous cell
CC carcinoma, hepatocellular carcinoma, melanoma, head and neck cancer,
CC adenocarcinoma, gastrointestinal cancer (e.g. gastric, colon, or
CC pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer,
CC non-squamous carcinoma, glioblastoma, medullablastoma, ovarian cancer
CC (e.g. basal cell carcinoma, clear cell carcinoma, endometrioid ovarian
CC cancer, or mucinous ovarian cancer), or breast cancer (e.g. lobular
CC lesion, stromal lesion, ductal carcinoma, ductal adenocarcinoma,
CC proliferative fibrocystic change, epitheliosis, intraductal papilloma, or
CC atypical ductal hyperplasia) in a subject. The antagonist of GOBLIN
CC function, method, and compound are useful for treating hyperproliferative
CC disease, like cancer. The present sequence represents a small interfering
CC RNA (siRNA) oligonucleotide targeted to human GOBLIN, which is used in
CC the exemplification of the present invention.
XX
SQ Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 828 CATGACCCAGGAGGCCG 845
Db 1 CTTGACCGAGGAAGGCCG 18
RESULT 201
ADR18487/C
ID ADR18487 standard; DNA; 21 BP.
XX
AC ADR18487;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human GOBLIN siRNA sense strand oligonucleotide SEQ ID NO:268.
XX
KW cancer; GOBLIN; micrometastasis; metastasis; cytostatic; gene therapy;
KW squamous cell carcinoma; hepatocellular carcinoma; melanoma;
KW head and neck cancer; adenocarcinoma; gastrointestinal cancer;
KW renal cell cancer; bladder cancer; prostate cancer;
KW non-squamous carcinoma; glioblastoma; medullablastoma; ovarian cancer;
KW basal cell carcinoma; clear cell carcinoma; endometrioid ovarian cancer;
KW mucinous ovarian cancer; breast cancer; lobular lesion; stromal lesion;
KW ductal carcinoma; ductal adenocarcinoma;
KW proliferative fibrocystic change; epitheliosis; intraductal papilloma;
KW atypical ductal hyperplasia; hyperproliferative disease; human;
KW small interfering RNA; siRNA; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .19 /*tag= a
FT /note= "human GOBLIN mRNA target sequence"
FT misc_feature 20. .21
FT

ABK27525
ID ABK27525 standard; DNA; 15 BP.
XX
AC ABK27525;
XX
DT 09-APR-2002 (first entry)
XX
DE Human CTLA4 gene allele-specific oligonucleotide sequencing primer #2.
XX
KW Human; cytotoxic T-lymphocyte-associated protein 4; CTLA4; haplotyping;
KW haplotype pair; single nucleotide polymorphism; autoimmune disorder; ss;
KW genotyping; gene therapy; drug screening; antisense gene therapy; primer;
KW immunosuppressive; sequencing; PCR; probe.
XX
OS Homo sapiens.
XX
PN WO200190122-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016905.
XX
PR 23-MAY-2000; 2000US-0206353P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Messer C;
XX
DR WPI; 2002-089914/12.
XX
PT New genetic variants of human cytotoxic T-lymphocyte-associated protein
PT 4, CTLA4 gene for studying expression, function of the gene and
PT expressing CTLA4 protein useful in identifying drugs to treat autoimmune
PT disorder.
XX
PS Claim 17; Page 13; 62pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human cytotoxic T-lymphocyte-associated protein 4 or CTLA4
CC protein. A method for haplotyping the CTLA4 gene in an individual
CC comprises identifying the nucleotide at one or more polymorphic sites and
CC determining whether one of the copies of the gene is defined by one of
CC the CTLA4 haplotypes given in the specification or whether both copies
CC are defined by a haplotype pair. This method is useful in genotyping,
CC whereby all possible haplotype pairs can be assigned to specific
CC genotypes. An association between a trait and a haplotype or haplotype
CC pair of the CTLA4 gene can be identified by comparing the frequency of
CC the haplotype or haplotype pair in a population exhibiting the trait with
CC the frequency of the haplotype or haplotype pair in a reference
CC population, where a higher haplotype frequency in the trait population
CC indicates the trait is associated with the haplotype or haplotype pair.
CC CTLA4 and its corresponding DNA are used for studying the expression and
CC function of CTLA4, for use in screening for candidate drugs to treat
CC diseases related to CTLA4 activity, such as autoimmune disorders. The
CC sequences are also useful for studying the effect of variation on the
CC biological activity of CTLA4 as well as on the binding affinity of
CC candidate drugs targeting CTLA4. Sequences ABK27518-ABK27549 represent
CC allele-specific oligonucleotide probes, sequencing primers and PCR
CC primers used to detect CTLA4 gene polymorphisms
XX
SQ Sequence 15 BP; 3 A; 3 C; 1 G; 7 T; 0 U; 1 Other;

Query Match 1.3%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 586 TCATGTTCACTTTAA 600
DB 1 TCATGTTCACTTTAA 15
|||||
RESULT 204
ABQ78935

ID ABQ78935 standard; DNA; 16 BP.
XX
AC ABQ78935;
XX
DT 04-NOV-2002 (first entry)
XX
DE Mouse intermediate-conductance potassium channel protein mIK1 primer 1.
XX
KW Mouse; intermediate-conductance potassium channel; dermatological;
KW antiinflammatory; keratolytic; vulnery; antipsoriatic; atopic eczema;
KW contact dermatitis; vitiligo; skin; hyperkeratosis; actinic keratose;
KW hypertrophic scar; keloids; lentigo; aged skin; ulcer; psoriasis; mIK1;
KW PCR; primer; ss.
XX
OS Mus musculus.
XX
PN WO200253171-A2.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-EP015317.
XX
PR 28-DEC-2000; 2000DE-01065475.
PR 20-MAR-2001; 2001US-0277453P.
XX
PA (SWIT-) SWITCH BIOTECH AG.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
XX
PI Goppelt A, Alzheimer C, Koegel H;
XX
DR WPI; 2002-643295/69.
XX
PT Use of intermediate-conductance potassium channel proteins for the
PT diagnosis, prevention and treatment of disorders associated with
PT disturbed keratinocyte activity, especially psoriasis.
XX
PS Example 3; Page 119; 121pp; German.
XX
CC The invention relates to a novel use of intermediate-conductance
CC potassium channel proteins. The proteins of the invention have
CC dermatological, antiinflammatory, keratolytic, vulnery, and
CC antipsoriatic activity. The method is used especially in the field of
CC damaged skin, e.g. contact dermatitis, atopic eczema, vitiligo,
CC hyperkeratosis, actinic keratosis, hypertrophic scars, keloids, lentigo,
CC aged skin, ulcers and especially psoriasis. The sequence represents a PCR
CC primer for the mouse potassium channel protein mIK1 of the invention
XX
SQ Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 265 CTGTCGGGAACCTGGCA 280
DB 1 CTGTCGGGAACCTGGCA 16
|||||
RESULT 205
AAA18571
ID AAA18571 standard; RNA; 17 BP.
XX
AC AAA18571;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1797.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytotatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;

CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.6e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 959 TGGACCCAGGACATT 974
:||||| |||||:::
Db 1 UGGACUCAGGACAUU 16

RESULT 209
ABK17677
ID ABK17677 standard; RNA; 17 BP.
XX
XX
AC ABK17677;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 324.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnarary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberos sclerosi; port-wine stain; wound healing;
KW Sturge-Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
PI
XX WPI; 2002-082995/11.
DR
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
XX Claim 4; Page 64; 149pp; English.
PS
XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberos sclerosi, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 5 A; 4 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 958 CTGGACCCAGGACATT 973
|:||||| |||||:::
Db 2 CUGGACUCAGGACAUU 17

RESULT 210
ACD52117
ID ACD52117 standard; RNA; 17 BP.
XX
AC ACD52117;
XX
DT 24-SEP-2003 (first entry)
XX
DE HBV inozyme substrate sequence #247.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
XX WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
DR

XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Example 1; Page 154; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC disclosed in the present invention
XX
SQ Sequence 17 BP; 4 A; 2 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATAT 584
DB 1 UUUAAUGCCUUUAU 16

RESULT 211
ACC67229
ID ACC67229 standard; DNA; 17 BP.
XX
AC ACC67229;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4476.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 554; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 519 ATACATGTGCACATGC 534
DB 2 ATCCATGTGCACATGC 17

RESULT 212
ADB45885/c
ID ADB45885 standard; DNA; 17 BP.
XX
AC ADB45885;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #6208.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 757; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 839 AAGGCCGGGTGGATC 854
Db 16 AAGGCCTGGGTGGATC 1
||||| |||||||

RESULT 213
ADE30660
ID ADE30660 standard; DNA; 17 BP.
XX
AC ADE30660;
XX
DT 29-JAN-2004 (first entry)
XX
DE Cholesterol homeostasis/adipogenesis related DNA seq id 47.
XX
KW expression vector; anorectic; antiarteriosclerotic; cardiant;
KW antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;
KW obesity; atherosclerosis; diabetes mellitus;
KW coronary artery heart disease; cholesterol homeostasis; ss;
KW differential expression.
XX
OS Homo sapiens.
XX
PN US2003180764-A1.
XX
PD 25-SEP-2003.
XX
PF 08-JAN-2003; 2003US-00339793.
XX
PR 09-JAN-2002; 2002US-0347286P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Shang J, Bowen B;
XX
XWPI; 2003-830986/77.
XX
PT Polynucleotides differentially regulated in response to cholesterol and
PT adipogenesis are useful to detect and treat associated conditions such as
PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart
PT disease.
XX
PS Claim 8; SEQ ID NO 47; 59pp; English.
XX
CC The invention describes a composition comprising at least one expression
CC vector comprising a polynucleotide of the invention. The composition has
CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.
CC The invention is used to detect and treat conditions associated with
CC elevated cholesterol and lipid or during adipogenesis, particularly
CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart
CC disease. This sequence represents a polynucleotide differentially
CC expressed during cholesterol homeostasis and adipogenesis.
XX
SQ Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 981 GATCCAAAGGAGTTGT 996
Db 1 GATCCAAAGCAGTTGT 16
||||| |||||||

RESULT 214
ADI50064/c
ID ADI50064 standard; DNA; 17 BP.
XX
AC ADI50064;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID2567.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XWPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 2567; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 839 AAGGCCGGGTGGATC 854
Db 16 AAGGCCTGGGTGGATC 1
||||| |||||||

RESULT 215
ACC53731/c
ID ACC53731 standard; DNA; 17 BP.

XX AC ACC53731;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2498.
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 617; 798pp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
XX CC with tumour suppression or regression, apoptosis or virus resistance. The
XX CC invention relates to these sequences or sequences having at least 80%
XX CC identity to them, and polypeptides encoded by the sequences or
XX CC polypeptides having 80% identity to the polypeptide sequences. The
XX CC invention is used to diagnose or treat viral disease or disease
XX CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 969 ACATTTTGATGATC 984
DB 16 ACATTCTGATGATC 1
RESULT 216
ADM58814
ID ADM58814 standard; RNA; 17 BP.
XX AC ADM58814;
XX DT 03-JUN-2004 (first entry)
XX DE Hepatitis B virus (HBV) RNA target sequence #948.
XX KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
XX KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
XX KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
XX KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX OS Hepatitis B virus.
XX PN US2004054156-A1.
XX PD 18-MAR-2004.
XX

PF 15-JAN-2003; 2003US-00342902.
XX 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX Draper K, Blatt L, Mcswiggen JA, Morrissey D;
PI WPI; 2004-247781/23.
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX Disclosure; SEQ ID NO 948; 122pp; English.
XX The invention relates to an enzymatic nucleic acid molecule that
XX specifically cleaves RNA derived from hepatitis B virus (HBV) and
XX comprising one or more binding arms, without requiring the presence of a
XX 2'-OH group within the molecule for activity. The nucleic acids are
XX useful for treating hepatitis B virus infection, hepatitis,
XX hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
XX combination with other therapies such as lamivudine and interferons. The
XX nucleic acids are useful as diagnostic tools to examine genetic drift and
XX mutations within diseased cells, for detecting the presence of HBV RNA in
XX a cell, for the study of RNA and for down-regulating gene expression of
XX target genes in bacterial, fungal, viral, plant or mammalian cells. This
XX sequence represents an HBV RNA target sequence, used in the scope of the
XX invention. Note: The sequence data for this patent is also available in
XX electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 17 BP; 4 A; 2 C; 2 G; 0 T; 9 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 569 TTTAATACCTTTTATAT 584
DB 1 UUUAAUGCCUUUAU 16
RESULT 217
ACN65663/C
ID ACN65663 standard; DNA; 17 BP.
XX AC ACN65663;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMLP-1 probe SEQ ID NO:2565.
XX KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
XX KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX

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PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
PI
XX WPI; 2004-533378/51.
DR
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 2565; Opp; English.
PS
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
XX Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
Db 17 AGGCAGCTGCCGCCTT 2
RESULT 218
ACN65664/c
ID ACN65664 standard; DNA; 17 BP.
XX
AC ACN65664;
XX
XX 02-DEC-2004 (first entry)
DT
XX Human GDMLP-1 probe SEQ ID NO:2566.
DE
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
```

```
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
PI
XX WPI; 2004-533378/51.
DR
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 2566; Opp; English.
PS
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 743 AGGCAGCTGCCACCTT 758
Db 16 AGGCAGCTGCCGCCTT 1
RESULT 219
AAA85722/c
ID AAA85722 standard; DNA; 19 BP.
XX
AC AAA85722;
XX
```


| | | | |
|------------|---|----------|---|
| DT | 04-DEC-2000 (first entry) | DT | 03-MAY-2001. |
| DE | Cyclin B1 ribozyme binding site #51. | PD | |
| XX | | XX | |
| KW | Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss. | PF | 26-OCT-2000; 2000WO-US029500. |
| XX | | XX | |
| OS | Mammalia. | PR | 26-OCT-1999; 99US-0161532P. |
| XX | | XX | |
| PN | WO200032765-A2. | PA | (IMMU-) IMMUSOL INC. |
| XX | | XX | |
| PD | 08-JUN-2000. | PI | Robbins JM, Tritz R; |
| XX | | XX | |
| PF | 06-DEC-1999; 99WO-US028772. | DR | WPI; 2001-300427/31. |
| XX | | XX | |
| PR | 04-DEC-1998; 98US-0110954P. | PT | Treating proliferative skin or eye diseases and scarring, using ribozymes |
| XX | | PT | that cleave RNA encoding cytokines involved in inflammation, matrix |
| PA | (IMMU-) IMMUSOL INC. | PT | metalloproteinases, growth factors and cell-cycle dependent kinases. |
| XX | | XX | |
| PI | Tritz R, Welch PJ, Barber JR, Robbins JM; | PS | Example 1; Page 312; 408pp; English. |
| XX | | XX | |
| DR | WPI; 2000-412314/35. | CC | The present invention describes a method for treating a proliferative |
| XX | | CC | skin or eye disease and scarring. The method involves administering a |
| PT | New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves | CC | ribozyme (I) which cleaves RNA encoding a cytokine involved in |
| PT | RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, | CC | inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle |
| PT | PCNA and Cyclin B1. | CC | dependent kinase, growth factor or a reductase, or administering a |
| XX | | CC | nucleic acid molecule (II) comprising a promoter operably linked to a |
| PS | Disclosure; Page 96; 109pp; English. | CC | nucleic acid segment encoding (I). (I) can have antipsoriatic, |
| XX | | CC | dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, |
| CC | The present invention relates to a hairpin or hammerhead ribozyme, | CC | ophthalmological, vulnery, keratolytic and virucide activities, and |
| CC | designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase | CC | cleaves RNA encoding cytokine involved in inflammation. (I) can be used |
| CC | other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. | CC | in gene therapy. (I) and (II) are useful for treating proliferative skin |
| CC | Representative examples of ribozyme recognition sites are given in | CC | diseases such as psoriasis, atopic dermatitis, actinic keratosis, |
| CC | AAA82415 to AAA86787. The ribozyme of the invention is useful for | CC | squamous or basal cell carcinoma and viral or seborrheic wart. They can |
| CC | inhibiting restenosis by introduction of the ribozyme into cells. The | CC | also be used for treating proliferative eye diseases such as diabetic |
| CC | ribozyme is resistant to endonuclease activity and hence is efficient in | CC | retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of |
| CC | restenosis treatment | CC | prematurity and retinal detachment, and for treating and preventing |
| XX | | CC | scarring such as keloid, adhesion and hypertrophic or hypertrophic burn |
| SQ | Sequence 19 BP; 4 A; 9 C; 2 G; 4 T; 0 U; 0 Other; | CC | scar. AAH57577 to AAH52099 represent sequences used in the |
| | | XX | exemplification of the present invention |
| | | | |
| | Query Match 1.3%; Score 14.4; DB 1; Length 19; | | Sequence 19 BP; 4 A; 9 C; 2 G; 4 T; 0 U; 0 Other; |
| | Best Local Similarity 93.8%; Pred. No. 1.7e+02; | | |
| | Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | |
| | | | |
| QY | 791 GTGCTTGGAGAGGCAG 806 | QY | 791 GTGCTTGGAGAGGCAG 806 |
| | | | |
| Db | 19 GGGCTTGGAGAGGCAG 4 | Db | 19 GGGCTTGGAGAGGCAG 4 |
| | | | |
| | RESULT 220 | | RESULT 221 |
| AAH60884/c | | ABA82563 | |
| ID | AAH60884 standard; DNA; 19 BP. | ID | ABA82563 standard; DNA; 19 BP. |
| XX | | XX | |
| AC | AAH60884; | AC | ABA82563; |
| XX | | XX | |
| DT | 10-SEP-2001 (first entry) | XX | |
| XX | | DT | 25-JAN-2002 (first entry) |
| DE | | XX | |
| XX | Cyclin B1 ribozyme binding site SEQ ID NO:3308. | DE | Zmax1 gene region physical map preparation STS marker #522. |
| KW | Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; | XX | |
| KW | recognition site; target; ribozyme binding site; eye disease; vulnery; | KW | Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3; |
| KW | proliferative disease; skin disease; psoriasis; diabetic retinopathy; | KW | sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; |
| KW | cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; | KW | antitense therapy; vaccine; bone disorder; Paget's disease; adapter; |
| KW | matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; | KW | sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss. |
| KW | antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; | XX | |
| KW | antisickling; ophthalmological; keratolytic; gene therapy; viral wart; | OS | Homo sapiens. |
| KW | atopic dermatitis; actinic keratosis; squamous cell carcinoma; | OS | Synthetic. |
| KW | basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; | XX | |
| KW | sickle cell retinopathy; ss. | PN | WO200177327-A1. |
| XX | | XX | |
| OS | Homo sapiens. | PD | 18-OCT-2001. |
| OS | Synthetic. | XX | |
| XX | | XX | |
| PN | WO200130362-A2. | PF | 21-JUN-2000; 2000WO-US016951. |

Fri Aug 19 11:00:00 2005

XX 05-APR-2000; 2000US-00543771.
PR 05-APR-2000; 2000US-00544398.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Carulli JP, Little RD, Recker RR, Johnson ML;
PI WPI; 2001-657171/75.
XX
DR New high bone mass (HBM) and Zmax1 genes and proteins useful for
XX modulating bone mass for the treatment of e.g. osteoporosis.
PT
XX Disclosure; Page 37; 443pp; English.
PS
XX The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 295 TCGAATTGTTGTTTCT 310
DB 1 TCGAATTGTTGTGCT 16
RESULT 222
ABK23360
ID ABK23360 standard; DNA; 19 BP.
XX
AC ABK23360;
XX
DT 09-APR-2002 (first entry)
XX
DE Human Zmax1 cDNA reverse PCR primer #261.
XX
KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200192891-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016946.
XX
PR 26-MAY-2000; 2000US-00578900.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2002-097784/13.
XX
PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.

XX Disclosure; Page 42; 409pp; English.
PS
XX The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 295 TCGAATTGTTGTTTCT 310
DB 1 TCGAATTGTTGTGCT 16
RESULT 223
ACC45943
ID ACC45943 standard; DNA; 19 BP.
XX
AC ACC45943;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human HBM STS marker reverse primer #261.
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
XX
PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Disclosure; Page 58; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTTCT 310
Db 1 TCGAATTGTTGTGCT 16

RESULT 224
ADB98641
ID ADB98641 standard; DNA; 19 BP.
XX
AC ADB98641;
XX
DT 04-DEC-2003 (first entry)
XX
DE Sequence tagged site #522 used to prepare Zmax1 (LRP5) gene region map.
XX
KW Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
XX
OS Homo sapiens.
XX
PN WO200292000-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX
DR WPI; 2003-129214/12.
XX
PT New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
PS Example 2; Page 65; 629pp; English.
XX

CC The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)
CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
CC region.
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTTCT 310
Db 1 TCGAATTGTTGTGCT 16

RESULT 225
ADR17506
ID ADR17506 standard; DNA; 19 BP.
XX
AC ADR17506;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human chromosome 11 Zmax1 region reverse mapping primer #261.
XX
KW Human; high bone mass; Zmax1; ss; primer; HBM; osteoporosis; osteopathic;
KW LDL receptor; bone development; metabolic bone disease; PCR.
XX
OS Homo sapiens.
XX
PN US6780609-B1.
XX
PD 24-AUG-2004.
XX
PF 05-APR-2000; 2000US-00543771.
XX
PR 13-JAN-1998; 98US-0071449P.
PR 23-OCT-1998; 98US-0105511P.
PR 13-JAN-1999; 99US-00229319.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2004-623529/60.
XX
PT New high bone mass gene of chromosome 1.1Q13.3, encoding protein useful
PT for treating, diagnosing, preventing, or screening for normal and
PT abnormal conditions of bone, including metabolic bone diseases, e.g.
PT osteoporosis.
XX
PS Disclosure; SEQ ID NO 588; 284pp; English.
XX
CC The invention relates to an isolated amino acid protein sequence selected
CC from an amino acid sequence appearing as ADR16922 or an amino acid
CC sequence comprising or consisting of the extracellular domain of
CC ADR16922(amino acids 23-1385). ADR16922 is encoded by the HBM (high bone
CC mass) allele of the human Zmax1 gene and has sequence similarity to LDL
CC receptors. Also disclosed are nucleic acids, proteins, cloning vectors,
CC expression vectors, transformed hosts, methods of developing
CC pharmaceutical compositions, methods of identifying molecules involved in
CC bone development, and methods of diagnosing and treating diseases
CC involved in bone development. Specifically disclosed is the Zmax1 gene
CC and the high bone mass (HBM) allele on chromosome 11q13.3 encoding
CC ADR16922. The protein is useful for treating, diagnosing, preventing, or
CC screening for normal and abnormal conditions of bone, including metabolic
CC bone diseases, e.g. osteoporosis. The present sequence is a PCR primer

CC used in the mapping of the Zmax1/HBM gene.
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTTCT 310
Db 1 TCGAATTGTTGTGCT 16

RESULT 226
ADR48157
ID ADR48157 standard; DNA; 19 BP.
XX
AC ADR48157;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human chromosome 11 Zmax1 region reverse mapping primer #261.
XX
KW Human; ss; PCR; high bone mass; Zmax1; HBM; bone modulation;
KW bone development disorder; osteoporosis; chromosome 11; gene therapy;
KW primer.
XX
OS Homo sapiens.
XX
PN US2004176582-A1.
XX
PD 09-SEP-2004.
XX
PF 10-DEC-2003; 2003US-00731739.
XX
PR 13-JAN-1998; 98US-0071449P.
PR 23-OCT-1998; 98US-0105511P.
PR 13-JAN-1999; 99US-00229319.
PR 05-APR-2000; 2000US-00544398.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
XX WPI; 2004-661408/64.
XX
XX New nucleic acid sequence encoding high bone mass, useful in diagnosing,
PT treating and/or preventing osteoporosis.
PT
XX
PS Disclosure; SEQ ID NO 588; 303pp; English.
XX
CC The invention relates to an isolated nucleic acid sequence encoding a
CC high bone mass protein (HBM). The gene exists in two alleles, Zmax1, the
CC notional wild-type (the cDNA for which appears as ADR47570 encoding
CC ADR47572) and the HBM allele (the cDNA for which appears as ADR47571
CC encoding ADR47573). The two alleles differ by a single nucleotide
CC polymorphism (G to T at position 582 of ADR47570) causing a Gly to Val
CC change at position 171 of the protein. Also included are a replicative
CC cloning vector comprising HBM/Zmax1 (and a replicon operative in an
CC isolated host cell), an expression vector comprising HBM/Zmax1 operably
CC linked to a transcription regulatory region, an isolated host cell
CC transformed with the vector(s), a method for testing a substance as a
CC therapeutic agent for bone modulation in a host, a method of identifying
CC a molecule involved in bone modulation, a method for identifying a
CC (candidate) protein involved in bone modulation, a method of testing for
CC HBM activity, a method of developing a pharmaceutical for the treatment
CC of bone development disorders, a method for treating a bone development
CC disorder in an animal, a method of altering bone development in a host, a
CC method for diagnostic screening for a genetic predisposition to a bone
CC development disorder, a diagnostic assay for bone development disorders,
CC a method of expressing the HBM protein in bone tissue, a bacterial
CC artificial chromosome comprising HBM/Zmax1 sequence (appearing as

CC ADR47574-ADR47580), a method for amplifying a nucleotide polymorphism in
CC the Zmax1 or HBM gene, a method for identifying a regulatory element of a
CC HBM gene and an isolated nucleic acid segment of at least 15 contiguous
CC nucleotides including a polymorphic site from HBM/Zmax1. The nucleic acid
CC molecule and the encoded polypeptide, composition, and methods are useful
CC in diagnosing, treating and preventing a bone development disorder, i.e.
CC osteoporosis. The gene for HBM/Zmax1 is located on chromosome 11q13.3.
CC The present sequence is a primer used in the mapping of the HBM/Zmax1
CC gene.
XX
SQ Sequence 19 BP; 2 A; 1 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTTCT 310
Db 1 TCGAATTGTTGTGCT 16

RESULT 227
AAX92502/c
ID AAX92502 standard; DNA; 20 BP.
XX
AC AAX92502;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
PT
XX Page 1516; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 287 TTCACTACTGGAATTG 302
||||||| |||||
Db 19 TTCACTACGGGAATTG 4

RESULT 228
AAA96394
ID AAA96394 standard; DNA; 20 BP.
XX
AC AAA96394;
XX
DT 08-FEB-2001 (first entry)
XX
DE Primer used to amplify a sara25/26 polymorphic microsatellite repeat.
XX
KW Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
KW ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus;
KW insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;
KW Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma;
KW thyroiditis; postpartum thyroiditis; rheumatoid arthritis;
KW Hashimoto's disease; coeliac disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200056856-A2.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US007938.
XX
PR 25-MAR-1999; 99US-0126215P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Ling V, Wu P, Gray GS;
XX
DR WPI; 2000-628257/60.
XX
PT Determining predisposition of humans to develop autoimmune disease
PT involves detecting polymorphic microsatellite repeat sequence within
PT human costimulatory receptor gene locus.
XX
PS Claim 18; Page 151; 160pp; English.
XX
CC PCR primers AAA96393-94 were used to amplify polymorphic microsatellite
CC repeat (PMR) sequences from the human costimulatory receptor gene locus
CC (hCGRL). The primers are used in the method of the invention. The
CC specification describes a method for determining the predisposition of a
CC human subject to develop autoimmune disease. The method comprises
CC detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the
CC human costimulatory receptor gene locus (hCGRL). PMR sequences vary in
CC length among individuals and can be amplified to generate products that
CC differ in size. These products can then be detected by rapid and
CC convenient high resolution processes. The method is useful for
CC determining the predisposition of insulin-dependent diabetes mellitus
CC (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism,
CC myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis,
CC rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy.
CC PMR sequences within hCGRL are useful as markers in a variety of assays
CC and in the field of forensic medicine, disease diagnosis and human genome
CC mapping
XX
SQ Sequence 20 BP; 9 A; 3 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 721 AAATATATTAAACGCAG 736
||||||| |||||
Db 5 AAATATATTAAACCCAG 20

RESULT 229
AAZ72439
ID AAZ72439 standard; DNA; 20 BP.
XX
AC AAZ72439;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:6795.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 1679; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 218 TTCATTGCCAAAAGAG 233
||| ||||| |||||
Db 5 TTCTTTGCCAAAAGAG 20

RESULT 230
AAA47500
ID AAA47500 standard; cDNA; 20 BP.
XX
AC AAA47500;
XX

Fri Aug 19 11:00:00 2005

DT 20-OCT-2000 (first entry)

XX Primer for amplifying CCR2 chemokine.

XX Secondary lymphoid chemokine; SLC; cancer; hyperproliferative disorders; prostatic hyperplasia; proliferative breast disease;

KW proliferative retinopathy; melanoma; breast cancer; cancer; metastases;

KW suppression; angiogenesis; tumourigenesis; inflammation; immune response;

KW chemotaxis; graft rejection; autoimmune disease; primer; ss.

XX Synthetic.

OS WO200038706-A2.

XX 06-JUL-2000.

XX 28-DEC-1999; 99WO-US031096.

XX 31-DEC-1998; 98US-0114498P.

XX (CHIR) CHIRON CORP.

XX Keting C, Xin H, Chan VWF, Kothakota S, Williams LT, Winter JA;

PI WPI; 2000-465631/40.

XX Treating cancer or hyperproliferative disorder and modulating dendritic cell function in a mammal involves administering secondary lymphoid chemokine to the mammal.

XX Disclosure; Page 28; 53pp; English.

XX Secondary lymphod chemokines (SLC's), variants, fragments, and the polynucleotides encoding the chemokines, variants and fragments, anti-SLC antibodies or ligands for the CCR7 receptor can be used to modulate dendritic cell function in a mammal which results in a decreased primary immune response. SLC can be used to treat cancer or hyperproliferative disorders such as prostatic hyperplasia, proliferative breast diseases, proliferative retinopathy or pigmented skin lesions. SLC is also useful for treating solid tumours such as melanoma, breast cancer, tumours of the head and neck, cancers or metastases of ovary, endometrium, urinary tract, stomach, testicle, prostate, lung, bladder, pancreas, bone, liver, colon or rectum, or metastases of unknown primary origin. SLC can also be used to suppress angiogenesis particularly angiogenesis involved in cancer, tumourigenesis, metastases and tumour growth, and for mediating recruitment of leukocytes into sites of inflammation and immune responses, particularly, the chemotaxis of dendritic and other cells. SLC is also useful in preventing graft rejection, prevention and treatment of the autoimmune diseases and for enhancing an immune response. Two primers (AAA47499, AAA47500) were used to amplify the sequence encoding the chemokine CCR2

XX Sequence 20 BP; 1 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

SQ Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 781 GCTTGGGATGTGCTT 796
||||| |||||

Db 2 GCTTGGTGTGTGCTT 17

RESULT 231

ABK85315

ID ABK85315 standard; DNA; 20 BP.

XX ABK85315;

AC

XX 13-AUG-2002 (first entry)

DT

XX Human PTP1B antisense oligonucleotide ISIS 142070.

DE

XX

KW Antisense; protein phosphatase 1B; PTP1B; ss; probe; human; type 2 diabetes; obesity; ovarian cancer; chronic myeloid leukaemia; hyperproliferative disease; antidiabetic; anorectic; cytostatic; blood glucose; gene therapy.

XX Homo sapiens.

OS US2002055479-A1.

XX 09-MAY-2002.

XX 14-MAY-2001; 2001US-00854883.

XX 18-JAN-2000; 2000US-00487368.

PR 31-JUL-2000; 2000US-00629644.

XX (COWS/) COWSERT L M.

PA (WYAT/) WYATT J.

PA (FREI/) FREIER S M.

PA (MONI/) MONIA B P.

PA (BUTL/) BUTLER M M.

PA (MCKA/) MCKAY R.

XX Cowsert LM, Wyatt J, Freier SM, Monia BP, Butler MM, Mckay R;

PI WPI; 2002-462914/49.

XX Compound for inhibiting the expression of protein phosphatase 1B (PTP1B) and for treating diabetes, cancer, or obesity, comprises an antisense oligonucleotide targeted to nucleic acid encoding PTP1B.

XX Claim 3; Page 27; 133pp; English.

XX The invention relates to a compound of 8-50 nucleobases in length targeted to a nucleic acid encoding protein phosphatase 1B (PTP1B), where the compound specifically hybridises with and inhibits the expression of PTP1B (e.g. an antisense oligonucleotide). Also included are (1) a compound of 8-50 nucleobases in length which specifically hybridises with an 8 nucleobase portion of an active site on a nucleic acid encoding PTP1B; (2) inhibiting the expression of PTP1B in cells or tissues comprising contacting the cells or tissues with the compound; treating an animal having or suspected of having a disease or condition associated with PTP1B comprising administering the compound; (4) decreasing blood sugar levels in an animal comprising administering the compound; (5) preventing or delaying the onset of a disease or condition associated with PTP1B in an animal comprising administering the compound; and (6) preventing or delaying the onset of an increase in blood glucose levels in an animal comprising administering the compound. The compound is used to inhibit the expression of PTP1B in cells or tissues, to treat or prevent or delay the onset of a disease or condition associated with PTP1B, such as type 2 diabetes, obesity, cancer (especially ovarian cancer, chronic myeloid leukaemia and hyperproliferative diseases in an animal having or suspected of having the disease or condition, and for decreasing blood sugar levels or preventing or delaying the onset of an increase in blood glucose levels in an animal. The compound is also used in diagnostics, therapeutics, prophylaxis, and in research reagents and kits. The present sequence is an antisense compound of the invention targetting human PTP1B

XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

SQ Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 343 GGCTGTGATCAATGG 358
||||| |||||

Db 1 GGCTGTGATCAAAAGG 16

RESULT 232

ACC86742

ID ACC86742 standard; DNA; 20 BP.

XX ACC86742;
AC 04-AUG-2003 (first entry)
DT
XX Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:37.
DE
XX Vascular endothelial growth factor receptor 1; VEGF receptor; VEGFR;
KW inhibitor; cytostatic; antirheumatic; antiarthritic; antiangiogenic;
KW antiinflammatory; antisense gene therapy; hyperproliferative disorder;
KW cancer; rheumatoid arthritis; angiogenesis; infection; inflammation;
KW tumour formation; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-O-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 5 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
FT
PN WO2003022227-A2.
XX
XX 20-MAR-2003.
PD
XX 12-SEP-2002; 2002WO-US029148.
PF
XX 13-SEP-2001; 2001US-00953318.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Bennett CF, Watt AT;
PI WPI; 2003-301004/29.
XX
DR New antisense oligonucleotide targeted to a nucleic acid encoding
PT vascular endothelial growth factor receptor-1, useful for diagnosing or
PT treating cancer, rheumatoid arthritis, or diseases or conditions
PT involving angiogenesis.
XX
PS Claim 3; Page 82; 150pp; English.
XX
CC The present invention describes a compound (C) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding vascular endothelial growth
CC factor receptor-1 (VEGFR-1), where the compound inhibits the expression
CC of VEGFR-1 and specifically hybridises with the nucleic acid encoding
CC VEGFR-1 or with an 8-nucleobase portion of an active site on the nucleic
CC acid molecule encoding VEGFR-1. Also described: (1) a composition
CC comprising (C) and a carrier or diluent; (2) inhibiting the expression of
CC VEGFR-1 in cells or tissues by contacting the cells or tissues with (C)
CC so that the expression of VEGFR-1 is inhibited; and (3) treating an
CC animal having a disease or condition associated with VEGFR-1 by
CC administering (C) to the animal so that the expression of VEGFR-1 is
CC inhibited. (C) has antiangiogenic, antirheumatic, antiarthritic,
CC cytostatic and antiinflammatory activities, and can be used in antisense
CC gene therapy. The antisense compounds are useful for modulating the
CC expression of VEGFR-1 and for treating diseases or conditions associated
CC with the expression of VEGFR-1, such as hyperproliferative disorders
CC (e.g. cancer), rheumatoid arthritis, or diseases or conditions involving
CC angiogenesis. The antisense compounds are also useful for diagnostics,
CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
CC inflammation or tumour formation, as research reagents and kits, and in
CC distinguishing between functions of various members of a biological
CC pathway. The present sequence represents a human VEGFR-2 chimeric
CC phosphorothioate antisense oligonucleotide, which is used in an example
CC from the present invention
XX
SQ Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. NO. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 626 GTTTTATTCTCAGCAA 641
Db ||||| |||||
4 GTTTATGCTCAGCAA 19

RESULT 233
ADB68675/c
ID ADB68675 standard; DNA; 20 BP.
XX
AC ADB68675;
XX
DT 04-DEC-2003 (first entry)
XX
DE Microsomal triglyceride transfer protein antisense oligonucleotide #91.
XX
KW microsomal triglyceride transfer protein; antisense oligonucleotide;
KW hybridisation; microsomal triglyceride transfer protein inhibitor;
KW cardiant; antiarteriosclerotic; antilipaemic; antisense gene therapy;
KW abnormal lipid metabolism; abnormal cholesterol metabolism;
KW atherosclerosis; cardiovascular disease; mouse; phosphorothioate; ss;
KW 2'-O-methoxyethyl.
XX
OS Synthetic.
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages, and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2003018600-A2.
XX
PD 06-MAR-2003.
XX
PF 17-JUL-2002; 2002WO-US022799.
XX
PR 30-JUL-2001; 2001US-00917963.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-300705/29.
XX
XX New antisense oligonucleotide compounds, useful for diagnosing,
PT preventing and/or treating conditions with aberrant activity of the
PT microsomal triglyceride transfer protein, such as atherosclerosis and
PT heart disease.
XX
PS Claim 3; Page 97; 135pp; English.
XX
CC The present invention describes compounds (I) comprising 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding a microsomal
CC triglyceride transfer protein, where the compounds specifically hybridise
CC with and inhibit the expression of the microsomal triglyceride transfer
CC protein. Also described: (1) a compound 8-50 nucleobases in length which
CC specifically hybridises with at least an 8-nucleobase portion of an
CC active site on a nucleic acid molecule encoding microsomal triglyceride
CC transfer protein; (2) a composition comprising (I) and a carrier or

CC diluent; (3) inhibiting the expression of microsomal triglyceride
CC transfer protein in cells or tissues, comprising contacting the cells or
CC tissues with (I) so that expression of microsomal triglyceride transfer
CC protein is inhibited; and (4) treating an animal having a disease or
CC condition associated with microsomal triglyceride transfer protein,
CC comprising administering (I) to the animal so that expression of
CC microsomal triglyceride transfer protein is inhibited. (I) have cardiant,
CC antiarteriosclerotic and antilipaemic activities, and can be used in
CC antisense gene therapy. The methods and compositions of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC diseases or conditions associated with aberrant expression or activity of
CC microsomal triglyceride transfer protein, such as an abnormal lipid or
CC cholesterol metabolism condition like atherosclerosis and cardiovascular
CC disease. The present sequence represents a mouse microsomal triglyceride
CC transfer protein chimeric phosphorothioate antisense oligonucleotide,
CC which is used in an example from the present invention.

XX
SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 130 TCTTATGCTGGGATGT 145
Db 18 TCTTATGCTGGCATGT 3

RESULT 234
ACF36599/c
ID ACF36599 standard; DNA; 20 BP.
XX
AC ACF36599;
XX
DT 18-DEC-2003 (first entry)
XX
DE Coll11a2 cDNA amplifying RT-PCR primer COL-2.
XX
KW KRAB; repressor fusion protein; Kruppel-associated box; KAP1; Coll11a2;
KW cloned cell production; drug screening; luciferase; RT-PCR; primer; ss.
XX Synthetic.
XX WO2003072788-A1.
PN
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005347.
XX
PR 21-FEB-2002; 2002US-0358599P.
XX
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
PI Rauscher FJ, Ayyanathan K, Schultz DC;
PI
XX
DR WPI; 2003-712733/67.
XX
PT Producing a cloned cell containing a stably silenced target gene, useful
PT in research and drug screening, comprises introducing a nucleic acid
PT molecule expressing a chimeric repressor fusion protein into a parent
PT cell.
XX
PS Example 7; Page 54; 113pp; English.
XX
CC The invention relates to producing a cloned cell containing a stably
CC silenced target gene. The method involves introducing a nucleic acid
CC molecule expressing a chimeric repressor fusion protein into a parent
CC cell. The repressor fusion protein comprises a first amino acid sequence
CC comprising a Kruppel-Associated Box (KRAB) domain or its variant that
CC binds to the protein KAP1 and has DNA-dependent repressor activity fused
CC to a second amino acid targeting sequence that binds to the target gene,
CC fused to a switch component, that, in the presence of a ligand or
CC inducer, permits the second amino acid sequence to bind to the target

CC gene, where the fusion protein is under the control of regulatory
CC sequences capable of directing its expression in the parent cell. The
CC methods are useful for producing cloned cells that are particularly
CC useful in research and drug screening, e.g. identifying a test molecule
CC that activates the expression of a stably silenced target gene, or
CC manipulating expression of target gene in a cell. Sequences ACF36598-99
CC represent primers used in a RT-PCR assay for detecting levels of Coll1a2
CC mRNA in NIH3T3 cells

XX Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 600 AGAAAGACTTCATAAG 615
Db 18 AGCAAGACTTCATAAG 3

RESULT 235
ADII14044
ID ADII14044 standard; DNA; 20 BP.
XX
AC ADII14044;
XX
DT 22-APR-2004 (first entry)
XX
DE Antisense DNA oligo to target human PTP1B DNA SeqID 297.
XX
KW human; ss; antisense; PTP1B; protein phosphatase 1B; PTPN1;
KW phosphorothioate backbone; hyperproliferative condition; cancer;
KW cytostatic; antidiabetic; anorectic; type 2 diabetes; obesity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone"
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl nucleotides. All cytidine
FT nucleobases are 5' methylcytidine."
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl nucleotides. All cytidine
FT nucleobases are 5' methylcytidine."
XX
PN US2003220282-A1.
XX
PD 27-NOV-2003.
XX
PF 07-FEB-2003; 2003US-00360510.
XX
PR 18-JAN-2000; 2000US-00487368.
PR 31-JUL-2000; 2000US-00629644.
PR 14-MAY-2001; 2001US-00854883.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bhanot S, Cowser LM, Wyatt JR, Monia BP, Butler MM, McKay R;
PI Freier SM;
XX
DR WPI; 2004-051719/05.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding PTP1B, useful for treating a disease/condition
PT associated with PTP1B, such as cancer, diabetes or obesity.

XX PS Claim 3; SEQ ID NO 297; 143pp; English.

XX CC This invention relates to novel compositions and methods for modulating

CC the expression of PTP1B (also known as protein phosphatase 1B and PTPN1).

CC Specifically, it refers to antisense compounds that can target and

CC hybridise with a nucleic acid molecule encoding PTP1B, as well as splice

CC variants thereof and inhibit expression accordingly. PTP1B is a tyrosine

CC phosphatase that plays an essential regulatory role in signalling

CC mediated by the insulin receptor and as such is useful for treating

CC diseases such as type 2 diabetes and obesity. Furthermore, PTP1B can

CC suppress transformation of oncogenic genes, such that compositions of

CC this invention can also be used to treat hyperproliferative conditions

CC including cancer. Accordingly, these compounds can be described as having

CC cytostatic, antidiabetic and anorectic activities. This oligonucleotide

CC sequence is an antisense DNA oligo that targets human PTP1B DNA, and

CC which has a phosphorothioate backbone and 2'-O-methoxyethyl wings, used

CC in an exemplification of the invention.

XX SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 343 GGCTGTGATCAAATGG 358

Db 1 GGCTGTGATCAAAGG 16

RESULT 236

ADJ25024

ID ADJ25024 standard; DNA; 20 BP.

XX AC ADJ25024;

XX 20-MAY-2004 (first entry)

XX Human endothelial lipase antisense oligonucleotide, SEQ ID 3422.

DE Antilipaemic; Cardiovascular; Analgesic; Antiangular; Antisense therapy;

KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;

KW cardiovascular disorder; metabolic syndrome X; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "This oligonucleotide has a phosphorothioate

FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'

FT and 3' ends, which are 4 nucleotides in length. Also all

FT cytidine residues are 5-methylcytidines"

XX WO2004009541-A2.

PN 29-JAN-2004.

XX 18-JUL-2003; 2003WO-US022410.

XX 19-JUL-2002; 2002US-0397106P.

XX (PHAA) PHARMACIA CORP.

XX Bhat BG;

XX WPI; 2004-132912/13.

XX New antisense oligonucleotide for modulating endothelial lipase

PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low

PT high density lipoprotein or cardiovascular disorders.

XX PS Claim 3; SEQ ID NO 3422; 1007pp; English.

XX CC The present invention relates to antisense oligonucleotides (ADJ21603-

CC ADJ2510) targeted to human Endothelial Lipase (EL) coding sequence

CC (ADJ2517), where the antisense oligonucleotide specifically hybridises

CC with and inhibits the expression of EL. The antisense oligonucleotides

CC are useful for modulating the expression of endothelial lipase in cells

CC or tissues to treat diseases associated with EL expression, such as

CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular

CC disorder or metabolic syndrome X. In addition, the oligonucleotides are

CC used for diagnostics, prophylaxis, or as research reagents or kits.

XX SQ Sequence 20 BP; 2 A; 6 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GCCCGGGCGGTGGCAG 34

Db 5 GCCCGGGCGGTGGCAG 20

RESULT 237

ADN61693/C

ID ADN61693 standard; DNA; 20 BP.

XX AC ADN61693;

XX 01-JUL-2004 (first entry)

XX Corn chromosome 6 SSR marker bnlg 2249 6.04 PCR primer 1 SEQ ID:23.

DE Corn; plant; transformable; introgression; chromosomal locus;

KW bin 6.02-6.04; bin 10.04-10.06; bin 1.03-1.06; bin 1.08-1.11;

KW bin 3.05-3.07; corn seed; plant breeding; transgenic plant; chromosome 6;

KW SSR marker; marker assisted breeding; PCR; primer; ss.

XX Zea mays.

XX WO2003103377-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-US017626.

XX 06-JUN-2002; 2002US-0386522P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Lowe BA, Chomet P;

XX WPI; 2004-062179/06.

XX Producing a transformable corn line comprises introgressing at least one

PT chromosomal locus mapping to bin 6.02-6.04 or 10.04-10.06, where the

PT locus is introgressed from a more transformable corn line into a less

PT transformable corn line.

XX Example 3; SEQ ID NO 23; 77pp; English.

XX The invention relates to a method of producing a transformable corn line

CC by introgressing at least one chromosomal locus mapping to bin 6.02-6.04

CC or bin 10.04-10.06, where the locus is introgressed from a more

CC transformable corn line into a less transformable corn line. The

CC invention also relates to corn variety 178-187-20 seed (ATCC accession

CC no. PTA-5183) and corn variety 178-74-25 seed (ATCC accession no. PTA-

CC 5182); progeny of a plant grown from the seed cited above, where the

CC progeny comprises loci mapping to chromosomal bins 1.03-1.06, 1.08-1.11,

CC 3.05-3.07, and 6.02-6.04; a transgenic corn plant produced by

CC transforming the progeny cited above; and hybrid corn seed and plants

CC produced by crossing a corn line with the progeny cited above. Because

CC more transformable lines are typically agronomically poor, while lines
CC with superior or desired agronomic traits tend to be less transformable,
CC the methods of the invention provide a means of testing for the effects
CC of an introduced gene on traits such as yield, kernel quality and plant
CC phenotype in earlier plant generations in a breeding programme. Sequences
CC ADN61671-ADN61702 represent PCR primers used in an example of the
CC invention to amplify corn SSR markers useful in marker assisted breeding.
XX
SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 775 CCTTTTGCTTGGGGAT 790
Db 19 CCTTTTGCTAGGGGAT 4

RESULT 238
ADN01882
ID ADN01882 standard; cDNA; 20 BP.
XX
AC ADN01882;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human HIP1 antisense target sequence ISIS168127.
XX
KW Human; antisense; ss; Huntington interacting protein 1; HIP1;
KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
XX
OS Homo sapiens.
XX
XX US2004092465-A1.
PN
XX 13-MAY-2004.
PD
XX 11-NOV-2002; 2002US-00293864.
PF
XX 11-NOV-2002; 2002US-00293864.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dobie KW;
PI
XX WPI; 2004-374983/35.
DR
XX New compound that modulates huntingtin interacting protein 1 expression,
XX useful in treating an animal having a disease or condition involving
XX dysregulation of cellular apoptosis.
PS Example 15; SEQ ID NO 120; 85pp; English.
XX

The invention relates to a compound targeted to a nucleic acid molecule
CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
CC nucleobases in length, is an antisense oligonucleotide, where the
CC compound specifically hybridises with the nucleic acid molecule encoding
CC huntingtin interacting protein 1 comprising a sequence appearing as
CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
CC Also included are inhibiting the expression of huntingtin interacting
CC protein 1 in cells or tissues, screening for a modulator of huntingtin
CC interacting protein 1, a diagnostic method for identifying a disease
CC state, a kit or assay device comprising the compound and treating an
CC animal having a disease or condition associated with huntingtin
CC interacting protein 1 compound so that expression of huntingtin
CC useful in treating an animal having a disease or condition involving
CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
CC gene is located on chromosome 7q11.23. The present sequence is an
CC antisense target region from the HIP1 cDNA.
XX Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 GCTGACGACGCGCTCT 827
Db 5 GCTGACGACGCGCTCT 20

RESULT 239
ADN01807/c
ID ADN01807 standard; DNA; 20 BP.
XX
AC ADN01807;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human HIP1 antisense oligonucleotide ISIS251612.
XX
KW Human; antisense; ss; Huntington interacting protein 1; HIP1;
KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages and all cytidines are 5
FT -methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN US2004092465-A1.
XX
PD 13-MAY-2004.
XX
XX 11-NOV-2002; 2002US-00293864.
PF
XX 11-NOV-2002; 2002US-00293864.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dobie KW;
PI
XX WPI; 2004-374983/35.
DR
XX New compound that modulates huntingtin interacting protein 1 expression,
PT useful in treating an animal having a disease or condition involving
PT dysregulation of cellular apoptosis.
XX
PS Example 15; SEQ ID NO 45; 85pp; English.
XX

The invention relates to a compound targeted to a nucleic acid molecule
CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
CC nucleobases in length, is an antisense oligonucleotide, where the
CC compound specifically hybridises with the nucleic acid molecule encoding
CC huntingtin interacting protein 1 comprising a sequence appearing as
CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
CC Also included are inhibiting the expression of huntingtin interacting
CC protein 1 in cells or tissues, screening for a modulator of huntingtin
CC interacting protein 1, a diagnostic method for identifying a disease
CC state, a kit or assay device comprising the compound and treating an
CC animal having a disease or condition associated with huntingtin
CC interacting protein 1 compound so that expression of huntingtin
CC interacting protein 1 is inhibited. The compound and the methods are

CC useful in treating an animal having a disease or condition involving
CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
CC gene is located on chromosome 7q11.23. The present sequence is an
CC antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 813 CTGAAGCAGGCCTCTC 828
DB 20 CTGCAGCAGGCCTCTC 5
RESULT 240
ADN01806/c
ID ADN01806 standard; DNA; 20 BP.
XX
AC ADN01806;
XX
DT 29-JUL-2004 (first entry)
XX Human HIP1 antisense oligonucleotide ISIS251611.
XX
KW Human; antisense; ss; Huntington interacting protein 1; HIP1;
KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages and all cytidines are 5
FT -methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN US2004092465-A1.
XX
PD 13-MAY-2004.
XX
PF 11-NOV-2002; 2002US-00293864.
XX
PR 11-NOV-2002; 2002US-00293864.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW;
XX
DR WPI; 2004-374983/35.
XX
PT New compound that modulates huntingtin interacting protein 1 expression,
PT useful in treating an animal having a disease or condition involving
PT dysregulation of cellular apoptosis.
XX
PS Example 15; SEQ ID NO 44; 85pp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
CC nucleobases in length, is an antisense oligonucleotide, where the
CC compound specifically hybridises with the nucleic acid molecule encoding
CC huntingtin interacting protein 1 comprising a sequence appearing as
CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
CC Also included are inhibiting the expression of huntingtin interacting
CC

CC protein 1 in cells or tissues, screening for a modulator of huntingtin
CC interacting protein 1, a diagnostic method for identifying a disease
CC state, a kit or assay device comprising the compound and treating an
CC animal having a disease or condition associated with huntingtin
CC interacting protein 1 compound so that expression of huntingtin
CC interacting protein 1 is inhibited. The compound and the methods are
CC useful in treating an animal having a disease or condition involving
CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
CC gene is located on chromosome 7q11.23. The present sequence is an
CC antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 812 GCTGAAGCAGGCCTCT 827
DB 16 GCTGCAGCAGGCCTCT 1
RESULT 241
ADN01883
ID ADN01883 standard; cDNA; 20 BP.
XX
AC ADN01883;
XX
DT 29-JUL-2004 (first entry)
XX Human HIP1 antisense target sequence ISIS168128.
XX
KW Human; antisense; ss; Huntington interacting protein 1; HIP1;
KW cellular apoptosis; Huntington's disease; chromosome 7q11.23.
XX Homo sapiens.
XX
PN US2004092465-A1.
XX
PD 13-MAY-2004.
XX
PF 11-NOV-2002; 2002US-00293864.
XX
PR 11-NOV-2002; 2002US-00293864.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW;
XX
DR WPI; 2004-374983/35.
XX
PT New compound that modulates huntingtin interacting protein 1 expression,
PT useful in treating an animal having a disease or condition involving
PT dysregulation of cellular apoptosis.
XX
PS Example 15; SEQ ID NO 121; 85pp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding huntingtin interacting protein 1, HIP1. The compound, 8-80
CC nucleobases in length, is an antisense oligonucleotide, where the
CC compound specifically hybridises with the nucleic acid molecule encoding
CC huntingtin interacting protein 1 comprising a sequence appearing as
CC ADN01766 and inhibits the expression of huntingtin interacting protein 1.
CC Also included are inhibiting the expression of huntingtin interacting
CC protein 1 in cells or tissues, screening for a modulator of huntingtin
CC interacting protein 1, a diagnostic method for identifying a disease
CC state, a kit or assay device comprising the compound and treating an
CC animal having a disease or condition associated with huntingtin
CC interacting protein 1 compound so that expression of huntingtin
CC interacting protein 1 is inhibited. The compound and the methods are
CC useful in treating an animal having a disease or condition involving
CC dysregulation of cellular apoptosis e.g. Huntington's disease. The HIP1
CC gene is located on chromosome 7q11.23. The present sequence is an

Fri Aug 19 11:00:00 2005

CC antisense target region from the HIP1 cDNA.

SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity93.8%; Pred. No. 1.7e+02;

Matches15; Conservative0; Mismatches1; Indels0; Gaps0;

QY813 CTGACGAGGCCTCTC 828

Db1 CTGCACGAGGCCTCTC 16

RESULT 242

ADP78871

ID ADP78871 standard; DNA; 20 BP.

XX

AC ADP78871;

XX

DT 12-AUG-2004 (first entry)

XX

DE Chimeric phosphorothioate oligonucleotide #2670.

XX

KW GFAT; Antidiabetic; Cardiant;

KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;

KW reperfusion; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1. .4

FT /*tag= a

FT /mod_base= other

FT /note= "2-methoxyethyl wing"

FT modified_base 17. .20

FT /*tag= b

FT /mod_base= other

FT /note= "2-methoxyethyl wing"

XX

PN WO2004035763-A2.

XX

PD 29-APR-2004.

XX

PF 02-OCT-2003; 2003WO-US033332.

XX

PR 17-OCT-2002; 2002US-0419268P.

XX

PA (PHAA) PHARMACIA CORP.

XX

PI Broschat KO, Crosby SD;

XX

DR WPI; 2004-348453/32.

XX

PT New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,

PT ischemia/reperfusion injury.

XX

PS Claim 4; SEQ ID NO 2670; 175pp; English.

XX

CC The present invention relates to a compound which specifically hybridizes

CC with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX

SQ Sequence 20 BP; 5 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match1.3%; Score 14.4; DB 1; Length 20;

Best Local Similarity93.8%; Pred. No. 1.7e+02;

Matches15; Conservative0; Mismatches1; Indels0; Gaps0;

QY554 TAATATGCTGGGTTTT 569

Db1 TAATAAGCTGGGTTTT 16

RESULT 243

ADP78738

ID ADP78738 standard; DNA; 20 BP.

XX

AC ADP78738;

XX

DT 12-AUG-2004 (first entry)

XX

DE Chimeric phosphorothioate oligonucleotide #2537.

XX

KW GFAT; Antidiabetic; Cardiant;

KW Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;

KW reperfusion; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1. .4

FT /*tag= a

FT /mod_base= other

FT /note= "2-methoxyethyl wing"

FT modified_base 17. .20

FT /*tag= b

FT /mod_base= other

FT /note= "2-methoxyethyl wing"

XX

PN WO2004035763-A2.

XX

PD 29-APR-2004.

XX

PF 02-OCT-2003; 2003WO-US033332.

XX

PR 17-OCT-2002; 2002US-0419268P.

XX

PA (PHAA) PHARMACIA CORP.

XX

PI Broschat KO, Crosby SD;

XX

DR WPI; 2004-348453/32.

XX

PT New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase

PT (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,

PT ischemia/reperfusion injury.

XX

PS Claim 4; SEQ ID NO 2537; 175pp; English.

XX

CC The present invention relates to a compound which specifically hybridizes

CC with a nucleic acid molecule encoding GFAT, and inhibits the expression

CC of GFAT. Specifically claimed are antisense oligonucleotides capable of

CC modulating the expression of GFAT, and which comprise any of the 3063

CC sequences of 20 base pairs, given in the specification. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with GFAT, such as a disease or condition, e.g. diabetes, a

CC cardiovascular or neurological disorder, ischemia/reperfusion injury.

CC They are also useful in research and diagnostics for modulating the

CC expression of GFAT. The present sequence represents a chimeric

CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these

CC oligonucleotides inhibit human GFAT expression.

XX


```
Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      553 TTAATATGCTGGGTTT 568
Db      5 TTAATAAGCTGGGTTT 20

RESULT 244
ADQ14074
ID      ADQ14074 standard; DNA; 20 BP.
XX
AC      ADQ14074;
DT      07-OCT-2004 (first entry)
XX
DE      CAPN3/DYSF PCR primer, SEQ ID 471.
XX
KW      Human; SCAIP; CAPN3; DYSF; calpain; calcium-activated neutral protease;
KW      limb-girdle muscular dystrophy type 2A; LGMD2A; dysferlin;
KW      limb-girdle muscular dystrophy type 2B; LGMD2B; PCR; primer; ss;
KW      Single Condition Amplification/ Internal Primer.
XX
OS      Homo sapiens.
XX
PN      WO2004058985-A2.
XX
PD      15-JUL-2004.
XX
PF      17-DEC-2003; 2003WO-US040278.
XX
PR      17-DEC-2002; 2002US-0433774P.
XX
PA      (UTAH ) UNIV UTAH RES FOUND.
XX
PI      Flanigan KM, Weiss RB, Dunn DM, Von Niederhausern A;
XX      WPI; 2004-525893/50.
XX
PT      Characterizing a nucleic acid region, useful for detecting genetic
PT      mutations in any large multi-exon gene e.g., those indicating
PT      dystrophinopathy, comprises using a Single Condition
PT      Amplification/Internal Primer (SCAIP) sequencing method.
XX
PS      Example 9; Page 45; 174pp; English.
XX
CC      The present invention relates to a Single Condition Amplification/
CC      Internal Primer (SCAIP) sequencing method for direct sequence analysis of
CC      large multi-exon genes from genomic DNA samples and identifying mutations
CC      in multi-exon genes e.g. the dystrophin gene, CAPN3 gene and DYSF gene.
CC      Mutations in the dystrophin gene result in both Duchenne Muscular
CC      Dystrophy (DMD) and Becker Muscular Dystrophy (BMD). Mutations in the
CC      CAPN3 gene, encoding calpain (calcium-activated neutral protease) result
CC      in limb-girdle muscular dystrophy type 2A (LGMD2A) and mutations in the
CC      DYSF gene, encoding dysferlin, result in limb-girdle muscular dystrophy
CC      type 2B (LGMD2B). The method comprises bringing into contact in each of
CC      the reaction chambers an amplicon from a different one of the
CC      amplification reactions and one or more internal sequencing primers
CC      corresponding to the amplicon and analysing the sequences of the
CC      amplicons. The method allows for the rapid, accurate, and economical
CC      analysis of any large multi-exon gene. The method is useful in detecting
CC      genetic mutations in any large multi-exon gene. It is also useful for the
CC      identification and analysis of specific individual genomic mutations
CC      including deletions, point mutations, or its combinations, gene complexes
CC      with multiple exons/introns spanning large genomic regions. The present
CC      sequence is a PCR primer, used in the method of the invention.
XX
SQ      Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      699 ATGTAGTCACGGTGCT 714
Db      20 ATGAAGTCACGGTGCT 5

RESULT 246
AAT30234
ID      AAT30234 standard; DNA; 19 BP.
```

```
QY      449 AGCTGGGAGCAGTGGT 464
Db      1 AGCTGGGAGCAGTTGT 16

RESULT 245
ADQ91206/c
ID      ADQ91206 standard; DNA; 20 BP.
XX
AC      ADQ91206;
DT      21-OCT-2004 (first entry)
XX
DE      PCR primer used to amplify murine TRPM calcium ion channel DNA Seq 13.
XX
KW      murine; mouse; transient receptor potential melastatin; TRPM; primer; ss;
KW      pregnenolone sulphate; memory; learning ability; antidermentia;
KW      calcium permeable nonselective cation channel; dementia; nootropic;
KW      neuroprotective; PCR.
XX
OS      Mus sp.
XX
PN      WO2004065598-A1.
XX
PD      05-AUG-2004.
XX
PF      16-JAN-2004; 2004WO-JP000333.
XX
PR      17-JAN-2003; 2003JP-00009884.
XX
PA      (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI      Sano Y, Inamura K, Mochizuki S;
XX      WPI; 2004-571687/55.
XX
PT      New polypeptide with calcium ion channel transmissive activity, activated
PT      by pregnenolone sulfate, useful for screening memory improving agent,
PT      learning ability improving agent and/or anti-dementia agent.
XX
PS      Example 9; SEQ ID NO 13; 114pp; Japanese.
XX
CC      This invention relates to a protein that exhibits calcium ion channel
CC      transmissive activity and is activated by pregnenolone sulphate.
CC      Specifically, it refers to a novel screening method for identifying a
CC      substance that is useful as a memory improving agent, a learning ability
CC      improving agent and/ or an antidermentia agent. The present invention
CC      describes this screening tool as one that involves contacting a test
CC      substance with cells expressing the calcium permeable nonselective cation
CC      channel and analysing the channel activity to select only those
CC      substances, for example pregnenolone sulphate, which can activate the
CC      channel. As such, it provides a means to develop pharmaceutical
CC      compositions comprising these substances that can be used to treat
CC      dementia, as well as improving memory and learning functions.
CC      Accordingly, they act as calcium channel agonists and exhibit nootropic
CC      and neuroprotective activities. This oligonucleotide sequence is a PCR
CC      primer given in an exemplification of the invention.
XX
SQ      Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match      1.3%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      699 ATGTAGTCACGGTGCT 714
Db      20 ATGAAGTCACGGTGCT 5

RESULT 246
AAT30234
ID      AAT30234 standard; DNA; 19 BP.
```


Fri Aug 19 11:00:00 2005

```
XX AC AAT30234;
XX DT 12-NOV-1996 (first entry)
XX DE Target nucleic acid for probe with attached intercalating agent.
XX KW probe; intercalating agent; fluoro-chrome; hybridisation; assay;
KW detection; thiazole orange; oxazole yellow; flourescent; flourescence;
KW ss.
XX OS Synthetic.
XX PN EP714986-A1.
XX PD 05-JUN-1996.
XX PF 01-DEC-1995; 95EP-00308660.
XX PR 01-DEC-1994; 94JP-00298665.
XX PR 21-JUL-1995; 95JP-00185599.
XX PA (TOYJ ) TOSOH CORP.
XX PI Ishiguro T, Otsuka M, Inoue T, Yawata H, Sugiyura Y;
XX DR WPI; 1996-261625/27.
XX Oligo:nucleotide probes with intercalating fluoro:chrome label - only
PT fluoresces when bound to target sequences, removes need to separate un-
PT hybridised probes.
XX Example 4; Page 10; 32pp; English.
XX Oligonucleotide probes labelled with an intercalating fluorochrome, the
CC characteristics of which change when the probe is hybridised to the
CC target sequence, can be used to detect target nucleic acid in a
CC convenient single step method. The new probes allow homogeneous assays to
CC be performed without the need to separate unhybridised probe. If the
CC probe is added before PCR amplification of target DNA, the PCR time
CC profile can be monitored by measuring the flourescent intensity of the
CC reaction mixture. The fluoro-chrome is preferably thiazole orange or
CC oxazole yellow. The method avoids the problem of nonspecific
CC intercalation associated with the use of free flourchromes
XX Sequence 19 BP; 0 A; 11 C; 0 G; 8 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 189 TTTTCCACGCCATCTCCCC 207
Db 1 TTTTCTCTCCCTCTCCCC 19
RESULT 247
AAV10771/C
ID AAV10771 standard; DNA; 19 BP.
XX AC AAV10771;
XX DT 21-JUL-1998 (first entry)
XX DE Human breast cancer gene CH13-2a12-1 primer pch14-sp6-3fb.
XX KW Breast cancer; malignant transformation; diagnostic; therapeutic;
KW screening; primer; ss.
XX OS Synthetic.
OS Homo sapiens.
XX WO9738085-A2.
XX PN
```

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XX PD 16-OCT-1997.
XX PF 09-APR-1997; 97WO-US005930.
XX PR 10-APR-1996; 96US-0015167P.
XX PR 05-JUN-1996; 96WO-US009286.
XX PR 06-JUN-1996; 96US-0019202P.
XX PR 11-JUL-1996; 96US-00678280.
XX PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
XX PI Smith H, Chen L;
XX DR WPI; 1997-512705/47.
XX Breast cancer genes - used to develop products to design or screen
PT diagnostic reagents or therapeutic compounds.
XX Disclosure; Fig 18; 118pp; English.
XX AAV10748-V10777 are primers used in a method to identify the novel human
CC breast cancer gene CH13-2a12-1 by differential display. The identified
CC genes or fragments of these genes can be used for identifying genes and
CC gene products that are intimately related to malignant transformation or
CC maintenance of the malignant properties of cancer cells. It can also be
CC used to design or screen diagnostic reagents or therapeutic compounds.
CC Kits are included within the scope of the invention
XX Sequence 19 BP; 7 A; 4 C; 1 G; 7 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1009 GTTTGAGAAGCATCATCAT 1027
Db 19 GTTTGAAAAGCATGATTAT 1
RESULT 248
AAA46190
ID AAA46190 standard; DNA; 19 BP.
XX AC AAA46190;
XX DT 04-SEP-2000 (first entry)
XX PCR primer used to amplify a fragment of the human HFE gene.
DE Hereditary hemochromatosis gene; HFE gene; iron overload;
XX hereditary atransferrinemia; hypotransferrinemia; aceruloplasminemia;
KW polymetabolic syndrome; chronic liver disease; hematological disease;
KW delayed cutaneous porphyria; hematochromatosis; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200026403-A1.
XX PD 11-MAY-2000.
XX PF 29-OCT-1999; 99WO-FR002656.
XX PR 29-OCT-1998; 98FR-00013607.
XX PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX PA (INRM ) INST NAT SANTE & RECH MEDICAL.
XX PI Rosmorduc O, Hermelin B, Poupon R, Clauser E;
XX DR WPI; 2000-387228/33.
XX Assessing risk of severe iron overload, e.g. in subjects with hereditary
PT
```

PT hemochromatosis, by measuring a profile of the various HFE gene
PT transcripts.
XX
PS Claim 4; Page 11; 38pp; French.
XX
CC PCR primers AAA46189-90 were used to amplify a fragment of the human
CC hereditary hemochromatosis (HFE) gene. The primers were used in the
CC method of the invention. The specification describes a method for
CC evaluating the risk of developing severe iron overload, particularly in a
CC predisposed subject. The method comprises determining the profile of the
CC different transcripts of the HFE gene in a biological sample. The method
CC is used to determine risk of iron overload, of inherited or acquired
CC origin, e.g. in cases of hereditary or juvenile hematochromatosis,
CC hereditary atransferrinemia, hypotransferrinemia, aceruloplasminemia,
CC polymetabolic syndrome, chronic liver disease, delayed cutaneous
CC porphyria or hematological disease
XX
SQ Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 238 CTATGACTCAGATGCAACC 256
Db 1 CTCTGACTCAGCTGCAGCC 19

RESULT 249
ABT23695
ID ABT23695 standard; DNA; 19 BP.
XX
AC ABT23695;
XX
DT 22-MAY-2003 (first entry)
XX
DE Stabilising reagent method related oligo SEQ ID No 147.
XX
KW Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
KW specific amplification; pathogenic microorganism; chimeric;
KW genetic engineering; clinical medicine; ss.
XX
OS Unidentified.
XX
XX WO2002101042-A1.
PN
XX
PD 19-DEC-2002.
XX
PF 12-JUN-2002; 2002WO-JP005832.
XX
PR 12-JUN-2001; 2001JP-00177737.
PR 20-AUG-2001; 2001JP-00249689.
XX
XX (TAKI) TAKARA BIO INC.
PA
XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
PI Enoki T, Asada K, Kato I;
XX WPI; 2003-148805/14.
DR
XX
PT Method for stabilizing and storing reaction reagents for specific
PT amplification and detection of nucleic acids particularly in e.g.
PT identifying pathogenic microorganisms or viruses in sample.
XX
PS Example 15; Page 168; 177pp; Japanese.
XX
CC The invention relates to a novel stabilising reaction reagent for use in
CC the amplification and/or detection of a target nucleic acid comprising:
CC preparing a reaction mixture with e.g. a nucleic acid as template, at
CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC defined period of time to form a reaction product during the
CC amplification of such target nucleic acid. The method is useful for
CC stabilising and long-term storage of reaction reagents for highly

CC sensitive and specific amplification and detection of nucleic acids
CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent
CC method of the invention
XX
SQ Sequence 19 BP; 6 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1064 CCAGTGGCTAAACCACTTA 1082
Db 1 CCAGAGGCTGAACCACTTA 19

RESULT 250
ADI82218
ID ADI82218 standard; DNA; 19 BP.
XX
AC ADI82218;
XX
DT 22-APR-2004 (first entry)
XX
DE RTQ PCR primer #2 for Human LEFTB.
XX
KW Human; ss; PCR; embryonic stem cell; pluripotent stem cell;
KW abnormal cell growth; malignancy; differentiation; primer; RTQ-PCR;
KW realtime quantitative PCR.
XX
OS Homo sapiens.
XX
XX US2003224411-A1.
PN
PD 04-DEC-2003.
XX
PF 13-MAR-2003; 2003US-00388578.
XX
PR 13-MAR-2003; 2003US-00388578.
XX
PA (STAN/) STANTON L W.
PA (BRAN/) BRANDENBERGER R.
PA (GOLD/) GOLD J D.
PA (IRVI/) IRVING J M.
PA (MAND/) MANDALAM R.
PA (MOKM/) MOK M.
PA (SHEL/) SHELTON D.
XX
PI Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;
PI Mok M, Shelton D;
XX WPI; 2004-119701/12.
DR
XX
PT Assessing culture of undifferentiated primate pluripotent stem cells by
PT detecting expression of markers e.g., Zic family member 3, other than
PT human telomerase reverse transcriptase/octamer binding transcription
PT factor.
XX
PS Example 4; SEQ ID NO 48; 106pp; English.
XX
CC The invention relates to assessing a culture of undifferentiated primate
CC pluripotent stem cells (pPS, e.g. embryonic stem cells), involving
CC detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as
CC given in specification, other than human telomerase reverse transcriptase
CC (hTERT) or octamer binding transcription factor (Oct)3/4, or a marker
CC (MR2) such as crypto or podocalyxin-like protein and hTERT and/or Oct3/4
CC or second marker chosen from (MR2). Also included are maintaining (M2)
CC pPS cells in a pluripotent state (involves causing them to express one of
CC the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypothetical
CC protein FLJ20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsa12,
CC KRAB-zinc finger protein SZF1-1 or zinc finger protein of cerebellum

CC ZIC2, or any other marker (MR4) chosen from PHD protein Jade-1 (Jade-1),
CC kruppel-like zinc finger protein (ZNF300), etc., as given in the
CC specification), causing pps cells to differentiate into a particular
CC tissue type by causing them to express one of the markers chosen from
CC (MR3) or (MR4) (or markers chosen from GATA binding protein 3 (GATA3),
CC core promoter element binding protein (COPEB), etc., as given in the
CC specification), maintaining pps cells in a pluripotent state (involves
CC culturing pps cells or their progeny in the presence of a normally
CC secreted protein that is encoded by a gene that down-regulated upon
CC differentiation of human embryonic stem (hES) cells, chosen from
CC Fibrillin 3 gene, LEFT B gene, ZIC3 gene, EPHA1 gene, etc., as given in
CC the specification), causing pps cells to differentiate (involves
CC culturing pps cells or their progeny in the presence of a normally
CC secreted protein that is encoded by a gene that up-regulated upon
CC differentiation of hES cells, chosen from p311 protein gene, Tax
CC interaction protein 1 gene, KIAA0853 protein gene, keratin 19 (KRT 19)
CC gene, etc., as given in the specification), causing an encoding sequence
CC to be preferentially expressed in undifferentiated pps cells, causing an
CC encoding sequence to be preferentially expressed in differentiated cells,
CC sorting (M4) differentiated cells from less differentiated cells
CC (involves separating cells expressing a surface marker chosen from any
CC one of MR1 from cells not expressing the marker), causing pps cells to
CC proliferate without differentiation, identifying genes that are up or
CC down regulated during differentiation of pps cells, and a kit (I) for
CC assessing a culture of pps cells by M1. The method (M1) is useful for
CC assessing culture of undifferentiated primate pluripotent stem cells and
CC for assessing the growth characteristics of a cell population. The cell
CC population has been obtained by culturing cells from human blastocyst or
CC from a human patient suspected of having a clinical condition related to
CC abnormal cell growth. The method further involves determining whether the
CC cell population is pluripotent from the marker expression and assessing
CC whether the patient has a malignancy from the marker expression. The
CC present sequence is an RTQ-PCR primer (realtime quantitative PCR) used to
CC assay the expression of a human mRNA in a pps population.

XX
SQ Sequence 19 BP; 6 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 827 TCATGACCCAGGAGGCCG 845
Db 1 TCATAAGCCAGGAGGCCG 19

RESULT 251
ADQ27747
ID ADQ27747 standard; DNA; 19 BP.
XX
AC ADQ27747;
XX
DT 26-AUG-2004 (first entry)
XX
DE RNA interference target sequence #655.
DE
XX ss; detection; RNA interference; siRNA; gene silencing; gene expression;
KW cytotoxicity.
KW
XX Homo sapiens.
OS
XX WO2004048566-A1.
PN
XX 10-JUN-2004.
PD
XX 21-NOV-2003; 2003WO-JP014893.
PF
XX 22-NOV-2002; 2002JP-00340053.
PR
XX (NATO/) NATORI Y.
PA (SAIG/) SAIGO K.
PA (TEIK/) TEI K.
PA (NAIT/) NAITO Y.

XX Saigo K, Tei K, Naito Y;
PI WPI; 2004-487423/46.
XX
DR
XX Detecting sequence of RNA interference useful for synthesizing siRNA, by
PT detecting regions in sequence fulfilling specific criteria such as base
PT at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
PT guanine or cytosine.
PT
XX Disclosure; SEQ ID NO 669; 325pp; Japanese.
PS
XX The invention relates to a method of detecting the base sequence for RNA
CC interference by detecting the regions in the DNA sequence fulfilling the
CC following requirements such as: (i) the base at 3' terminal is adenine,
CC thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine;
CC (iii) the seven base sequence at 3' terminal is rich in adenine, thymine
CC and uracil, and; (iv) there are bases in a such a number that it causes
CC RNA interference without showing cytotoxicity. The method is used for
CC designing and synthesizing siRNA causing RNA interference. This sequence
CC corresponds to an RNA interference target sequence of the invention.

XX
SQ Sequence 19 BP; 5 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 709 GGTGCTCTCAGAAATATA 727
Db 1 GTTGCTCTCCGAAATTTA 19

RESULT 252
ADQ61744/C
ID ADQ61744 standard; RNA; 19 BP.
XX
AC ADQ61744;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-NR2E1 siRNA related DNA sequence SEQ ID NO:1446.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
XX (DHAR-) DHARMACON INC.
PA
XX Anastasia K, Angela R, Devin L, William M, Stephen S;
PI WPI; 2004-420527/39.
XX
DR Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
XX by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
XX Example 12; SEQ ID NO 1446; 199pp; English.

XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the

CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGGAGAUGAUGAAGUA; GAAGUACAUCCAUUAUAAAG;
CC GUACGACAACCGAGAU; AGAUAGUGAUGAAGUACAU; UGAAGACUCUCUCAGUUU;
CC CAUGCGCCUCUGUUUGA; UGCGCCUCUGUUUGAUUU; GAGAUGAUGAAGUAACA;
CC GGAGAUGAUGAAGUAC; and GAAGACUCUCUCAGUUUG. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention. The sequence is shown in
CC the specification as DNA, but described as siRNA.

XX
SQ Sequence 19 BP; 6 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 723 ATATATTAAACGCAGTCTTG 741
Db 19 ATATCTGAAAGCAGTCTTG 1
||||| ||| ||||| |||||

RESULT 253
ADR70528

ID ADR70528 standard; DNA; 19 BP.

XX ADR70528;

XX 02-DEC-2004 (first entry)

DE Reverse RTQ primer for human LEFTB.

XX Human; ss; PCR; telomerase reverse transcriptase; TERT; POU domain;
KW class 5 transcription factor; POU5F1; Oct3; Oct4;
KW teratocarcinoma-derived growth factor; Cripto; podocalyxin-like; PODXL;
KW gastrin-releasing peptide receptor; GRPR; human embryonic stem cell; hES;
KW primate pluripotent stem cell; cancer; gene expression; cell separation;
KW differentiation; primer; RTQ PCR; real time quantitative PCR.

OS Homo sapiens.

XX US2004180347-A1.

PN 16-SEP-2004.

XX 13-MAR-2003; 2003US-00389431.

XX 13-MAR-2003; 2003US-00389431.

XX (STAN/) STANTON L W.

PA (BRAN/) BRANDENBERGER R.

PA (GOLD/) GOLD J D.

PA (IRVI/) IRVING J M.

PA (MAND/) MANDALAM R.

PA (MOKM/) MOK M.

XX Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;
PI Mok M;

XX WPI; 2004-675599/66.

XX Assessing culture of undifferentiated human embryonic stem cells or their
PT progeny, by detecting Cripto, gastrin-releasing peptide (GRP) receptor
PT and podocalyxin-like protein markers, and either hTERT and/or Oct3/4, or

PT GRP receptor.

XX Disclosure; SEQ ID NO 48; 57pp; English.

XX The invention relates to assessing a culture of undifferentiated human
CC embryonic stem (hES) cells (undifferentiated primate pluripotent stem
CC cells) or their progeny, involves detecting or measuring a marker such as
CC Cripto (teratocarcinoma-derived growth factor), gastrin-releasing peptide
CC (GRP) receptor and podocalyxin-like protein, and either hTERT (telomerase
CC reverse transcriptase) and/or Oct3/4 (also known as POU domain, class 5,
CC transcription factor 1(POU5F1)), or GRP receptor. The method involves
CC detecting or measuring at least two markers, and detecting or measuring
CC hTERT and/or Oct3/4. The expression of the marker(s) is detected or
CC measured at mRNA level by PCR amplification. The expression of the
CC marker(s) is detected or measured at the protein level by antibody assay.
CC The method involves quantifying the proportion of undifferentiated hES
CC cells or differentiated cells in the culture from the marker expression.
CC The level of the marker is determined to be at least 100-fold higher than
CC the level of the marker in BJ fibroblasts or is determined to be no less
CC than 100-fold lower than the level of the marker in hES cells, cultured
CC on an extracellular matrix in medium conditioned with mouse embryonic
CC fibroblasts and containing 4 ng/ml basic fibroblast growth factor. The
CC method further involves modifying the culture conditions so as to cause
CC the hES cells to increase expression of the marker detected or measured
CC in the culture. The method is useful for assessing a culture of
CC undifferentiated hES cells or their progeny. The marker used in the above
CC method is useful for characterising pluripotent stem cells and their
CC differentiated progeny, for clinical diagnosis of cancer, for assessing
CC and manipulating culture conditions, regulating gene expression, cell
CC separation and purification, and to influence differentiation. The
CC present sequence is a real time quantitative PCR primer used to assay
CC mRNA expression in undifferentiated stem cells.

XX
SQ Sequence 19 BP; 6 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 827 TCATGACCCAGGAAGCGG 845
Db 1 TCATAAGCCAGGAAGCCCG 19
||||| ||| ||||| |||||

RESULT 254

ADR75949/C

ID ADR75949 standard; DNA; 19 BP.

XX ADR75949;

XX 16-DEC-2004 (first entry)

XX Human apolipoprotein B (ApoB) oligonucleotide seqid 434.

KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.

OS Homo sapiens.

XX WO2004080406-A2.

XX 23-SEP-2004.

XX 08-MAR-2004; 2004WO-US007070.

XX 07-MAR-2003; 2003US-0452682P.

| | | | |
|----|---|----|--|
| PR | 12-MAR-2003; 2003US-0454265P. | DT | 16-DEC-2004 (first entry) |
| PR | 13-MAR-2003; 2003US-0454962P. | XX | Human apolipoprotein B (ApoB) oligonucleotide seqid 3052. |
| PR | 13-MAR-2003; 2003US-0455050P. | DE | |
| PR | 14-APR-2003; 2003US-0462894P. | XX | antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic; |
| PR | 17-APR-2003; 2003US-0463772P. | KW | cytostatic; anticonvulsant; nootropic; muscular; anti-HIV; |
| PR | 25-APR-2003; 2003US-0465665P. | KW | RNA interference; iRNA; antisense technology; lipid metabolism; |
| PR | 25-APR-2003; 2003US-0465802P. | KW | cholesterol imbalance; dyslipidaemia hypercholesterolaemia; |
| PR | 09-MAY-2003; 2003US-0469612P. | KW | coronary artery disease; CAD; coronary heart disease; CHD; |
| PR | 08-AUG-2003; 2003US-0493986P. | KW | atherosclerosis; hepatic glucose production; |
| PR | 11-AUG-2003; 2003US-0494597P. | KW | glucose-metabolism-related disorder; diabetes; cancer; breast cancer; |
| PR | 26-SEP-2003; 2003US-0506341P. | KW | colon cancer; lung cancer; neurological disease; Huntington disease; |
| PR | 09-OCT-2003; 2003US-0510246P. | KW | spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss. |
| PR | 10-OCT-2003; 2003US-0510318P. | XX | |
| PR | 07-NOV-2003; 2003US-0518453P. | OS | Homo sapiens. |
| XX | (ALNY-) ALNYLAM PHARM. | XX | |
| PA | Manoharan M, Bumcrot D; | PN | WO2004080406-A2. |
| XX | | XX | 23-SEP-2004. |
| PI | WPI; 2004-677362/66. | PD | |
| DR | | XX | 08-MAR-2004; 2004WO-US007070. |
| XX | Interference RNA agent useful for treating dyslipidemias, coronary artery | PF | |
| PT | disease, diabetes, cancer or neurological disease, comprises sense | XX | 07-MAR-2003; 2003US-0452682P. |
| PT | sequence and antisense sequence which has specific modifications. | PR | 12-MAR-2003; 2003US-0454265P. |
| XX | | PR | 13-MAR-2003; 2003US-0454962P. |
| PS | Example 5; SEQ ID NO 434; 378pp; English. | PR | 13-MAR-2003; 2003US-0455050P. |
| XX | | PR | 14-APR-2003; 2003US-0462894P. |
| CC | The invention describes a RNA interference (iRNA) agent (I) comprising a | PR | 17-APR-2003; 2003US-0463772P. |
| CC | sense sequence and an antisense sequence, where the sense sequences have | PR | 25-APR-2003; 2003US-0465665P. |
| CC | one or more asymmetrical 2'-O alkyl modifications, the antisense | PR | 25-APR-2003; 2003US-0465802P. |
| CC | sequences have one or more asymmetrical phosphorothioate modifications | PR | 09-MAY-2003; 2003US-0469612P. |
| CC | and the antisense sequence targets a human gene sequence. Also described | PR | 08-AUG-2003; 2003US-0493986P. |
| CC | are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100 | PR | 11-AUG-2003; 2003US-0494597P. |
| CC | levels or glucose-6-phosphatase levels in a subject; producing (I); | PR | 26-SEP-2003; 2003US-0506341P. |
| CC | stabilising (I), involves selecting a sequence with activity and | PR | 09-OCT-2003; 2003US-0510246P. |
| CC | introducing one or more asymmetrical modification in the sequence, where | PR | 10-OCT-2003; 2003US-0510318P. |
| CC | the modification decreases nuclease sensitivity while not decreasing its | PR | 07-NOV-2003; 2003US-0518453P. |
| CC | activity; a kit comprising (I) and instruction for its use; and a device | XX | (ALNY-) ALNYLAM PHARM. |
| CC | that can be dispense or administer a composition comprising (I). (I) is | PA | Manoharan M, Bumcrot D; |
| CC | useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1) | XX | |
| CC | is useful for reducing apoB-100 levels or glucose-6-phosphatase levels. | PI | WPI; 2004-677362/66. |
| CC | The subject is suffering from a disorder characterised by elevated or | XX | |
| CC | otherwise unwanted expression of apoB-100, elevated or otherwise unwanted | DR | |
| CC | levels of cholesterol, and/or dysregulation of lipid metabolism. The | XX | |
| CC | disorder is chosen from the HDL/LDL cholesterol imbalance, | PT | |
| CC | dyslipidaemias, hypercholesterolaemia, statin-resistant | PT | |
| CC | hypercholesterolaemia, coronary artery disease (CAD), coronary heart | XX | |
| CC | disease (CHD) and atherosclerosis. (I) is administered to a subject to | PS | |
| CC | inhibit hepatic glucose production or for treating glucose-metabolism- | XX | |
| CC | related disorder e.g. diabetes or type-2 diabetes. (I) is useful for | CC | |
| CC | treating the diseases as mentioned above, cancer (e.g. breast, colon or | CC | |
| CC | lung cancer), neurological disease (e.g., Huntington disease or | CC | |
| CC | spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence | CC | |
| CC | represents a human apolipoprotein B (ApoB) antisense oligonucleotide that | CC | |
| CC | can be used to control ApoB gene expression. | XX | |
| XX | | SQ | |
| | Sequence 19 BP; 2 A; 4 C; 3 G; 10 T; 0 U; 0 Other; | | |
| | Query Match 1.3%; Score 14.2; DB 1; Length 19; | | |
| | Best Local Similarity 84.2%; Pred. No. 1.8e+02; | | |
| | Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | |
| Qy | 1014 AGAAGCATCATCATGAGA 1032 | | |
| Db | 19 AGAAGCATCATCAAGGAAA 1 | | |
| | RESULT 255 | | |
| | ADR78567/c | | |
| ID | ADR78567 standard; DNA; 19 BP. | | |
| XX | | | |
| AC | ADR78567; | | |
| XX | | | |

CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.
XX
SQ Sequence 19 BP; 2 A; 4 C; 3 G; 10 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1014 AGAAGCATCATCATAGAGA 1032
Db 19 AGAAGCATCATCAAGGAAA 1
RESULT 256
ADR76227/c
ID ADR76227 standard; DNA; 19 BP.
XX
AC ADR76227;
XX
DT 16-DEC-2004 (first entry)
DE Human apolipoprotein B (ApoB) oligonucleotide seqid 712.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytosstatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS Homo sapiens.
XX
PN WO2004080406-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US007070.
XX
PR 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Bumcrot D;
XX
DR WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
PS Example 5; SEQ ID NO 712; 378pp; English.
XX

CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholesterolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.
XX
SQ Sequence 19 BP; 10 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 552 TTTAATATGCTGGGTTTTT 570
Db 19 TTGAATATGGTGAGTTTTT 1
RESULT 257
ADR78845/c
ID ADR78845 standard; DNA; 19 BP.
XX
AC ADR78845;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human apolipoprotein B (ApoB) oligonucleotide seqid 3330.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytosstatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS Homo sapiens.
XX
PN WO2004080406-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US007070.
XX
PR 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.

XX CTV primer 5'.

XX TSWV; tomato spotted-wilt virus; BYMV; bean yellow mosaic virus; CLRV;

XX cherry leaf roll virus; CMV; cucumber mosaic virus; CTV;

KW citrus tristeza virus; GFLV; grapevine fanleaf virus; PLRV;

KW potato leaf roll virus; PMMV; pepper mild mottling virus; PSTV;

KW potato spindle tuber viroid; Lycopersicum esculentum; detection; virus;

KW immobilisation; amplification; tobamovirus; potyvirus; closterovirus;

KW luteovirus; nepovirus; identification; ss.

XX Synthetic.

XX EP574345-A2.

PN 15-DEC-1993.

XX 10-JUN-1993; 93EP-00500079.

XX 12-JUN-1992; 92ES-00001232.

XX (NAIN-) INST NACIONAL INVESTIGACION & TECNOLOGIA.

PA Bardosa Nolasco N, De Blas Beorlegui C, Borja Tome MJ;

XX Pons Ascaso F, Torres Pascual V;

PI WPI; 1993-396985/50.

DR Detection and identification of viral and sub-viral pathogens, partic. in

XX plants - by immobilisation with antibodies and spectrophotometric

PT quantitation or electrophoretic identification.

PT Example 2; Page 6; 13pp; English.

XX The primers (AAQ53267-86) are used to amplify the genomes of various

CC viral plant pathogens or satellite viruses. The pathogen is then

CC imobilised using antibodies against proteins in the virus coating or

CC against double-chain RNAs in the case of viral pathogens. Detection of

CC the pathogen is carried out by electrophoretic identification of the

CC amplification products. (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 20 BP; 11 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

SQ Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 857 TCTTTGTGTGTAGTCCAT 875

Db 19 TCTTTGTTCGTCGTCAT 1

RESULT 260

AAQ97957/c

ID AAQ97957 standard; DNA; 20 BP.

XX AAQ97957;

AC 25-MAR-2003 (revised)

XX 18-OCT-1995 (first entry)

DT PNA oligomer targetting coding region of PKC-epsilon.

DE Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;

XX cell proliferation; cell differentiation; isozyme; antisense;

KW triple helix; cancer; psoriasis; inflammation.

XX Synthetic.

OS Key Location/Qualifiers

XX misc_feature 1. .20

FT /*tag= a

FT

FT /note= "at least one (and preferably all) of the backbone

FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine

FT peptide residues, the nucleobase being attached

FT covalently to the acetyl group and the peptide linkage

FT being formed by condensation of the glycine carboxy group

FT of one residue with the amino group of the 2-aminoethyl

XX moiety in the next residue"

PN WO9503833-A1.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US008465.

XX 29-JUL-1993; 93US-00099098.

PR (ISIS-) ISIS PHARM INC.

PA Dean NM;

XX WPI; 1995-082040/11.

DR New peptide nucleic acid oligomers specific for protein kinase C

XX isozyme(s) - useful as anti:sense molecules for treating PKC mediated

PT disease, e.g. cancer, psoriasis and inflammation.

PT Claim 38; Page 274; 287pp; English.

XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist

CC of naturally occurring nucleobases covalently bound to a polyamide

CC backbone and (b) hybridise to the translation initiation AUG region,

CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region

CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target RNA

CC and single stranded DNA (ssDNA) to produce antisense-type gene regulation

CC moieties. They inhibit expression of PKC-alpha and its isoforms

CC (including beta, gamma, delta, epsilon, zeta and eta) and so are useful

CC for treating and diagnosing cell proliferation and differentiation

CC processes such as neoplastic, hyperproliferative and inflammatory

CC diseases. PNA oligomers have high affinity for complementary single

CC stranded DNA. They are also able to form triple helices in which a first

CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the

CC resulting double helix or with the first PNA strand. The PNAs possess no

CC significant charge and are water soluble, which facilitates cellular

CC uptake. Further, since they contain amides of non-biological amino acids,

CC they are biostable and resistant to enzymatic degradation by proteases.

CC The present sequence targets the coding region of PKC-epsilon. (Updated

CC on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

SQ Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 434 AGAGGAGATGATTTTAGCT 452

Db 19 AGAGAAGAGGATTTTGCT 1

RESULT 261

AAQ84260/c

ID AAQ84260 standard; DNA; 20 BP.

XX AAQ84260;

AC 25-MAR-2003 (revised)

XX 21-SEP-1995 (first entry)

DT PKC-epsilon coding region antisense oligo, ISIS #7941.

DE Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon; zeta;

XX modulation; expression; isozyme; hybridise; 5' UTR; human;

KW 3' untranslated region; translation initiation site; detection;

KW

XX This invention describes antisense oligonucleotides that specifically
CC bind to human protein kinase C (PKC) mRNA. These oligonucleotides can be
CC used to inhibit PKC mRNA and therefore be used to treat PKC-related
CC hyperproliferative conditions, e.g. cancer, especially colorectal cancer,
CC breast cancer, bladder cancer, lung cancer, or brain cancer (preferably
CC glioblastoma multiforme). The products of the invention may also be used
CC to treat skin cancer and psoriasis
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
DB 19 AGAGAAGAGGATTTTGCT 1

RESULT 264
AAX76903/c
ID AAX76903 standard; DNA; 20 BP.
XX
AC AAX76903;
XX
DT 17-OCT-2003 (revised)
DT 05-AUG-1999 (first entry)
XX
DE Hz-1 Pagl gene direct repeat sequence.
XX
KW Hz-1 pagl promoter; persistence-associated gene 1; insect cell;
KW constitutive expression promoter; direct repeat; ss.
XX
OS Heliothis zea virus 1.
XX
PN US5911982-A.
XX
PD 15-JUN-1999.
XX
PF 18-APR-1996; 96US-00634350.
XX
PR 06-OCT-1995; 95US-0004894P.
PR 11-OCT-1995; 95US-0005128P.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Chao Y;
XX
DR WPI; 1999-357167/30.
XX
PT HZ-1 virus persistence-associated gene promoter.
PS Example 1; Fig 3c; 56pp; English.
XX
CC This sequence represents a direct repeat from the Hz-1 persistence-
CC associated gene 1 (Hz-1 pagl). The invention relates to the Hz-1 pagl
CC promoter. The pagl gene promoter is useful in insect cells for driving
CC constitutive expression of e.g. genes encoding foreign proteins. The
CC promoter of the pagl gene is constitutively expressed and stronger than
CC that of the polyhedrin gene in insect cells, enabling it to express
CC foreign genes more strongly e.g. lacZ and luciferase, in addition to
CC which it can be expressed more prominently as a short promoter. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 20 BP; 13 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 566 TTTTAAATACCTTTATAT 584
||| ||||| ||||| |||

Db 19 TTGTTTAATACCTTTGTTT 1

RESULT 265
AAX78609/c
ID AAX78609 standard; DNA; 20 BP.
XX
AC AAX78609;
XX
DT 03-SEP-1999 (first entry)
XX
DE Human PKC-epsilon oligonucleotide primer ISIS # 7941.
XX
KW PKC; human; PKC-alpha; primer; protein kinase C; expression modulator;
KW PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-eta; PKC-delta;
KW PKC-epsilon; PKC-zeta; anti-inflammatory; cytostatic;
KW antisense targeting; isozyme; growth control; hyperproliferative disease;
KW colon cancer; glioblastoma; bladder cancer; inflammatory condition;
KW psoriasis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5922686-A.
XX
PD 13-JUL-1999.
XX
PF 14-JUN-1996; 96US-00664336.
XX
PR 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean N, Bennett CF;
XX
DR WPI; 1999-404471/34.
XX
PT Oligonucleotides targetted against nucleic acids encoding protein kinase
C.
XX
PS Example 16; Col 63-64; 56pp; English.
XX
CC This invention describes novel oligonucleotides (AAX78524-X78644) having
CC up to 50 nucleotides hybridisable with, and able to modulate the
CC expression of, a nucleic acid encoding protein kinase C and its isozymes
CC alpha, beta type I, beta type II, gamma, eta, delta, epsilon and zeta.
CC The oligonucleotides of the invention have anti-inflammatory and
CC cytostatic activity and are used for antisense targeting to modulate the
CC expression of PKC or of a particular PKC isozyme or set of isozymes in
CC cells or tissues. The products of the invention also hybridise with
CC nucleic acids involved in the modulation of PKC expression, which is
CC known to be involved growth control in hyperproliferative diseases e.g.
CC colon cancer, glioblastoma and bladder cancer as well as in inflammatory
CC conditions e.g. psoriasis. Due to their specificity the oligonucleotides
CC are able to overcome the problems of toxicity associated with previous
CC agents designed to modulate PKC expression
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
||| ||||| ||||| |||
DB 19 AGAGAAGAGGATTTTGCT 1

RESULT 266
AAX83735/c
ID AAX83735 standard; DNA; 20 BP.
XX

AC AAX83735;
XX
DT 27-AUG-1999 (first entry)
XX
DE Human protein kinase C antisense oligonucleotide SEQ ID NO:86.
XX
XX Human; protein kinase C; PKC; antisense oligonucleotide; diagnosis; ss;
KW hybridisation; cancer; psoriasis; hyperproliferative disease; tumour.
KW
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5916807-A.
XX
PD 29-JUN-1999.
XX
XX 07-JUN-1995; 95US-00481072.
PF
XX 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dean N, Bennett CF;
PI
XX WPI; 1999-403817/34.
DR
XX New antisense oligonucleotides specific for human protein kinase C useful
PT for diagnosis and treatment of cancer and psoriasis.
PT
XX Example 16; Col 21; 54pp; English.
PS
XX The present invention describes a method of inhibiting the expression of
CC human protein kinase C (PKC) in cells. The method comprises contacting
CC the cells with an antisense oligonucleotide which has up to 50 nucleotide
CC units. AAX83633 to AAX83720 represent specifically claimed antisense
CC oligonucleotides for use in the method of the invention. The antisense
CC oligonucleotides modulate hybridize to messenger RNA from the PKC gene
CC which results in modulation of expression of the PKC gene. This means
CC they can be used for diagnosis, therapeutic or prophylactic treatment of
CC PKC associated diseases such as cancer and psoriasis, and as research
CC agents. Abnormal proliferative states in tissue from patients suspected
CC of having a hyperproliferative disease e.g. cancer, psoriasis can be
CC diagnosed. Tumours associated with PKC can be distinguished from tumours
CC which are not PKC associated to allow an efficacious treatment regime to
CC be used. The antisense oligonucleotides have specific activity so are
CC able to modulate PKC activity without producing side effects and with
CC greater effectiveness than observed from administration of current
CC agents. AAX83721 to AAX83753 represent other oligonucleotides used in
CC examples from the present invention
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 AGAGGAGATGATTTTAGCT 452
Db 19 AGAGAAGAGGATTTTGCT 1

RESULT 267
AAX92824
ID AAX92824 standard; DNA; 20 BP.
XX
AC AAX92824;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB001890.
PF
XX 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
XX Griffais R;
PI
XX WPI; 1999-357842/30.
DR
XX Genome sequence of Chlamydia pneumoniae.
PT
XX Page 1542; Disclosure; 1912pp; English.
PS
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 8 A; 7 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 940 AGAATCTGAAGCCCCACTC 958
Db 1 AGAATCGGAACCCCCACGC 19

RESULT 268
AAX94795
ID AAX94795 standard; DNA; 20 BP.
XX
AC AAX94795;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.
PA Griffais R;
PI WPI; 1999-357842/30.
XX Genome sequence of Chlamydia pneumoniae.
DR Page 1697; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 4 A; 3 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 771 GAACCTTTTGGTTGGGA 789
DB 1 GAGACCTTTTCTTTGGGA 19

RESULT 269
AAX95833
ID AAX95833 standard; DNA; 20 BP.
XX
AC AAX95833;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.
XX
PS Page 1779; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as

CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 1 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 CTACTGGAATTGTTGTTTC 309
DB 2 CTTCTGGAGTCGTTGTTTC 20

RESULT 270
AAX97255
ID AAX97255 standard; DNA; 20 BP.
XX
AC AAX97255;
XX
DT 13-SEP-1999 (first entry)
XX
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.
XX
PS Page 1890; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Fri Aug 19 11:00:00 2005

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QY      460 GTGCTAGCACTTTATTCTG 478
      |||||
Db      2 GTGCTAGCACTATAACCTG 20

RESULT 271
AAX95840
ID      AAX95840 standard; DNA; 20 BP.
XX
AC      AAX95840;
XX
DT      13-SEP-1999 (first entry)
XX
DE      PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW      Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW      sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW      neutralising epitope; PCR primer; ss.
XX
OS      Synthetic.
OS      Chlamydophila pneumoniae.
XX
PN      WO9927105-A2.
XX
PD      03-JUN-1999.
XX
PF      20-NOV-1998; 98WO-IB001890.
XX
PR      21-NOV-1997; 97FR-00014673.
PR      04-NOV-1998; 98US-0107078P.
XX
PA      (GEST ) GENSET.
PI      Griffais R;
XX
DR      WPI; 1999-357842/30.
XX
PT      Genome sequence of Chlamydia pneumoniae.
XX
PS      Page 1779; Disclosure; 1912pp; English.
XX
CC      AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC      and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC      (see AAX91990). C. pneumoniae causes respiratory disease such as
CC      pneumonia and bronchitis and is thought to be a contributing factor in
CC      heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC      nodosum or pharyngitis. The polypeptides encoded by the open reading
CC      frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC      in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC      nucleotides sequences can also be used as immunogenic compositions,
CC      especially where the vector directs the expression of a neutralising
CC      epitope of C. pneumoniae
XX
SQ      Sequence 20 BP; 1 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      291 CTTCTGGAATTGTTGTTTC 309
      |||||
Db      2 CTTCTGGAGTCGTTGTTTC 20

RESULT 272
AAX19212/c
ID      AAX19212 standard; DNA; 20 BP.
XX
AC      AAX19212;
XX
DT      20-MAR-2003 (revised)
DT      14-MAY-1999 (first entry)

XX      Human PKC-epsilon antisense oligonucleotide SEQ ID NO:86.
DE
XX      Human; PKC; protein kinase C; diagnosis; antisense oligonucleotide;
KW      phosphorothioate linkage; hyperproliferative disease; cancer; psoriasis;
KW      tumour; inhibition; ss.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
PN      US5882927-A.
XX
PD      16-MAR-1999.
XX
PF      07-JUN-1995; 95US-00478178.
XX
PR      16-MAR-1992; 92US-00852852.
PR      09-JUL-1993; 93US-00089996.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Dean N, Bennett CF;
XX
DR      WPI; 1999-214073/18.
XX
PT      New synthetic oligonucleotides inhibiting expression of protein kinase C
PT      (PKC)-alpha - useful for treating and diagnosing conditions associated
PT      with abnormal PKC expression.
XX
PS      Example 16; Col 23; 56pp; English.
XX
CC      The present invention specifically describes antisense oligonucleotides
CC      of up to 50 nucleotides in length which specifically bind human protein
CC      kinase C-alpha (PKC-alpha) mRNA. AAX19127 to AAX19247 represent antisense
CC      oligonucleotides from the present invention which bind human PKC-alpha, -
CC      beta, -gamma, -delta, -epsilon, -zeta and -eta. The antisense
CC      oligonucleotides modulate the expression of the PKC gene (i.e. inhibit
CC      the PKC gene). The antisense oligonucleotides can be used to diagnose
CC      abnormal proliferative states in tissue or other samples from patients
CC      suspected of having a hyperproliferative disease e.g cancer or psoriasis.
CC      The antisense oligonucleotides can be used to distinguish PKC-associated
CC      tumours and to detect and diagnose PKC expression (through the use of 32P
CC      labeled antisense oligonucleotides). Radiolabeled antisense
CC      oligonucleotides can also be used to perform autoradiography of tissues
CC      to determine the localization, distribution and quantitation of PKC
CC      expression for research, diagnostic and therapeutic purposes. The use of
CC      the antisense oligonucleotides eliminate the side effects associated with
CC      prior art methods because it modulates the amount of PKC protein made
CC      from the gene rather than inhibiting the enzyme itself. (Updated on 20-
CC      MAR-2003 to correct PF field.)
XX
SQ      Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match      1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      434 AGAGGAGATGATTTTAGCT 452
      |||||
Db      19 AGAGAAGAGAGATTTTGCT 1

RESULT 273
AAZ27351/c
ID      AAZ27351 standard; DNA; 20 BP.
XX
AC      AAZ27351;
XX
DT      01-DEC-1999 (first entry)
XX
DE      Human protein kinase C epsilon antisense oligonucleotide #9.
XX
KW      Human; protein kinase C; PKC; diagnosis; antisense oligonucleotide;
```

KW phosphorothioate; hybridisation; isozyme; target; inflammation;
XW hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5959096-A.
XX
PD 28-SEP-1999.
XX
XX 07-JUN-1995; 95US-00481066.
XX
PR 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean N;
XX
DR WPI; 1999-561076/47.
XX
XX Antisense oligonucleotides useful for treatment of hyperproliferative and
PT inflammatory conditions including psoriasis, tumors and cancer.
PT
XX
PS Example 16; Col 23; 56pp; English.
XX
CC The present invention describes antisense oligonucleotides up to 50
CC nucleotides in length which specifically bind mRNA encoding human protein
CC kinase C (PKC). AAZ27266 to AAZ27386 represent human PKC antisense
CC oligonucleotides used in the exemplification of the present invention.
CC The antisense oligonucleotides are useful for the treatment of diseases
CC associated with PKC expression, such as hyperproliferative and
CC inflammatory conditions including psoriasis, tumours and cancer
CC (glioblastoma, bladder, breast, colon and lung cancer)
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 ACAGGAGATGATTTTAGCT 452
Db ||||| ||||| ||||| |||||
19 ACAGAAGAGGATTTTGGCT 1

RESULT 274
AAZ75053/C
ID AAZ75053 standard; DNA; 20 BP.
XX
AC AAZ75053;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9409.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB0000822.
XX
XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX

PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 2236; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 427 ATTTGGAAGAGGAGATGAT 445
Db | | | | | | | | | | | | | | | |
19 AGTTGGAGGGGAGATGAT 1

RESULT 275
AAA64912/C
ID AAA64912 standard; DNA; 20 BP.
XX
AC AAA64912;
XX
DT 07-NOV-2000 (first entry)
XX
DE Antisense oligonucleotide #102333 to X-linked inhibitor of apoptosis.
XX
KW X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; 2'-methoxyethyl;
KW antisense; antiinflammatory; cytostatic; tumour; MOE; phosphorothioate;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /note= "Optionally the internucleotide linkages are
FT phosphorothioate"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optionally the nucleotides are 2'-methoxyethyl"
FT modified_base 3
FT /*tag= d
FT /mod_base= m5c
FT /note= "Optional"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "Optionally the nucleotides are 2'-methoxyethyl"
XX
PN US6087173-A.

XX 11-JUL-2000.
PD
XX
PF 09-SEP-1999; 99US-00392580.
XX
PR 09-SEP-1999; 99US-00392580.
XX
PA (ISIS-) ISIS PHARM INC.
PI Bennett CF, Cowsert LM, Ackermann EJ;
XX WPI; 2000-498201/44.
DR
XX
PT Antisense compound useful for research reagents, diagnostics, prophylaxis
PT and for treating disorders associated with X-linked inhibitor of
PT apoptosis, modulates expression of X-linked inhibitor of apoptosis.
XX
PS Claim 3; Col 40; 33pp; English.
XX
CC The present sequence is an antisense oligonucleotide designed to inhibit
CC expression of the human X-linked inhibitor of apoptosis. This sequence is
CC targeted to the start codon region of the gene. The oligonucleotides may
CC be modified to consist of 10 nucleotides flanked on both sides by 5
CC nucleotide wings. The wings are composed of 2'-methoxyethyl (2'-MOE)
CC nucleotides. Cytidine residues in the 2'-MOE wings are 5-methylcytidines.
CC Throughout the modified oligonucleotides, the internucleoside linkages
CC are phosphorothioate. The modified oligonucleotides are more effective
CC inhibitors than unmodified oligonucleotides. The oligonucleotides may be
CC used to inhibit X-linked inhibitor of apoptosis expression in cells and
CC tissues in vitro. The oligonucleotides are also useful for treating
CC animals or humans, prone to a disease associated with X-linked inhibitor
CC of apoptosis. The oligonucleotides may also be used prophylactically to
CC prevent infection, inflammation or tumour formation
XX
SQ Sequence 20 BP; 6 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 426 TATTGGAGAGGAGATGA 444
Db 20 TATTTCAGAGAGATGA 2

RESULT 276
AAF62444/C
ID AAF62444 standard; DNA; 20 BP.
XX
AC AAF62444;
XX
DT 05-NOV-2001 (first entry)
XX
DE A thaliana VRN1 gene PCR primer S49.
XX
KW VRN1; vernalisation; flowering; crop; PCR primer; ss.
XX Arabidopsis thaliana.
OS
PN WO200121822-A1.
XX
XX 29-MAR-2001.
PD
XX 13-SEP-2000; 2000WO-GB003525.
PF
XX 17-SEP-1999; 99GB-00022071.
PR
XX (PLAN-) PLANT BIOSCIENCE LTD.
PA
XX Dean C, Levy YY;
PI
XX WPI; 2001-273467/28.
DR
XX

PT Novel VRN1 polynucleotide sequence encoding a polypeptide which alters
PT vernalization response of plant in which VRN1 nucleic acid is expressed,
PT useful for influencing and assessing vernalization phenotype of plants.
XX
PS Claim 10; Page 76; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC Arabidopsis thaliana VRN1. This protein is capable of altering the
CC vernalisation responses of a plant. Also provided are a number of PCR
CC primers used to isolate the sequences. The sequences are useful in the
CC production of crop plants, where they are able to control the timing of
CC flowering, the duration of vernalisation required, the optimum
CC temperature, or even eliminate the need for vernalisation completely. The
CC present sequence is a PCR primer used to isolate the VRN1 coding sequence
XX
SQ Sequence 20 BP; 5 A; 10 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 448 TAGCTGGGAGCAGTGGTAG 466
Db 19 TAGGTGGGAAC TGTGGTAG 1

RESULT 277
AAF23509
ID AAF23509 standard; DNA; 20 BP.
XX
AC AAF23509;
XX
DT 22-MAR-2001 (first entry)
XX
DE Primer cadF-R1C.
XX
KW Fibronectin binding protein; CadF; vaccine; diagnostic assay; ss.
XX
OS Campylobacter coli.
OS Campylobacter jejuni.
XX
PN US6156546-A.
XX
PD 05-DEC-2000.
XX
PF 15-MAY-1998; 98US-00080025.
XX
PR 16-MAY-1997; 97US-0046763P.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Garvis SG, Konkel ME;
XX
DR WPI; 2001-079546/09.
XX
PT Novel isolated polynucleotide useful for producing fibronectin binding
PT proteins which are useful in production of vaccine, in diagnostic assays
PT and for prophylactic and therapeutic purposes.
XX
PS Example 2; Col 28; 29pp; English.
XX
CC The present invention relates to a Campylobacter jejuni or Campylobacter
CC coli fibronectin binding protein (CadF). A recombinant expression vector
CC with cadF is useful in an assay for determining the presence of C.jejuni
CC or C.coli in a test sample or for determining whether a test isolate of
CC Campylobacter is a strain of C.coli. cadF is useful in the construction
CC of DNA probes for identifying and quantifying the level of expression of
CC CadF in a cell. The gene can also be used in a vaccine
XX
SQ Sequence 20 BP; 1 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 676 TTATGTTACTTGTGGCT 694
||| ||||| |||||

Db 2 TTCTTTTACTTGTTCGGCT 20

RESULT 278
AAC92586/c
ID AAC92586 standard; DNA; 20 BP.
XX
AC AAC92586;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:36.
XX
KW Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
KW ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
KW cell growth; transcriptional repression; replication;
KW signal transduction; chromatin decondensation; Ag-NOR family;
KW nucleolin antibody; systemic connective tissue disease; SLE;
KW systemic lupus erythematosus;
KW scleroderma-like chronic graft versus host disease;
KW expression inhibition; tumour formation; cancer; inflammation;
KW immune disorder; phosphorothioate; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN US6165786-A.
XX
PD 26-DEC-2000.
XX
PF 03-NOV-1999; 99US-004333699.
XX
PR 03-NOV-1999; 99US-004333699.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM;
XX
DR WPI; 2001-079848/09.
XX
PT Novel antisense compound targeted to human nucleolin which specifically
PT hybridizes with and inhibits the expression of human nucleolin, useful
PT for modulating the expression of nucleolin in cells.
XX
PS Example 15; Col 41-42; 41pp; English.
XX
CC Sequences AAC92560-C92639 represent antisense oligonucleotides targetted
CC to the human nucleolin gene, which inhibit its expression. The antisense
CC oligonucleotides were designed to target different regions of the human
CC nucleolin mRNA, and were analysed for their effect on nucleolin mRNA
CC levels by quantitative real-time PCR. Nucleolin (also known as P92 or
CC C23) is the most abundant nucleolar phosphoprotein in actively growing
CC cells. Nucleolin primarily participates in ribosome biogenesis and
CC transport of ribosomal components, being able to transiently bind to pre-
CC ribosomes in the nucleolus via a ribonucleoprotein consensus sequence.
CC However, it has also been shown to be involved in cytokinesis,
CC nucleogenesis, cell proliferation and growth, transcriptional repression,
CC replication, signal transduction, and chromatin decondensation. Nucleolin
CC is a member of the Ag-NOR (active ribosomal gene located in the nucleolar
CC organiser region) family of proteins which are markers of active
CC ribosomal genes, and whose expression is associated with the prediction
CC of tumour growth rate. The presence of antibodies against nucleolin are
CC associated with systemic connective tissue diseases such as systemic
CC lupus erythematosus (SLE) and scleroderma-like chronic graft versus host
CC disease. The oligonucleotides of the invention are useful for diagnosis,
CC prevention and treatment of conditions associated with nucleolin
CC expression, such as tumour formation, immune disorders and inflammation
XX
SQ Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 800 GAGGCAGATAACGCTGAAG 818
||||| ||||| |||||

Db 19 GAGGAAGATGACTCTGAAG 1

RESULT 279
AAI65644/c
ID AAI65644 standard; DNA; 20 BP.
XX
AC AAI65644;
XX
DT 03-JAN-2002 (first entry)
XX
DE Primer for microsatellite marker D16S408, used to localise IBD1.
XX
KW Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox;
KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;
KW inflammatory disease; immune disease; cryptogenetic inflammation;
KW hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN FR2806739-A1.
XX
PD 28-SEP-2001.
XX
PF 27-MAR-2000; 2000FR-00003832.
XX
PR 27-MAR-2000; 2000FR-00003832.
XX
PA (DAUS-) FOND DAUSSET-CEPH JEAN.
XX
PI Hugot JP, Thomas G, Zouali M, Lesage S, Chamaillard M;
XX
DR WPI; 2001-608364/70.
XX
PT New human nucleic acids associated with intestinal inflammatory disease,
PT useful for diagnosis, prognosis and control of these diseases, also
PT related proteins.
XX
PS Example 1; Page 84; 97pp; French.
XX
CC PCR primers AAI65595-AAI65646 were used to amplify polymorphic
CC microsatellite markers, for localisation of a human gene encoding
CC inflammatory bowel disease 1 (IBD1) polypeptide, which is associated with
CC intestinal inflammatory disease. The specification also describes a
CC polypeptide which is in proximity to IBD1, and is designated IBD1prox.
CC The IBD1 gene is probably involved in regulation of apoptosis and
CC activation of NF-kappa B. The IBD1 and IBD1prox polynucleotides are is
CC useful as source of probes and primers, as source of (anti)sense
CC oligonucleotides, for recombinant production of polypeptides, and in
CC screening for interactive compounds. The polypeptides are used to raise
CC specific antibodies which useful for diagnostic detection or purification
CC of IBD1 and IBD1prox, to screen for specific binding agents, potential
CC therapeutic agents. The IBD1 and IBD1prox polynucleotides are
CC polypeptides are useful for treatment and prevention of inflammatory
CC and/or immune diseases or cancer, where associated with mutations in
CC genes corresponding to IBD1 and IBD1prox, especially cryptogenetic
CC inflammation of the intestines (hemorrhagic rectocolitis, Crohn's disease
CC and Blau syndrome)
XX
SQ Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 776 CTTTGTGGGATGTC 794
||| ||||| |||||

Db 20 CTTGTGCTTGGTGATGTCC 2

RESULT 280
ABA822285/c
ID ABA822285 standard; DNA; 20 BP.
XX AC ABA822285;
XX DT 25-JAN-2002 (first entry)
XX DE Zmax1 gene region physical map preparation STS marker #244.
XX KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO200177327-A1.
XX PD 18-OCT-2001.
XX PF 21-JUN-2000; 2000WO-US016951.
XX PR 05-APR-2000; 2000US-00543771.
PR 05-APR-2000; 2000US-00544398.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2001-657171/75.
XX DR New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
XX PS Disclosure; Page 34; 443pp; English.
XX CC The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACACAGAC 900
Db 19 AATATTGTGGCCACACAC 1

RESULT 281
AAL46974/c
ID AAL46974 standard; DNA; 20 BP.
XX AC AAL46974;
XX DT 15-AUG-2002 (first entry)
XX DE Cell cycle regulatory protein coding sequence related PCR primer #2.
DE Human; cell cycle regulatory protein; cancer; cell cycle abnormality;
KW cytostatic; PCR; primer; ss.

XX OS Homo sapiens.
XX PN JP2002101891-A.
XX PD 09-APR-2002.
XX PF 02-OCT-2000; 2000JP-00302674.
XX PR 02-OCT-2000; 2000JP-00302674.
XX PA (NNSH) NIPPON SHINYAKU CO LTD.
XX WPI; 2002-440460/47.
XX DR Cell-cycle regulatory protein, useful for diagnosis and treatment of
XX cancers and other diseases caused by abnormal cell cycles.
PT cancers and other diseases caused by abnormal cell cycles.
XX PS Example 1; Page 20; 34pp; Japanese.
XX CC The present invention provides the protein and coding sequences of
CC several human cell cycle regulatory proteins. These sequences can be used
CC in the diagnosis and treatment of cancers and other diseases associated
CC with cell cycle abnormalities. The present sequence is a PCR primer
CC described in the exemplification of the invention
XX SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1079 CTTAACCTCTCTGGGTGT 1097
Db 19 CTGAACCTCTCCTGGTGT 1

RESULT 282
ABL90939/c
ID ABL90939 standard; DNA; 20 BP.
XX AC ABL90939;
XX DT 27-MAY-2002 (first entry)
XX DE Human protein kinase C-epsilon antisense oligonucleotide 9.
XX KW Human; PKC antisense oligonucleotide; protein kinase C; PKC; PKC-alpha;
KW PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-delta; PKC-epsilon;
KW PKC-zeta; PKC-eta; PKC expression modulation; ss;
KW hyperproliferative condition; tumour; glioblastoma; bladder cancer;
KW breast cancer; colon cancer; lung cancer; inflammatory condition;
KW psoriasis; phosphorothioate backbone.
XX OS Homo sapiens.
XX PN US6339066-B1.
XX PD 15-JAN-2002.
XX PF 31-MAR-1997; 97US-00829637.
XX PR 11-JAN-1990; 90US-00463358.
PR 13-AUG-1990; 90US-00566977.
PR 11-JAN-1991; 91WO-US000243.
PR 15-OCT-1991; 91US-00777760.
PR 16-OCT-1991; 91US-00777007.
PR 16-MAR-1992; 92US-00852852.
PR 05-MAY-1993; 93US-00058023.
PR 09-JUL-1993; 93US-00089996.
PR 29-AUG-1994; 94US-00297703.
PR 07-JUN-1995; 95US-00481066.

PA (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dean NM, Cook PD, Hoke G;
XX WPI; 2002-215022/27.
DR
XX New antisense oligonucleotide having nucleoside units which specifically
PT binds mRNA encoding human protein kinase C isoform, useful for treating
PT hyperproliferative and inflammatory diseases e.g. psoriasis, tumor and
PT cancer.
XX
XX Example 16; Col 47-48; 77pp; English.
PS
XX The invention comprises antisense oligonucleotides designed to bind mRNA
CC encoding a human protein kinase C (PKC) isoform (i.e. PKC-alpha, PKC-beta
CC type I, PKC-beta type II, PKC-gamma, PKC-delta, PKC-epsilon, PKC-zeta,
CC and PKC-eta). The antisense oligonucleotides of the invention are useful
CC for modulating the expression of the PKC isoforms. The antisense
CC oligonucleotides are useful for treating hyperproliferative conditions
CC (e.g. tumour, glioblastoma, bladder cancer, breast cancer, colon cancer
CC and lung cancer), and inflammatory conditions (e.g. psoriasis). The
CC antisense oligonucleotides of the invention are also useful for detection
CC and diagnosis of PKC expression. The present sequence represents a human
CC PKC antisense oligonucleotide of the invention. NOTE: The present
CC sequence contains a phosphorothioate backbone
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
Db ||||| ||||| ||||| ||||| |||||
19 AGAGAAGAGGATTTTGGCT 1

RESULT 283
AAL45924/c
ID AAL45924 standard; DNA; 20 BP.
XX
AC AAL45924;
XX
DT 08-JUL-2002 (first entry)
XX
DE Murine dystrophin-specific antisense oligonucleotide mAON#6.
XX
KW Antisense oligonucleotide; exon skipping; exon inclusion signal;
KW disease treatment; splice-modulation; gene therapy; dystrophin;
KW haemostatic; antithyroid; muscular; mouse; ss.
XX
OS Mus sp.
XX
PN EP1191097-A1.
XX
PD 27-MAR-2002.
XX
PF 21-SEP-2000; 2000EP-00203283.
XX
PR 21-SEP-2000; 2000EP-00203283.
XX
PA (UYLE-) UNIV LEIDS MEDISCH CENT.
XX
PI Van Ommen GB, Van Deutekom JCT, Den Dunnen JT, Dauwerse JG;
PI Datson NA;
XX
DR WPI; 2002-354071/39.
XX
PT Decreasing the production of an aberrant protein in a cell, for treatment
PT of inherited diseases such as Duchenne Muscular Dystrophy or Hemophilia,
PT comprises a splice modulation therapy of exons.
XX
PS Example 1; Page 6; 18pp; English.

XX The present invention relates to a method of decreasing the production of
CC an aberrant protein in a cell containing pre-mRNA of exons coding for the
CC protein, involving providing the cell with an agent capable of
CC specifically inhibiting an exon inclusion signal of one of the exons, and
CC allowing translation of mRNA produced from splicing of pre-mRNA. The new
CC method decreases the production of an aberrant protein in a cell by using
CC a process known as exon-skipping. The process is carried out by providing
CC an agent such as a nucleic acid to inhibit the exon inclusion signal. The
CC nucleic acid agent can therefore be used as a preparation of a medicament
CC for treatment of inherited diseases such as haemophilia A, clotting
CC factor VIII deficiency, some forms of congenital hypothyroidism, Duchenne
CC Muscular Dystrophy, and Becker Muscular Dystrophy. The present sequence
CC is an antisense oligonucleotide directed at the murine dystrophin pre-
CC mRNA
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 793 GCTTGGAGAGGCAGATAAC 811
Db ||||| ||||| ||||| ||||| |||||
19 GCTGAAGAGAGCAGATAAC 1

RESULT 284
ABL45469/c
ID ABL45469 standard; DNA; 20 BP.
XX
AC ABL45469;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 21q22.1 PCR primer SEQ ID NO:2513.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 6; Page 54; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals

CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 96 CATTATCCTTCAGTGGGC 114
| | | | | | | | | | | | | | | |
Db 20 CATTAGCCTACAGTTGGC 2

RESULT 285
ABL44467/c
ID ABL44467 standard; DNA; 20 BP.
XX
AC ABL44467;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1511.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 34; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX

SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 385 CAATGCAGTCATTTCCTT 403
| | | | | | | | | | | | | | | |
Db 20 CGATGCATTCATTTCCTT 2

RESULT 286
ABT06471
ID ABT06471 standard; DNA; 20 BP.
XX
AC ABT06471;
XX
DT 07-NOV-2002 (first entry)
XX
DE NES-1 gene methylation specific primer #3.
XX
KW Human; methylated gene; methylation; breast cancer; marker; WT-1;
KW cell proliferative disorder; TWIST; HOXA5; NES-1; RARBeta; cyclin D2;
KW retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;
KW 14.3.3 sigma; HIN-1; RASSFLA; tumour suppressor gene; hypermethylation;
KW PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200259347-A2.
XX
PD 01-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002455.
XX
PR 26-JAN-2001; 2001US-00771357.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
XX WPI; 2002-599803/64.
DR
XX
PT Diagnosing and/or determining a predisposition to a cellular
PT proliferative disorder of breast tissue, in particular breast cancer, by
PT determining the state of methylation of one or more nucleic acids
PT isolated from the subject.
XX
PS Claim 13; Page 68; 115pp; English.
XX
CC The present invention relates to a method of diagnosing a cellular
CC proliferative disorder of breast tissue, which involves determining the
CC state of methylation of one or more nucleic acids isolated from the
CC subject, where the state of methylation of the nucleic acids as compared
CC with a state of methylation from a subject not having the cellular
CC proliferative disorder of breast tissue is indicative of a cellular
CC proliferative disorder of breast tissue in the subject. The nucleic acids
CC may be TWIST, HOXA5, NES-1, retinoic acid receptor beta (RARBeta),
CC oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma,
CC HIN-1 or RASSFLA. The method is useful for diagnosing and/or determining
CC a predisposition to a cellular proliferative disorder, in particular
CC breast cancer including ductal carcinoma in situ, lobular carcinoma,
CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic
CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and
CC papillary carcinoma in situ. The present sequence is a primer used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGGCGTTT 167
Db 1 TTCGAAGTTTATGGCGTTT 19

RESULT 287
ABQ62452/c
ID ABQ62452 standard; DNA; 20 BP.
XX
AC ABQ62452;
XX
DT 16-AUG-2002 (first entry)
XX
DE Mouse syntaxin 4 interacting protein antisense oligonucleotide 39.
XX
KW Mouse; antisense gene therapy; Syntaxin 4 interacting protein; ss;
KW antisense oligonucleotide; diabetes; obesity; skeletal muscle disorder;
KW inflammation; tumour formation; phosphorothioate backbone;
KW 2'-O-methoxyethyl wing.
XX
OS Mus musculus.
XX
PN WO200224864-A2.
XX
PD 28-MAR-2002.
XX
PF 19-SEP-2001; 2001WO-US029251.
XX
PR 22-SEP-2000; 2000US-00668313.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Wyatt JR;
XX
DR WPI; 2002-404952/43.
XX
PT Novel antisense compound that hybridizes and inhibits nucleic acid
PT molecule encoding Syntaxin 4 interacting protein, useful for treating
PT diabetes, obesity and skeletal muscle disorder.
XX
PS Claim 3; Page 88; 154pp; English.
XX
CC The invention comprises antisense oligonucleotides designed to inhibit
CC expression of Syntaxin 4 interacting protein. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of Syntaxin 4 interacting protein in cells or tissues. The
CC antisense oligonucleotides are also useful for treating an animal having
CC a disease or condition associated with Syntaxin 4 interacting protein
CC (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense
CC oligonucleotides can also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents a
CC mouse Syntaxin 4 interacting protein antisense oligonucleotide. NOTE: The
CC present sequence contains a phosphorothioate backbone and 2'-O-
CC methoxyethyl wings
XX
SQ Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 932 AGAAATGCAGAACTCTGAAG 950
Db 19 AGAACTCCAGAAATGTGAAG 1

RESULT 288
ABK23082/c
ID ABK23082 standard; DNA; 20 BP.
XX
AC ABK23082;
XX
DT 09-APR-2002 (first entry)

XX Human Zmax1 cDNA reverse PCR primer #122.
DE
XX
KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200192891-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016946.
XX
PR 26-MAY-2000; 2000US-00578900.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2002-097784/13.
XX
PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX
PS Disclosure; Page 39; 409pp; English.
XX
CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
Db 19 AATATTGTGGCCACACAC 1

RESULT 289
ABS68905
ID ABS68905 standard; DNA; 20 BP.
XX
AC ABS68905;
XX
DT 20-NOV-2002 (first entry)
XX
DE Human RecQ protein-like 4 (RECQL4) DNA antisense oligonucleotide #48.
XX

KW Human; RecQ protein-like 4; RECQL4; ss; chromosome 8q24; infection;
KW inflammation; tumour formation; cancer; cytostatic; antiinflammatory;
KW antimicrobial; antisense therapy; antisense oligonucleotide.
XX
OS Homo sapiens.
XX
PN US6436706-B1.
XX
PD 20-AUG-2002.
XX
PF 23-FEB-2001; 2001US-00792594.
XX
PR 23-FEB-2001; 2001US-00792594.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Watt AT;
XX
XX WPI; 2002-689941/74.
XX
PT New antisense compounds targeted to nucleic acids encoding RecQ protein-
PT like 4, useful for modulating expression of the nucleic acid and treating
PT diseases associated with expression of the nucleic acid in humans.
XX
PS Claim 14; Col 45; 45pp; English.
XX
CC The invention relates to a compound targeted to specific nucleobases of
CC RecQ protein-like 4 (RECQL4) and which hybridises and inhibits the
CC expression of RECQL4. The compound is useful for inhibiting the
CC expression of RECQL4 in cells or tissues and for treating an animal,
CC particularly a human suspected of having or being prone to a disease or
CC condition associated with expression of RECQL4. The compound is useful
CC for diagnostics, therapeutics and as a research reagent, e.g.
CC prophylactically to prevent or delay infection, inflammation or tumour
CC formation. This sequence represents an antisense oligonucleotide used in
CC inhibition of human RECQL4 expression
XX
SQ Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GGGCAGGCTGCCGGGCCG 28
Db |||||
1 GGGCAGGCTGCCGTCACG 19

RESULT 290
AAD41640
ID AAD41640 standard; DNA; 20 BP.
XX
AC AAD41640;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human interleukin-12 p35 subunit DNA amplifying forward PCR primer.
XX
KW Human; interleukin-12; IL-12 p35 subunit; therapeutic; infection; tumour;
KW inflammation; antisense therapy; antisense; prophylactic; PCR; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN US6399379-B1.
XX
PD 04-JUN-2002.
XX
PF 07-MAY-2001; 2001US-00851520.
XX
PR 07-MAY-2001; 2001US-00851520.
XX
PA (ISIS-) ISIS PHARM INC.

XX Baker BF, Freier SM;
PI WPI; 2002-535980/57.
XX
XX Novel antisense compounds targeted to nucleic acids encoding interleukin-
PT 12 p35 subunit, useful for modulating interleukin-12 p35 subunit
PT expression and treating diseases associated with expression of the
PT subunit in humans.
XX
PS Example 13; Col 53; 44pp; English.
XX
CC The present invention relates to novel antisense oligonucleotides which
CC specifically hybridise with specific regions of nucleic acids encoding
CC interleukin-12 (IL-12) p35 subunit and inhibit the expression of human IL
CC -12 p35 subunit. Sequences of the invention are useful for inhibiting the
CC expression of human IL-12 p35 subunit in human cells or tissues and for
CC treating animals, particularly humans suspected of having or being prone
CC to diseases or conditions associated with expression of IL-12 p35
CC subunit. They are useful for diagnostics, therapeutics and as research
CC reagent, e.g. prophylactically to prevent or delay infection, tumour
CC formation or inflammation. Sequences of the invention are useful for
CC antisense therapy. The present DNA sequence is a PCR primer which is used
CC for amplifying human IL-12 p35 subunit DNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 822 GCCTCTCATGACCCAGGAA 840
Db |||||
1 GCCACTCCAGACCCAGGAA 19

RESULT 291
ADE31838/c
ID ADE31838 standard; DNA; 20 BP.
XX
AC ADE31838;
XX
DT 29-JAN-2004 (first entry)
XX
DE Solid surface assembly oligonucleotide Lib1-D.
XX
KW Lipopeptide synthetase; multifunctional enzyme; lipid module;
KW peptide module; DNA library; lipopeptide synthesis; antimicrobial;
KW solid surface; immobilisation; ss.
XX
OS Synthetic.
XX
PN WO200132845-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-EP011237.
XX
PR 05-NOV-1999; 99EP-00203674.
XX
PA (BIOM-) BIOMADE BV.
XX
PI Leenhouts CJ, Noback MA, Van Den Burg L, Hamoen LW, Duitman EH;
PI Kuipers OP;
XX
XX WPI; 2002-239393/29.
XX
PT Preparing lipopeptide synthetases, useful for producing new combinations
PT of lipid molecules and amino acid modules, comprises modifying the lipid
PT moiety and optionally a peptide moiety of one or more known (lipo)peptide
PT synthetase.
XX

PS Example 6; Page 46; 78pp; English.

XX The invention relates to a method of preparing novel lipopeptide

CC synthetases by modifying the lipid module and optionally the peptide

CC module of one or more known (lipo)peptide synthetases. The method

CC involves providing a range of DNA fragments encoding lipopeptide

CC synthetase modules or domains, which may contain at their 5'-end and 3'-

CC end restriction enzyme recognition sites that generate non-palindromic

CC sticky ends; selecting and ligating at least two of these DNA fragments,

CC at least one of which is specific for the lipid moiety of the lipopeptide

CC synthetase, to obtain a lipopeptide synthetase encoding DNA molecule;

CC introducing the lipopeptide synthetase-encoding DNA molecule in a host

CC cell; and expressing the DNA molecule in the host cell. The invention

CC also relates to DNA molecules encoding novel lipopeptide synthetases, a

CC library of DNA fragments encoding lipopeptide synthetase modules or

CC domains, and a method for non-ribosomal preparation of novel peptides

CC using the novel lipopeptide synthetases of the invention. The lipopeptide

CC synthetases produced according to methods of the invention have a lipid

CC module and peptide module configuration that does not exist in nature,

CC and the DNA library is useful in the production of a range of lipopeptide

CC synthetases. The lipopeptide synthetases of the invention are useful for

CC producing very large numbers of novel lipopeptides, which differ from

CC existing lipopeptides in their fatty acid composition and optionally

CC their amino acid composition. Such lipopeptides may have novel structures

CC and/or activities compared to known lipopeptides, and may therefore be

CC useful as novel antimicrobial agents. Sequences ADE31837-ADE31838

CC represent a pair of oligonucleotides used to couple DNA fragments to a

CC solid surface to permit the assembly of lipopeptide synthetase modules in

CC a predetermined order. These oligonucleotides anneal to each other to

CC form an SfiI sticky end which facilitates ligation of a double stranded

CC nucleic acid also containing an SfiI sticky end.

XX

SQ Sequence 20 BP; 0 A; 12 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GGGCAGGCTGCCCGGCCG 28

Db 19 GGGCGCGCGCGCGGCCG 1

RESULT 292

ABT21432/c

ID ABT21432 standard; DNA; 20 BP.

XX

AC ABT21432;

XX

DT 16-APR-2003 (first entry)

XX

DE Multiplex group PCR primer #179.

XX

XX Racing potential; horse; grandpaternal DNA; over-represented; breeding;

KW grandmother; performance; progeny horse; PCR; primer; ss.

KW

XX Unidentified.

OS

XX WO200292851-A2.

PN

XX

PD 21-NOV-2002.

XX

XX 15-MAY-2002; 2002WO-GB002273.

PF

XX

XX 15-MAY-2001; 2001GB-00011886.

PR

XX (ANIM-) ANIMAL HEALTH TRUST.

PA (BRHO-) BRITISH HORSERACING BOARD.

PA

XX Binns MM, Swinburne JE;

PI

XX WPI; 2003-129314/12.

DR

XX

PT Determining the racing potential of a horse comprises measuring whether

PT grandpaternal or grandmaternal DNA from the selected grandmother DNA is

PT over-represented in the genome of the horse.

XX

PS Example 2; Page 24; 49pp; English.

XX

CC The invention relates to a novel method for determining racing potential

CC of a horse. The method comprises measuring: whether grandpaternal DNA is

CC over-represented in the genome of the horse; or in the case where one of

CC the grandmothers was selected for breeding on the basis of racing

CC performance, whether grandmaternal DNA from the selected grandmother is

CC over-represented in the genome of the horse which indicates that the

CC horse has good racing potential. The method of the invention is useful

CC for determining the racing potential of a horse or for obtaining a

CC progeny horse with good racing potential. This polynucleotide sequence

CC represents a PCR primer used in the detection method of over-

CC representation of DNA from male grandparents of the invention

XX

SQ Sequence 20 BP; 11 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 317 GGATTTCTCTGTTATCTTG 335

Db 19 GGATTTCTTGTGTTTGCTTG 1

RESULT 293

ABX10661

ID ABX10661 standard; DNA; 20 BP.

XX

AC ABX10661;

XX

DT 22-APR-2003 (first entry)

XX

DE Reverse PCR primer amplifying vncs SNP containing gene fragment.

XX

KW vex2; ss; PCR; primer; SNP; single nucleotide polymorphism;

KW antibiotic tolerance; type 4 allele; R6 allele; pep27; penicillin;

KW vancomycin; vex/pep27/vncr/s operon; pneumococcus; autolytic enzyme;

KW LytA; signal peptide; VncS; VncR; beta-lactam.

XX

OS Streptococcus pneumoniae.

XX

PN US2002164623-A1.

XX

PD 07-NOV-2002.

XX

PF 13-NOV-2001; 2001US-00054225.

XX

PR 13-NOV-2001; 2001US-00054225.

XX

PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX

PI Atkinson RM, Tuomanen EI;

XX

XX WPI; 2003-238303/23.

DR

XX

XX Identifying antibiotic tolerant bacteria, especially antibiotic tolerant

PT Streptococcus pneumoniae, by determining whether the bacteria has type 4

PT or R6 allele of vex2 and pep27 gene.

XX

PS Claim 16; Page 4; 11pp; English.

XX

CC The invention discloses a method for determining whether a bacteria is

CC likely to be tolerant to an antibiotic. The method comprises determining

CC whether the bacteria has a type 4 or R6 allele of the vex2 gene and pep27

CC genes, where vex2 and pep27 genes are closely associated with tolerance

CC to penicillin and vancomycin, and the bacteria is determined to be likely

CC to be tolerant if it has a type 4 allele of the vex2 gene and an R6

CC allele of the pep27. Also disclosed are PCR primers which can be used to

CC amplify the regions of the vex2 and pep27 genes which contain the single
CC nucleotide polymorphisms (SNPs). The genes are located within the
CC vex/pep27/vncr/s operon encoding the major pneumococcal autolytic enzyme,
CC LytA. The operon encodes for a signal peptide, Pep27, that is transported
CC out of the cell via the Vex dedicated transporter. Once it reaches a
CC critical density in the supernatant, it signals through the two-component
CC regulatory system, VncS and VncR, which subsequently induces activation
CC of LytA. Mutations in any one of the operon genes prevents proper
CC signaling, resulting in a lack of LytA activation and antibiotic
CC tolerance. The method is useful for determining whether a bacteria is
CC likely to be tolerant to an antibiotic, preferably a beta-lactam such as
CC penicillin and vancomycin and, therefore, for determining whether a
CC subject suffering from a bacterial infection can be effectively treated
CC with those antibiotics. The method is rapid and correctly predicts
CC whether a subject can be successfully treated with a particular
CC antibiotic. Unsuccessful treatment of the subject with conventional
CC antibiotics can be avoided so that alternative therapies can be
CC administered without delay. The sequence presented is the reverse PCR
CC primer which was used to amplify the S. pneumoniae vncS SNP containing
CC gene fragment

XX
SQ Sequence 20 BP; 4 A; 5 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 ATTGAATTCTTAGAACTC 507
||||| ||||| |||||
Db 1 ATTGATTTCTTCTTAAC TC 19

RESULT 294
ACC45665/C
ID ACC45665 standard; DNA; 20 BP.
XX
AC ACC45665;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human HBM STS marker reverse primer #122.
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babi j P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
XX
XX New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Disclosure; Page 56; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development, is
CC or characterised by reduced bone density or mass. The present sequence, is
CC used in the exemplification of the invention

XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
||| ||||| ||||| ||
Db 19 AATATTGTGGCCACACAC 1

RESULT 295
ABZ80435
ID ABZ80435 standard; DNA; 20 BP.
XX
AC ABZ80435;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human protein PP13671 PCR primer #2.
XX
KW Human; cancer; cancer suppression; cancer inhibitor; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1368509-A.
XX
PD 11-SEP-2002.
XX
PF 08-FEB-2001; 2001CN-00105310.
XX
PR 08-FEB-2001; 2001CN-00105310.
XX
PA (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI Gu J;
XX
DR WPI; 2003-112778/11.
XX
XX Human protein that suppresses cancer cell growth and its coding sequence.
PT
XX
PS Example 2; Page 10 (Disclosure); 36pp; Chinese.

XX
CC ABZ80408 to ABZ80418 encode the human proteins ABP96551 to ABP96561 which
CC have cancer inhibiting functions. Also described is a method for
CC preparing the proteins using recombination techniques. The human proteins
CC from the present invention, and nucleotide sequences encoding them, can
CC be used for treating diseases such as cancer. The present sequence
CC represents a PCR primer for a human cancer inhibiting function related
CC protein from the present invention

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 819 CAGGCTCTCATGACCCAG 837
Db 1 CAGGCTTCTCTTGACGCAG 19
RESULT 296
ACH11218/c
ID ACH11218 standard; DNA; 20 BP.
XX
AC ACH11218;
XX
DT 08-OCT-2003 (first entry)
XX
DE Human protein kinase C-epsilon targeted oligonucleotide ISIS#7941.
KW Human; ss; antisense; PKC; protein kinase C; hyperproliferation; tumour;
KW inflammation; psoriasis; cancer; non-small cell lung cancer; lung cancer;
KW non-Hodgkin's lymphoma; glioblastoma; bladder cancer; colon cancer;
KW breast cancer; ovarian cancer; pancreatic cancer.
XX
OS Homo sapiens.
XX
PN US6537973-B1.
XX
PD 25-MAR-2003.
XX
PF 18-DEC-2001; 2001US-00025139.
XX
PR 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
PR 07-JUN-1995; 95US-00478178.
PR 31-MAR-1997; 97US-00829637.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Holmlund JT, Dorr FA;
XX
DR WPI; 2003-531084/50.
XX
PT New pharmaceutical composition, useful for treating cancer, e.g., non-small cell lung cancer or non-Hodgkin's lymphoma.
PT
XX
PS Example 16; Col 22; 56pp; English.
XX
CC The invention relates to a new pharmaceutical composition comprising: (a) an oligonucleotide sequence having up to 50 base pairs (bp); and (b) carboplatin and paclitaxel, cisplatin and gemcitabine, 5-fluorouracil and leucovorin, or docetaxel. The pharmaceutical composition is useful for treating diseases associated with protein kinase C such as hyperproliferative and inflammatory conditions e.g. psoriasis, tumours and cancer e.g. non-small cell lung cancer, non-Hodgkin's lymphoma, glioblastoma, bladder cancer, lung cancer, colon cancer, breast cancer, ovarian cancer and pancreatic cancer. The present sequence represents an antisense oligonucleotide targeted against protein kinase C
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 434 AGAGGAGATGATTTTAGCT 452
Db 19 AGAGAAGAGGATTTTGGCT 1
RESULT 297

ACA62693/c
ID ACA62693 standard; DNA; 20 BP.
XX
AC ACA62693;
XX
DT 20-AUG-2003 (first entry)
XX
DE RIZ(A)8 tract primer RIZA8-F.
XX
KW RIZ1; microsatellite instability; tumour; apoptosis; ss; PCR; primer;
KW retinoblastoma protein interacting zinc finger gene; colorectal tumour;
KW endometrial tumour; hereditary nonpolyposis colon carcinoma; MSI;
KW gastric tumour.
XX
OS Homo sapiens.
XX
PN US2003032606-A1.
XX
PD 13-FEB-2003.
XX
PF 17-DEC-2001; 2001US-00024450.
XX
PR 19-DEC-2000; 2000US-0256582P.
XX
PA (HUAN/) HUANG S.
PA (CHAD/) CHADWICK R B.
XX
PI Huang S, Chadwick RB;
XX
DR WPI; 2003-492075/46.
XX
PT Inhibiting growth of microsatellite instability-positive tumor, by introducing a nucleic acid molecule encoding a retinoblastoma protein-interacting zinc finger gene-1 polypeptide into the tumor.
PT
XX
PS Example 2; Page 7; 41pp; English.
XX
CC The invention relates to a method of inhibiting growth of a microsatellite instability (MSI)-positive tumour, which involves introducing into the tumour a nucleic acid molecule encoding a retinoblastoma protein-interacting zinc finger gene (RIZ)-1 polypeptide and expressing the polypeptide in the tumour in an effective amount to inhibit growth of the tumour. The method is useful for inhibiting growth of a microsatellite instability (MSI)-positive tumour. The tumour contains cells having an abnormal number of adenosine nucleotides in a RIZ poly(A) tract. The MSI-positive tumour is colorectal tumour, gastric tumour, endometrial tumour or hereditary nonpolyposis colon carcinoma. Also disclosed is a method for determining MSI status of the tumour. Both methods are are useful for detecting and treating MSI(+) tumours and for inducing apoptotic cell killing both in vitro and in vivo. The present sequence represents the RIZ(A)8 tract primer RIZA8-F
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 966 AGGACATTTTGATGAGATC 984
Db 19 ACGACATTTTGCTGAGCTC 1
RESULT 298
ABT44202/c
ID ABT44202 standard; DNA; 20 BP.
XX
AC ABT44202;
XX
DT 06-NOV-2003 (first entry)
XX
DE Chimeric antisense oligonucleotide ISIS 199198 to inhibit human NOD1.
XX

PR 16-AUG-2002; 2002US-0404200P.
XX (GENO-) GENOMAR ASA.
PA
XX
PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX
DR WPI; 2003-627388/59.
XX
PT Novel isolated nucleic acid molecule comprising single nucleotide
PT polymorphism associated with fish, useful for forming PCR primers which
PT are used for detecting single nucleotide polymorphisms in fish nucleic
PT acids.
XX
PS Claim 18; SEQ ID NO 1061; 233pp; English.
XX
CC The present invention describes an isolated nucleic acid (I) comprising a
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC (i), or its complement under highly stringent hybridisation conditions.
CC Also described: (1) an isolated oligonucleotide (II) comprising at least
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC origin of fish sample comprising providing a parentage genotype database
CC comprising a collection of candidate parent genotypes, where each of the
CC candidate parent genotype represents a distinct origin, and comparing a
CC sample genotype to the parentage genotype database, where a match between
CC the sample genotype and one of the candidate parent genotype identifies
CC to the origin of the sample. (M1) is useful for determining the origin of
CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC detecting nucleic acid molecule comprising SNP in a sample, which
CC involves contacting the sample containing nucleic acids with one or more
CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC useful for detecting nucleic acid molecule comprising a polymorphic
CC sequence in a sample, comprising contacting the sample containing nucleic
CC acids with one or more (ii) which is derived from O. niloticus
CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC sites or seabass polymorphic sites, and identifying a nucleic acid that
CC hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC comprising a microsatellite sequence in sample. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 782 CTTGGGGATGTGCTTGAG 800
DB ||||| || |||||
2 CTTGGGTTTGAGCTTGAG 20

RESULT 301
ADD90778
ID ADD90778 standard; DNA; 20 BP.
XX
AC ADD90778;
XX
DT 29-JAN-2004 (first entry)
XX
DE S. pneumoniae vncS gene PCR primer #2.
XX
KW ss; PCR; primer; antibiotic; antibiotic tolerance; bacterial resistance;
KW beta-lactam; penicillin; vancomycin; vncS.
XX

OS Streptococcus pneumoniae.
XX
PN US2003175796-A1.
XX
PD 18-SEP-2003.
XX
PF 02-MAY-2003; 2003US-00428617.
XX
PR 13-NOV-2001; 2001US-00054225.
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Atkinson RM, Tuomanen EI;
XX
DR WPI; 2003-852128/79.
XX
PT Determining whether a bacteria is likely to be tolerant to beta-lactam,
PT penicillin or vancomycin by determining the genotype of the vex2 and
PT pep27 genes.
XX
PS Claim 16; SEQ ID NO 12; 11pp; English.
XX
CC The invention relates to a method of determining whether a bacteria is
CC likely to be tolerant to antibiotics. The methods are used for
CC determining bacterial resistance to beta-lactam, penicillin and/or
CC vancomycin. The present sequence represents the S. pneumoniae vncS PCR
CC primer.
XX
SQ Sequence 20 BP; 4 A; 5 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 489 ATTGAATTTCTTAGAACTC 507
DB ||||| ||||| |||||
1 ATTGATTTTCTTCTAACTC 19

RESULT 302
ACH00690/c
ID ACH00690 standard; DNA; 20 BP.
XX
AC ACH00690;
XX
DT 12-FEB-2004 (first entry)
XX
DE Mammalian inverted nipple associated microsatellite PCR primer #144.
XX
KW Inverted nipple; microsatellite; PCR; primer; ss; pig.
XX
OS Mammalia.
XX
PN WO2003066891-A2.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-EP001045.
XX
PR 05-FEB-2002; 2002EP-00002632.
XX
PA (FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE.
XX
PI Hardge T, Schellander K, Wimmers K;
XX
DR WPI; 2003-671539/63.
XX
PT Determining predisposition to inverted nipples useful e.g. for selecting
PT breeding animals comprises detecting specific microsatellite markers.
XX
PS Disclosure; Page 24; 63pp; German.
XX
CC The present invention relates to the use of a nucleic acid to determine

CC the predisposition of appearance or inheritance of inverted nipples,
CC where the nucleic acid is identical to the region of microsattelites
CC S0200, SW2443, S0097, S0007, SW1301 or S0164 on chromosomes 6, 2, 4, 14,
CC 1 and 3, respectively, in pigs, or homologous positions in the genomes of
CC other mammals. The nucleic acids can be used to select pets, breeding or
CC farm animals that lack inverted nipples, particularly by genomic
CC screening of many related mammals in a population. The present sequence
CC is a PCR primer used in the exemplification of the invention to identify
CC microsattellite markers associated with the inverted nipple phenotype
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 406 AATCAAGGGTTTTTCCTT 424
|| ||||| ||||| |||||
Db 19 AACTCAAGGGGTTTGCCTT 1

RESULT 303
ABZ91305/C
ID ABZ91305 standard; DNA; 20 BP.

XX
AC ABZ91305;

DT 17-OCT-2003 . (first entry)

XX
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.
OS
XX WO200285308-A2.

XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.

XX
PR 24-APR-2001; 2001US-0286137P.

XX
PA (EPIG-) EPIGENESIS PHARM INC.

XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX
DR WPI; 2003-229219/22.

XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Disclosure; SEQ ID NO 6547; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 429 TTGGAAGAGGAGATGATT 447
||||| ||||| ||||| |||||
Db 20 TTGGCAAAGGAGATGACTT 2

RESULT 304
ABZ99318
ID ABZ99318 standard; DNA; 20 BP.

XX
AC ABZ99318;

DT 17-OCT-2003 (first entry)

XX
DE Human PDE4C oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.
OS
XX WO200285308-A2.

XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.

XX
PR 24-APR-2001; 2001US-0286137P.

XX
PA (EPIG-) EPIGENESIS PHARM INC.

XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX
DR WPI; 2003-229219/22.

XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Disclosure; SEQ ID NO 14560; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 191 TTCCAGCCCATCTCCCCCA 209
Db 1 TTGGAGGCCATCTCCCCCA 19

RESULT 305
ABZ88740/C
ID ABZ88740 standard; DNA; 20 BP.

XX AC ABZ88740;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.
XX WO200285308-A2.

PN 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 3982; 872pp; English.

PS The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 540 TTTACTATGAAATTTAATA 558
Db 20 TTCACCATGACATTTAATA 2

RESULT 306
ABQ84375/C
ID ABQ84375 standard; DNA; 20 BP.

XX AC ABQ84375;
XX
DT 20-FEB-2003 (first entry)
XX
DE DPP10 PCR primer #6.
XX
KW DPP10; dipeptidyl peptidase; prollyloloigopeptidase; enzyme; asthma;
KW antiinflammatory; antiasthmatic; antipsooriatic; antiarthritic;
KW antirheumatic; vaccine; gene therapy; inflammatory disease;
KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
KW chromosome 2q14; PCR primer; ss.

XX OS Homo sapiens.
OS Synthetic.

PN WO200286113-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-GB001887.

XX 24-APR-2001; 2001GB-00010044.

PR 24-APR-2001; 2001GB-00010046.

PR 12-OCT-2001; 2001GB-00024575.

PR 12-OCT-2001; 2001GB-00024594.

XX (ISIS-) ISIS INNOVATIONS LTD.

XX Cookson WOCM, Moffat MF, Allen M, Lench N;

XX WPI; 2003-093132/08.

XX New nucleic acid sequence comprising DPP10 mRNA, useful for the
PT manufacture of a medicament for regulating DPP10 protein expression or
PT for preventing or treating inflammatory disease e.g., inflammatory bowel
PT disease.

XX Claim 43; Page 313; 321pp; English.

PS The present invention describes a new isolated nucleic acid sequence (I)
XX comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
CC known as prollyloloigopeptidase). (I) has antiinflammatory, antiasthmatic,
CC antipsooriatic, antiarthritic and antirheumatic activities, and can be
CC used in vaccines and gene therapy. A composition comprising (I) can be
CC used for the manufacture of a medicament for regulating DPP10 expression
CC or for preventing or treating inflammatory disease e.g., inflammatory
CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
CC also be used in an assay for detecting or measuring DPP10 in a sample. A

CC host cell comprising (I) can be used for producing recombinant DPP10 gene
CC products, or in drug screening systems to identify agents for diagnosis
CC or treatment of individuals having or susceptible to inflammatory
CC disease. Human DPP10 is located on chromosome 2, more specifically
CC chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 472 TATTCTGATTACAGTGCAT 490
Db 19 TGTTCTGGTTACAATGCAT 1

RESULT 307
ABZ77118
ID ABZ77118 standard; DNA; 20 BP.
XX
AC ABZ77118;
XX
DT 07-MAY-2003 (first entry)
XX
DE Human stearyl-CoA desaturase phosphorothioate oligonucleotide SEQ:73.
XX
KW Human; stearyl-CoA desaturase; phosphorothioate; 2'-O-methoxyethyl;
KW 2'-MOE; cardiovascular; antiarteriosclerotic; antilipaemic; cytostatic;
KW antiinflammatory; antisense therapy; antisense oligonucleotide; tumour;
KW abnormal lipid metabolism; abnormal cholesterol metabolism; infection;
KW atherosclerosis; cardiovascular disease; inflammation; inhibition; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN WO2003012031-A2.
XX
PD 13-FEB-2003.
XX
PF 16-JUL-2002; 2002WO-US022676.
XX
PR 30-JUL-2001; 2001US-00918187.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-248160/24.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding human
PT stearyl-CoA desaturase, useful for treating diseases associated with the
PT desaturase, e.g. atherosclerosis, and in diagnostic and research
PT applications.
XX
PS Claim 3; Page 95; 117pp; English.
XX
CC The present invention describes a compound (I) that is 8-50 nucleobases

CC in length targeted to a nucleic acid molecule encoding human stearyl-CoA
CC desaturase, and which specifically hybridises with and inhibits the
CC expression of human stearyl-CoA desaturase, or which specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding human stearyl-CoA desaturase. Human
CC stearyl-CoA desaturase is mapped to chromosome 10. (I) has antilipaemic,
CC cardiovascular, antiarteriosclerotic, cytostatic and antiinflammatory
CC activities, and can be used in antisense therapy. The antisense compounds
CC (I) can be used for modulating the expression of human stearyl-CoA
CC desaturase and for treating diseases or conditions associated with
CC expression of human stearyl-CoA desaturase, e.g. abnormal lipid or
CC cholesterol metabolism, atherosclerosis, or cardiovascular diseases. The
CC antisense compounds (I) can also be used for diagnostics, therapeutics
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC tumour formation, as research reagents and kits, and in distinguishing
CC between functions of various members of a biological pathway. The present
CC sequence represents a human stearyl-CoA desaturase inhibiting chimeric
CC phosphorothioate antisense oligonucleotide, which is given in an example
CC from the present invention
XX
SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 814 TGAAGCAGGCCTCTCATGA 832
Db 2 TCAAGCAGGCATCTGATGA 20

RESULT 308
ABV99953
ID ABV99953 standard; DNA; 20 BP.
XX
AC ABV99953;
XX
DT 06-MAR-2003 (first entry)
XX
DE Coriolus versicolor cytochrome P450 PCR primer SEQ ID 6.
XX
KW Cytochrome P450; antidote; PCR; primer; ss.
XX
OS Coriolus versicolor.
XX
PN JP2002253248-A.
XX
PD 10-SEP-2002.
XX
PF 28-FEB-2001; 2001JP-00055452.
XX
PR 28-FEB-2001; 2001JP-00055452.
XX
PA (WARI/) WARIISHI H.
PA (KUBI) KUBOTA CORP.
XX
DR WPI; 2003-096531/09.
XX
PT A new polypeptide with cytochrome P450 activity useful for producing
PT antidotes.
XX
PS Example 1; Page 8; 16pp; Japanese.
XX
CC The present invention relates to a novel cytochrome P450 (see ABP70653).
CC (I) is useful for producing antidotes. Also disclosed are a recombinant
CC vector containing the coding sequence for (I); a transformant transformed
CC by the recombinant vector; and a method for preparing cytochrome P450,
CC comprising culturing the transformant and recovering cytochrome P450 from
CC the culture. The present sequence is a PCR primer, which was used in an
CC example from the invention
XX
SQ Sequence 20 BP; 5 A; 10 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 952 CCCACTCTGGACCCAGGAC 970
Db 2 CCCACCACGGACCCAGGAC 20

RESULT 309
ADM83692
ID ADM83692 standard; DNA; 20 BP.
XX
AC ADM83692;
XX
DT 03-JUN-2004 (first entry)
XX
DE Serine protease-like protease NES-1 primer #3.
XX
KW cellular proliferative disorder; breast cancer; methylation;
KW predisposition; methylation specific PCR; PCR; primer; CpG island; ss;
KW human; serine protease-like protease; NES-1.
XX
OS Homo sapiens.
XX
PN US2003138783-A1.
XX
PD 24-JUL-2003.
XX
PF 28-JAN-2002; 2002US-00059579.
XX
PR 26-JAN-2001; 2001US-00771357.
XX
PA (SUKU/) SUKUMAR S.
PA (EVRO/) EVRON E.
PA (DOOL/) DOOLEY W C.
PA (SACC/) SACCHI N.
PA (DAVI/) DAVIDSON N.
PA (FACK/) FACKLER M J.
XX
PI Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
XX WPI; 2003-851722/79.
XX
PT Diagnosing a cellular proliferative disorder of breast tissue in a
PT subject comprises determining the state of methylation of one or more
PT nucleic acid isolated from the subject.
XX
PS Claim 13; SEQ ID NO 79; 59pp; English.
XX
CC The invention describes a method of diagnosing a cellular proliferative
CC disorder of breast tissue in a subject comprising determining the state
CC of methylation of one or more nucleic acid isolated from the subject,
CC where the state of methylation of one or more nucleic acids is compared
CC with the state of methylation of one or more nucleic acids from a subject
CC not having the cellular proliferative disorder of breast tissue. Also
CC described are: a method for determining a predisposition to a cellular
CC proliferative disorder of breast tissue in a subject; a method of
CC diagnosing a cellular proliferative disorder of breast tissue in a
CC subject; and a kit for the detecting a cellular proliferative disorder of
CC diagnosing a cellular proliferative disorder of breast tissue in a
CC subject; and a kit for the detecting a cellular proliferative disorder of
CC breast tissue in a subject. The method is useful for diagnosing a
CC cellular proliferative disorder of breast tissue in a subject. This
CC sequence represents a methylation specific primer used in the analysis of
CC the methylation state of the serine protease-like protease NES-1 gene CpG
CC islands in normal mammary epithelium, breast cancer cell lines and in
CC primary mammary tumours.
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGGCGTTT 167
Db 1 TTCGAAGTTTATGGCGTTT 19

RESULT 310
ADM83766
ID ADM83766 standard; DNA; 20 BP.
XX
AC ADM83766;
XX
DT 03-JUN-2004 (first entry)
XX
DE Serine protease-like protease NES-1 primer #14.
XX
KW cellular proliferative disorder; breast cancer; methylation;
KW predisposition; methylation specific PCR; PCR; primer; CpG island; ss;
KW human; serine protease-like protease; NES-1.
XX
OS Homo sapiens.
XX
PN US2003138783-A1.
XX
PD 24-JUL-2003.
XX
PF 28-JAN-2002; 2002US-00059579.
XX
PR 26-JAN-2001; 2001US-00771357.
XX
PA (SUKU/) SUKUMAR S.
PA (EVRO/) EVRON E.
PA (DOOL/) DOOLEY W C.
PA (SACC/) SACCHI N.
PA (DAVI/) DAVIDSON N.
PA (FACK/) FACKLER M J.
XX
PI Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
XX WPI; 2003-851722/79.
XX
PT Diagnosing a cellular proliferative disorder of breast tissue in a
PT subject comprises determining the state of methylation of one or more
PT nucleic acid isolated from the subject.
XX
PS Disclosure; SEQ ID NO 158; 59pp; English.
XX
CC The invention describes a method of diagnosing a cellular proliferative
CC disorder of breast tissue in a subject comprising determining the state
CC of methylation of one or more nucleic acid isolated from the subject,
CC where the state of methylation of one or more nucleic acids is compared
CC with the state of methylation of one or more nucleic acids from a subject
CC not having the cellular proliferative disorder of breast tissue. Also
CC described are: a method for determining a predisposition to a cellular
CC proliferative disorder of breast tissue in a subject; a method of
CC diagnosing a cellular proliferative disorder of breast tissue in a
CC subject; and a kit for the detecting a cellular proliferative disorder of
CC breast tissue in a subject. The method is useful for diagnosing a
CC cellular proliferative disorder of breast tissue in a subject. This
CC sequence represents a methylation specific primer used in the analysis of
CC the methylation state of the serine protease-like protease NES-1 gene CpG
CC islands in normal mammary epithelium, breast cancer cell lines and in
CC primary mammary tumours.
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 TTAGAGGATTATGGCGTTT 167
Db 1 TTCGAAGTTTATGGCGTTT 19

CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 540 TTACTATGAAATTTTATA 558
DB 20 TTCACCATGACATTTTATA 2

RESULT 313
ABD32349
ID ABD32349 standard; DNA; 20 BP.
XX
AC ABD32349;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human PDE4C-derived oligonucleotide SEQ ID 14560.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.

XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 14560; 763pp; English.

XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 191 TTCCACGCCATCTCCCCCA 209
DB 1 TTGAGGCCATCTCCCCCA 19

RESULT 314
ADH47993/C
ID ADH47993 standard; DNA; 20 BP.

XX
AC ADH47993;
XX
DT 25-MAR-2004 (first entry)
XX
DE Protein kinase C epsilon antisense oligonucleotide seq id 86.
XX
KW cytostatic; protein-kinase-inhibitor-C-alpha; gene therapy; carboplatin;
KW paclitaxel; docetaxel; cisplatin; gemcitabine; 5-fluorouracil;
KW leucovorin; protein kinase C alpha inhibitor; PKC-alpha inhibitor;
KW cancer; non-small cell lung cancer; non-Hodgkin's lymphoma;
KW antisense technology; ss; PKC-epsilon.

XX Synthetic.

XX US2003148989-A1.

XX 07-AUG-2003.

XX 21-JAN-2003; 2003US-00348485.

XX 16-MAR-1992; 92US-00852852.

XX 09-JUL-1993; 93US-00089996.

XX 07-JUN-1995; 95US-00478178.

XX 31-MAR-1997; 97US-00829637.

XX 18-DEC-2001; 2001US-00025139.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dean NM, Holmlund JT, Dorr FA;
XX WPI; 2004-106519/11.

PT New pharmaceutical compositions comprising oligonucleotide in combination
PT with e.g. arboplatin or cisplatin, useful for inhibiting protein kinase C
PT expression, particularly for treating cancer, e.g. non-Hodgkin's
PT lymphoma.
XX Example 16; SEQ ID NO 86; 52pp; English.
PS
XX The invention describes new pharmaceutical compositions comprising an
CC oligonucleotide up to 50 nucleotide units in length of a sequence having
CC 20 bp (dnal), in combination with any of the following: carboplatin and
CC paclitaxel; docetaxel; cisplatin and gemcitabine; or 5-fluorouracil and
CC leucovorin. Also described are: a method of inhibiting protein kinase C
CC (PKC)-alpha expression in human cells by contacting the cells with any of
CC the pharmaceutical compositions; and methods of treating a condition
CC associated with expression of human PKC-alpha by administering to an
CC animal, or its cells, tissues or bodily fluid any of the pharmaceutical
CC compositions. The compositions are useful for inhibiting PKC-alpha
CC expression in human cells. The compositions are useful for treating a
CC condition associated with the expression of human PKC-alpha, particularly
CC cancer. In particular, the compositions are useful for treating non-small
CC cell lung cancer or non-Hodgkin's lymphoma in a human. This sequence
CC represents a human protein kinase C antisense oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 434 AGAGGAGATGATTTTAGCT 452
Db 19 AGAGAAGAGGATTTGGCT 1

RESULT 315
ADH58845
ID ADH58845 standard; DNA; 20 BP.
XX
AC ADH58845;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDC-like kinase 1 antisense oligonucleotide #127.
XX
KW antisense oligonucleotide; CDC-like kinase 1; cancer;
KW autoimmune disorder; infection; inflammation; tumour formation; human;
KW ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN US2003219895-A1.
XX
AC ADH58845;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDC-like kinase 1 antisense oligonucleotide #127.
XX
KW antisense oligonucleotide; CDC-like kinase 1; cancer;
KW autoimmune disorder; infection; inflammation; tumour formation; human;
KW ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN US2003219895-A1.
XX
PD 27-NOV-2003.
XX
PF 22-MAY-2002; 2002US-00154708.
XX
PR 22-MAY-2002; 2002US-00154708.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Watt AT;
XX
DR WPI; 2004-051714/05.
XX
PT New antisense oligonucleotides targeted to nucleic acid molecules
PT encoding CDC-like kinase 1, useful for treating diseases or conditions
PT associated with expression of CDC-like kinase 1, e.g. cancers or
PT autoimmune disorders.
XX
PS Example 15; SEQ ID NO 140; 64pp; English.
PS
XX The invention comprises antisense oligonucleotides that are targeted to
CC CDC-like kinase 1. The antisense oligonucleotides of the invention are

CC useful for modulating the expression of CDC-like kinase 1, and for
CC treating diseases or conditions associated with expression of CDC-like
CC kinase 1 (e.g. cancers and autoimmune disorders). The antisense
CC oligonucleotides may also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents an
CC antisense oligonucleotide of the invention that is targeted to human CDC-
CC like kinase 1. NOTE: The present sequence is a 2'-O-methoxyethyl gapmer
CC with a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 220 CATTGCCAAAAGAGTCACC 238
Db 2 CGTTCCAGAGAGTCACC 20

RESULT 316
ADH58791/C
ID ADH58791 standard; DNA; 20 BP.
XX
AC ADH58791;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDC-like kinase 1 antisense oligonucleotide #73.
XX
KW antisense oligonucleotide; CDC-like kinase 1; cancer;
KW autoimmune disorder; infection; inflammation; tumour formation; human;
KW ss; 2'-O-methoxyethyl gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN US2003219895-A1.
XX
PD 27-NOV-2003.
XX
PF 22-MAY-2002; 2002US-00154708.
XX
PR 22-MAY-2002; 2002US-00154708.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Watt AT;
XX
DR WPI; 2004-051714/05.
XX
PT New antisense oligonucleotides targeted to nucleic acid molecules
PT encoding CDC-like kinase 1, useful for treating diseases or conditions
PT associated with expression of CDC-like kinase 1, e.g. cancers or
PT autoimmune disorders.
XX
PS Claim 1; SEQ ID NO 86; 64pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC CDC-like kinase 1. The antisense oligonucleotides of the invention are
CC useful for modulating the expression of CDC-like kinase 1, and for
CC treating diseases or conditions associated with expression of CDC-like
CC kinase 1 (e.g. cancers and autoimmune disorders). The antisense
CC oligonucleotides may also be used to prevent or delay infection,
CC inflammation and tumour formation. The present DNA sequence represents an
CC antisense oligonucleotide of the invention that is targeted to human CDC-
CC like kinase 1. NOTE: The present sequence is a 2'-O-methoxyethyl gapmer
CC with a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 220 CATTGCCAAAAGAGTCACC 238
Db 19 CGTTTCCAGAAGAGTCACC 1

RESULT 317
ADH65127
ID ADH65127 standard; DNA; 20 BP.
XX
AC ADH65127;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #1961.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 1961; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity, The
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 11 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 198 CCATCTCCCCCATCCCCCA 216
Db 1 CCATCTCCCTCTTCCCCCTA 19

RESULT 318
ADH65989/c
ID ADH65989 standard; DNA; 20 BP.
XX
AC ADH65989;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #2823.

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 2823; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity, The
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1075 ACCACTTAACCTCTCTGGG 1093
Db 20 ACAACTTGACTTCTCTGGG 2

RESULT 319
ADH65276/c
ID ADH65276 standard; DNA; 20 BP.
XX
AC ADH65276;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #2110.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.

XX (PHAA) PHARMACIA CORP.
PA
XX Crosby SD, Nalseth AE;
PI
XX WPI; 2004-035034/03.
DR
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 2110; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity. The
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1075 ACCACTTAACCTCTCTGGG 1093
Db 19 ACAACTTGACTTCTCTGGG 1

RESULT 320
ADH64643
ID ADH64643 standard; DNA; 20 BP.
XX
AC ADH64643;
XX
XX 25-MAR-2004 (first entry)
XX Human glucocorticoid receptor-specific antisense oligonucleotide #1477.
DE
XX antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
XX WO2003099215-A2.
PN
XX
AC
XX 04-DEC-2003.
PD
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
XX 20-MAY-2002; 2002US-0381857P.
XX
XX (PHAA) PHARMACIA CORP.
PA
XX Crosby SD, Nalseth AE;
PI
XX WPI; 2004-035034/03.
DR
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 1477; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The

CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity. The
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCCCATCCCC 214
Db 1 CTCCATCTCCCTCTTCCCC 19

RESULT 321
ADH65757
ID ADH65757 standard; DNA; 20 BP.
XX
AC ADH65757;
XX
XX 25-MAR-2004 (first entry)
XX Human glucocorticoid receptor-specific antisense oligonucleotide #2591.
DE
XX antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
XX WO2003099215-A2.
PN
XX
XX 04-DEC-2003.
PD
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
XX 20-MAY-2002; 2002US-0381857P.
XX
XX (PHAA) PHARMACIA CORP.
PA
XX Crosby SD, Nalseth AE;
PI
XX WPI; 2004-035034/03.
DR
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 2591; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity.
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 11 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 198 CCATCTCCCCCATCCCCCA 216

PF 02-JUL-2002; 2002US-00190366.
XX
PR 02-JUL-2002; 2002US-00190366.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Freier SM, Dobie KW;
XX
XX WPI; 2004-081743/08.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding HMG-CoA reductase, useful for treating
PT atherosclerosis, or a disease involving cholesterol metabolism or
PT angiogenesis.
XX
PS Example 16; SEQ ID NO 308; 110pp; English.
XX
CC The invention relates to novel compounds of 8-80 nucleobases in length
CC targeted to, and which specifically hybridises with, a nucleic acid
CC molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
CC reductase, and inhibits the expression of HMG-CoA reductase. The novel
CC compounds have cardiant, antiarteriosclerotic, and antilipaemic
CC activities. The compound can be used to treat disorders by antisense gene
CC therapy. The compounds, compositions and methods are useful for treating
CC a disease or condition associated with HMG-CoA reductase, such as a
CC cardiovascular disorder e.g. atherosclerosis, or a disease or condition
CC involving cholesterol metabolism. They are also useful in research and
CC diagnostics for modulating the expression of HMG-CoA reductase. This
CC polynucleotide sequence represents an antisense oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 95 GCATTATCCTTCAGTGGG 113
Db 2 GCATTATTCCTCAGAAGG 20

RESULT 325
ADI44833
ID ADI44833 standard; DNA; 20 BP.
XX
AC ADI44833;
XX
DT 22-APR-2004 (first entry)
XX
DE Human cystic fibrosis CFTR 1-related PCR primer SeqID333.
XX
KW genetic marker;
KW human cystic fibrosis transmembrane conductance regulator; CFTR;
KW PCR assay; cystic fibrosis; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003235834-A1.
XX
PD 25-DEC-2003.
XX
PF 19-NOV-2002; 2002US-00300683.
XX
PR 12-NOV-1999; 99US-0165301P.
PR 03-NOV-2000; 2000WO-US030493.
PR 08-MAY-2001; 2001US-00851501.
PR 19-NOV-2001; 2001US-0333531P.
PR 08-MAY-2002; 2002US-00142722.
XX
PA (DUNL/) DUNLOP C I M.
PA (WEIS/) WEISEL J M.
XX

PI Dunlop CLM, Weisel JM;
XX
DR WPI; 2004-070574/07.
XX
PT Identifying the presence or absence of a genetic marker in the human
PT cystic fibrosis transmembrane conductance regulator gene of a subject by
PT contacting the DNA and primer set and separating the extension product.
XX
PS Claim 1; SEQ ID NO 333; 154pp; English.
XX
CC This invention relates to a novel method of identifying the presence or
CC absence of a genetic marker in the human cystic fibrosis transmembrane
CC conductance regulator (CFTR) gene of a subject using a PCR assay. The
CC method comprises providing a DNA sample from the subject, providing at
CC least one primer set given in the specification, contacting the DNA and
CC the primer set, generating an extension product from the at least one
CC primer set that comprises a region of DNA that includes the location of
CC the genetic marker, separating the extension product on the basis of
CC melting behaviour and identifying the presence or absence of the genetic
CC marker in the subject by analysing the melting behaviour of the extension
CC product. The present sequence is that of a PCR primer which was used in
CC the exemplification of the invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 670 CTCAAATTATGTTACTTGT 688
Db 1 CTCATACTTTGTTACTTGT 19

RESULT 326
ADJ61611/c
ID ADJ61611 standard; DNA; 20 BP.
XX
AC ADJ61611;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to IL5R-X61176 #303.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-203534/19.
DR
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 2467; 85pp; English.

XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 676 TTATGTTACTGTTGGCT 694
DB 20 TAAAGTTACTGGTTGGCT 2

RESULT 327
ADJ61203
ID ADJ61203 standard; DNA; 20 BP.
XX
AC ADJ61203;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to PDE4C #269.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 2059; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the

CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 191 TTCCACGCCCATCTCCCCCA 209
DB 1 TTGGAGGCCATCTCCCCCA 19

RESULT 328
ADJ19254
ID ADJ19254 standard; DNA; 20 BP.
XX
AC ADJ19254;
XX
DT 20-MAY-2004 (first entry)
XX
DE Antisense 2-MOE gapmer oligo targeted to human Itgb5 - SEQ ID 69.
XX
KW integrin beta 5; Itgb5; cytostatic; antiinflammatory; antimicrobial;
KW antisense; gene therapy; hyperproliferative; cancer; inflammation;
KW infection; 2-MOE wing; 2'-methoxyethyl gapmer; ss; human;
KW phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN US2004005707-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00188470.
XX
PR 02-JUL-2002; 2002US-00188470.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cooper S, Dobie KW;
XX
DR WPI; 2004-081731/08.
XX
PT New antisense compounds targeted to nucleic acid molecules encoding
PT integrin beta 5, useful for treating diseases associated with expression
PT of integrin beta 5, e.g. hyperproliferative disorder, infection or
PT inflammation.
XX
PS Example 15; SEQ ID NO 69; 105pp; English.
XX
CC The invention relates to a novel compound 8-80 nucleobases in length
CC targeted to a nucleic acid molecule encoding integrin beta 5 (Itgb5). The
CC compound specifically hybridises with the nucleic acid molecule encoding
CC integrin beta 5, thus inhibiting the expression of integrin beta 5. The
CC compound of the invention demonstrates cytostatic, antiinflammatory and
CC antimicrobial activities and may be useful for inhibiting the expression
CC of integrin beta 5, via antisense gene therapy and thus for treating
CC diseases associated with expression of integrin beta 5, including
CC hyperproliferative disorders such as cancer, inflammation or infection.
CC The current sequence is that of an antisense 2-MOE (2'-methoxyethyl)
CC gapmer oligo targeted to human Itgb5 of the invention. The

CC oligonucleotide has central "gap" region flanked on both sides by 2-MOE
CC "wings". The backbone linkages are phosphorothioate and all cytidine
CC residues are 5-methylcytidines.
XX
SQ Sequence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1029 GAGAGTAAACATCACACC 1047
Db 1 GAGAGGAAACATCAGTCC 19

RESULT 329
ADJ18790
ID ADJ18790 standard; DNA; 20 BP.
XX
AC ADJ18790;
XX
DT 20-MAY-2004 (first entry)
XX
DE Antisense DNA oligo used to modulate human LRH1 expression SeqID 3340.
XX
KW human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
KW gall stone; triglyceridaemia; obesity; hepatitis;
KW hepatocellular carcinoma; aromatase; cytostatic; antilipaemic;
KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;
KW antiinflammatory; virucidal.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /label= OTHER= phosphorothioate backbone
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT cytidine nucleobases are 5-methylcytidine."
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT cytidine nucleobases are 5-methylcytidine."
XX
PN WO2004003201-A2.
XX
PD 08-JAN-2004.
XX
PF 01-JUL-2003; 2003WO-US020865.
XX
PR 01-JUL-2002; 2002US-0392813P.
XX
XX (PHAA) PHARMACIA CORP.
XX Kane CD;
XX
XX WPI; 2004-083058/08.
DR
XX New antisense oligonucleotides targeted to a nucleic acid encoding liver
PT related homologue-1 (LRH1), useful for treating breast cancer,
PT dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
XX
PS Example 15; SEQ ID NO 3340; 909pp; English.
XX
CC This invention relates to novel antisense compounds useful for modulating

CC the expression of liver related homologue-1 (LRH1) and splice variants
CC thereof. Specifically, it refers to compositions 8-30 nucleobases in
CC length that target a portion of an active site on the nucleic acid
CC molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan
CC nuclear receptor protein that functions as a tissue specific
CC transcription factor. The present invention describes antisense
CC oligonucleotides that comprise at least one modified internucleoside
CC linkage, a phosphorothioate linkage; at least one modified sugar moiety,
CC a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-
CC methylcytidine. These antisense compounds are useful for treating or
CC diagnosing a disease associated with LRH1, such as breast cancer,
CC dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high
CC LDL (low density lipoprotein), hypercholesterolaemia, gall stones,
CC triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic
CC hepatitis, as well as hepatocellular carcinoma or a condition associated
CC with aromatase activity. Accordingly, these compositions exhibit
CC cytostatic, antilipaemic, antiarteriosclerotic, anorectic, hepatotropic,
CC litholytic, antiinflammatory and virucidal activities. This
CC oligonucleotide sequence is an antisense DNA oligo used to modulate the
CC expression of the human LRH1 protein of the invention.
XX
SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 433 AAGAGGAGATGATTTTAGC 451
Db 2 AATAGGCCATGATTTTAGC 20

RESULT 330
ADJ18263
ID ADJ18263 standard; DNA; 20 BP.
XX
AC ADJ18263;
XX
DT 20-MAY-2004 (first entry)
XX
DE Antisense DNA oligo used to modulate human LRH1 expression SeqID 2813.
XX
KW human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
KW gall stone; triglyceridaemia; obesity; hepatitis;
KW hepatocellular carcinoma; aromatase; cytostatic; antilipaemic;
KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;
KW antiinflammatory; virucidal.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /label= OTHER= phosphorothioate backbone
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT cytidine nucleobases are 5-methylcytidine."
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT cytidine nucleobases are 5-methylcytidine."
XX
PN WO2004003201-A2.
XX
PD 08-JAN-2004.
XX

XX DE Antisense DNA oligo used to modulate human LRH1 expression SeqID 2516.

XX KW human; ss; liver related homologue-1; LRH1; NR5A2; antisense;

KW phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;

KW low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;

KW gall stone; triglyceridaemia; obesity; hepatitis;

KW hepatocellular carcinoma; aromatase; cytostatic; antilipaemic;

KW antiarteriosclerotic; anorectic; hepatotropic; litholytic;

KW antiinflammatory; virucidal.

XX OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

PH modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /label= OTHER= phosphorothioate backbone

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All

FT cytidine nucleobases are 5-methylcytidine."

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All

FT cytidine nucleobases are 5-methylcytidine."

XX WO2004003201-A2.

PN 08-JAN-2004.

XX 01-JUL-2003; 2003WO-US020865.

XX 01-JUL-2002; 2002US-0392813P.

XX (PHAA) PHARMACIA CORP.

PA Kane CD;

PI WPI; 2004-083058/08.

XX New antisense oligonucleotides targeted to a nucleic acid encoding liver

PT related homologue-1 (LRH1), useful for treating breast cancer,

PT dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.

XX Example 15; SEQ ID NO 2516; 909pp; English.

PS This invention relates to novel antisense compounds useful for modulating

XX the expression of liver related homologue-1 (LRH1) and splice variants

CC thereof. Specifically, it refers to compositions 8-30 nucleobases in

CC length that target a portion of an active site on the nucleic acid

CC molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan

CC nuclear receptor protein that functions as a tissue specific

CC transcription factor. The present invention describes antisense

CC oligonucleotides that comprise at least one modified internucleoside

CC linkage, a phosphorothioate linkage; at least one modified sugar moiety,

CC a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-

CC methylcytidine. These antisense compounds are useful for treating or

CC diagnosing a disease associated with LRH1, such as breast cancer,

CC dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high

CC LDL (low density lipoprotein), hypercholesterolaemia, gall stones,

CC triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic

CC hepatitis, as well as hepatocellular carcinoma or a condition associated

CC with aromatase activity. Accordingly, these compositions exhibit

CC cytostatic, antilipaemic, antiarteriosclerotic, anorectic, hepatotropic,

CC litholytic, antiinflammatory and virucidal activities. This

CC oligonucleotide sequence is an antisense DNA oligo used to modulate the

CC expression of the human LRH1 protein of the invention.

XX Sequence 20 BP; 6 A; 4 C; 1 G; 9 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 391 AGTCATTTTCCTTACAATT 409

Db ||||||| ||||| |||

1 AGTCATTTTCCTTAATATT 19

RESULT 333

ADJ24119/c

ID ADJ24119 standard; DNA; 20 BP.

XX

AC ADJ24119;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2517.

XX

KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;

KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;

KW cardiovascular disorder; metabolic syndrome X; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "This oligonucleotide has a phosphorothioate

FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'

FT and 3' ends, which are 4 nucleotides in length. Also all

FT cytidine residues are 5-methylcytidines"

XX WO2004009541-A2.

PN 29-JAN-2004.

XX

XX 18-JUL-2003; 2003WO-US022410.

PF

XX 19-JUL-2002; 2002US-0397106P.

PR

XX (PHAA) PHARMACIA CORP.

PA

XX Bhat BG;

PI

XX WPI; 2004-132912/13.

DR

XX New antisense oligonucleotide for modulating endothelial lipase

PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low

PT high density lipoprotein or cardiovascular disorders.

XX Claim 3; SEQ ID NO 2517; 1007pp; English.

PS The present invention relates to antisense oligonucleotides (ADJ21603-

XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence

CC (ADJ25517), where the antisense oligonucleotide specifically hybridises

CC with and inhibits the expression of EL. The antisense oligonucleotides

CC are useful for modulating the expression of endothelial lipase in cells

CC or tissues to treat diseases associated with EL expression, such as

CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular

CC disorder or metabolic syndrome X. In addition, the oligonucleotides are

CC used for diagnostics, prophylaxis, or as research reagents or kits.

XX Sequence 20 BP; 12 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 315 TTGGATTTCCTGTATTCT 333

Db ||||| ||||| || |||||
19 TTGGCTTTCCTATTCT 1

RESULT 334
ADJ241136
ID ADJ241136 standard; DNA; 20 BP.
XX
AC ADJ241136;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2534.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2-'methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PT Bhat BG;
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 2534; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 867 GTAGTCCATGCTATTAAAA 885
DB 1 GTAGCCAATGCTATTACAA 19

RESULT 335
ADJ24120/c

ID ADJ24120 standard; DNA; 20 BP.
XX
AC ADJ24120;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human endothelial lipase antisense oligonucleotide, SEQ ID 2518.
XX
KW Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW Cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2-'methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-US022410.
XX
PR 19-JUL-2002; 2002US-0397106P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PT Bhat BG;
XX
DR WPI; 2004-132912/13.
XX
PT New antisense oligonucleotide for modulating endothelial lipase
PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT high density lipoprotein or cardiovascular disorders.
XX
PS Claim 3; SEQ ID NO 2518; 1007pp; English.
XX
CC The present invention relates to antisense oligonucleotides (ADJ21603-
CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC with and inhibits the expression of EL. The antisense oligonucleotides
CC are useful for modulating the expression of endothelial lipase in cells
CC or tissues to treat diseases associated with EL expression, such as
CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ Sequence 20 BP; 12 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 315 TTGGATTTCTGTTATCT 333
DB 20 TTGGCTTTCCTATTCT 2

RESULT 336
ADK80500
ID ADK80500 standard; DNA; 20 BP.
XX
AC ADK80500;
XX
DT 20-MAY-2004 (first entry)
XX

DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #7834.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;

KW diabetic neuropathy; arthritic pain; migraine headache;

KW infantile epilepsy; ataxia; ss.

XX Synthetic.

OS

XX WO2004016754-A2.

PN

XX 26-FEB-2004.

PD

XX 14-AUG-2003; 2003WO-US025465.

PF

XX 14-AUG-2002; 2002US-0403416P.

PR

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

PI WPI; 2004-203785/19.

XX

XX New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.

PT

PT Claim 4; SEQ ID NO 7834; 417pp; English.

PS

XX The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target different regions of the human Nav1.3 RNA.

CC

XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1062 TTCCAGTGGCTAAACCACT 1080

Db ||||| ||| |||||

2 TTCCAGTACCTACACCACT 20

RESULT 337

ADK80983

ID ADK80983 standard; DNA; 20 BP.

XX

AC ADK80983;

XX

XX 20-MAY-2004 (first entry)

DT

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8317.

DE

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;

KW diabetic neuropathy; arthritic pain; migraine headache;

KW infantile epilepsy; ataxia; ss.

XX

OS Synthetic.

OS

XX WO2004016754-A2.

PN

XX

PD 26-FEB-2004.

XX

PF 14-AUG-2003; 2003WO-US025465.

XX

PR 14-AUG-2002; 2002US-0403416P.

XX

PA (PHAA) PHARMACIA CORP.

XX Roberds SL;

PI WPI; 2004-203785/19.

XX

DR

XX New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.

PT

PT Claim 4; SEQ ID NO 8317; 417pp; English.

PS

XX The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target different regions of the human Nav1.3 RNA.

CC

XX Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1062 TTCCAGTGGCTAAACCACT 1080

Db ||||| ||| |||||

1 TTCCAGTACCTACACCACT 19

RESULT 338

ADL97965/c

ID ADL97965 standard; DNA; 20 BP.

XX

AC ADL97965;

XX

XX 17-JUN-2004 (first entry)

DT

XX Msx2 probe, SEQ ID 4.

DE

XX Osteopathic; calvarial osteoblast differentiation;

KW osteoblast differentiation; calvarial osteoblast mineralization;

KW osteoblast mineralization; NELL-1; bone fracture repair; bone density;

KW Msx2; probe; ss.

XX

OS Synthetic.

OS

XX WO2004024893-A2.

PN

XX 25-MAR-2004.

PD

XX 15-SEP-2003; 2003WO-US029281.

PF

XX 13-SEP-2002; 2002US-0410846P.

PR

XX (UYCA-) UNIV CALIFORNIA LOS ANGELES.

PA

XX Kang T;

PI

XX WPI; 2004-329478/30.
XX
PT Modulating calvarial osteoblast differentiation and mineralization,
PT useful for facilitating repair of bone fractures and/or to generally
PT increase bone density, comprises altering expression or activity of Nell-
PT 1.
XX
PS Example 2; Page 54; 85pp; English.
XX
CC The present invention relates to a method for modulating calvarial
CC osteoblast differentiation and mineralization. The method comprises
CC altering expression or activity of NELL-1, where the increased expression
CC or activity of NELL-1 increases osteoblast differentiation or
CC mineralization and decreased expression or activity of NELL-1 decreases
CC osteoblast differentiation or mineralization. The methods and NELL-1 gene
CC are useful for facilitating repair of bone fractures and/or to generally
CC increase bone density. The present sequence is a PCR primer, used to
CC illustrate the invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 697 TCATGTAGTCACGGTGCTC 715
Db 19 TCCTGTATCCACGGTGCTC 1

RESULT 339
ADO46593
ID ADO46593 standard; DNA; 20 BP.
XX
AC ADO46593;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #1959.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
PN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
PF 25-JUL-2003; 2003US-00627930.
XX
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;

XX WPI; 2004-293804/27.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Claim 2; SEQ ID NO 2059; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 191 TTCCACGCCATCTCCCCCA 209
Db 1 TTGGAGGCCATCTCCCCCA 19

RESULT 340
ADO47001/c
ID ADO47001 standard; DNA; 20 BP.
XX
AC ADO47001;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #2367.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
PN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
PF 25-JUL-2003; 2003US-00627930.


```
XX 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-293804/27.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Claim 2; SEQ ID NO 2467; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 676 TTATGTTACTGTTGGCT 694
DB 20 TAAAGTTACTGTTGGCT 2

RESULT 341
ADP12146/C
ID ADP12146 standard; DNA; 20 BP.
XX
AC ADP12146;
XX
DT 12-AUG-2004 (first entry)
XX
DE Tagman probe set 2 #4.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.
```

```
XX Homo sapiens.
OS
XX WO2004042346-A2.
PN
XX 21-MAY-2004.
PD
XX 24-APR-2003; 2003WO-US012946.
XX
PF 24-APR-2002; 2002US-00131831.
XX
PR 20-DEC-2002; 2002US-00325899.
PR
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 58; SEQ ID NO 2155; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC probe for a 50 mer oligonucleotide marker for diagnosis and monitoring of
CC allograft rejection and other disorders.
XX
SQ Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. NO. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 363 CCTGCGGCCTTGTGTGGC 381
DB 20 CCTGGGGCATTGTGCTGGC 2

RESULT 342
ADP68640/C
ID ADP68640 standard; DNA; 20 BP.
XX
AC ADP68640;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human PPAR-alpha antisense oligonucleotide seqid 76.
XX
KW cytostatic; gene therapy; PPAR-alpha;
KW peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator;
KW PPAR-alpha associated disorder; hyperproliferative disorder; human;
KW antisense oligonucleotide; antisense technology; ss.
XX
OS Homo sapiens.
XX
PN US2004115637-A1.
XX
PD 17-JUN-2004.
XX
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PF 11-DEC-2002; 2002US-00317500.
XX
PR 11-DEC-2002; 2002US-00317500.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Mckay R, Dobie KW;
XX
DR WPI; 2004-449378/42.
XX
PT New oligonucleotide compound that inhibits expression of PPAR-alpha,
PT useful for preparing a composition for treating hyperproliferative
PT disorders, e.g. cancer.
XX
PS Example 15; SEQ ID NO 76; 121pp; English.
XX
CC The invention describes a compound, having a sequence comprising 8-80 bp
CC targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-
CC activated receptor-alpha), that specifically hybridises with the nucleic
CC acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits
CC expression of PPAR-alpha. Also described are: a method of inhibiting the
CC expression of PPAR-alpha in cells or tissues; a method of screening for a
CC modulator of PPAR-alpha; a diagnostic method for identifying a disease
CC state; a kit or assay device comprising the compound; and a method of
CC treating an animal having a disease or condition associated with PPAR-
CC alpha. The oligonucleotide compound is useful for preparing a composition
CC for treating hyperproliferative disorder e.g. cancer. This sequence
CC represents a human peroxisome proliferator-activated receptor-alpha (PPAR
CC -alpha) antisense oligonucleotide.
XX
SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 266 TGTCGGGAACGGCATATT 284
DB ||||| ||||| ||||| ||||| |||||
20 TGTAGGTAACGGCATATT 2

RESULT 343
ADR27036
ID ADR27036 standard; DNA; 20 BP.
XX
AC ADR27036;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human single nucleotide polymorphism detection primer #126.
XX
KW ss; primer; single nucleotide polymorphism; SNP; diagnosis;
KW disease association; linkage analysis; autoimmune disease;
KW rheumatoid arthritis; diabetes; multiple sclerosis;
KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
KW glomerulonephritis; Graves' disease; myocarditis; Sjogren disease;
KW primary systemic vasculitis; genotyping; gene therapy; PCR primer.
XX
OS Homo sapiens.
XX
PN WO2004067779-A2.
XX
PD 12-AUG-2004.
XX
PF 30-JAN-2004; 2004WO-US002652.
XX
PR 30-JAN-2003; 2003US-0443566P.
PR 18-MAR-2003; 2003US-0455444P.
PR 25-APR-2003; 2003US-0465241P.
PR 15-AUG-2003; 2003US-0495115P.
PR 13-NOV-2003; 2003US-0519270P.
XX

PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Begovich AB, Carlton VE, Schrodi SJ, Alexander HC;
XX
DR WPI; 2004-594223/57.
XX
PT New single nucleotide polymorphisms (SNPs) associated with rheumatoid
PT arthritis (RA), useful in identification of individuals at risk of
PT developing RA or other autoimmune disease, and in development of
PT therapeutic agents.
XX
PS Claim 21; SEQ ID NO 49708; 141pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising at
CC least 8 contiguous nucleotides where one of the nucleotides is a single
CC nucleotide polymorphism (SNP) selected from any one of the nucleotide
CC sequences of SEQ ID NOS:1-669 and 1339-49582, or their complements. The
CC SNPs are useful as targets for the design of diagnostic reagents and the
CC development of therapeutic agents, as well as for disease association and
CC linkage analysis. In particular, the SNPs are useful for identifying an
CC individual who is at an increased or decreased risk for developing an
CC autoimmune disease such as rheumatoid arthritis, type 1 diabetes,
CC multiple sclerosis, systemic lupus erythematosus, inflammatory bowel
CC diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia,
CC asthma, vitiligo, glomerulonephritis, Graves' disease, myocarditis,
CC Sjogren disease, or primary systemic vasculitis. Methods associated with
CC the SNPs are useful for early detection of the disease, for providing
CC clinically important information for the prevention and/or treatment of
CC the autoimmune diseases particularly rheumatoid arthritis, and for
CC screening and selecting therapeutic agents. The SNPs are useful for human
CC identification applications. The genes containing the SNPs are useful for
CC treating the diseases defined above. The nucleic acid molecules are
CC useful as hybridization probes for genotyping SNPs in messenger RNA,
CC cDNA, genomic DNA, and genomic clones. The nucleic acid molecules are
CC useful for constructing host cells expressing a part or all of the
CC nucleic acid molecules and variant peptides, for constructing transgenic
CC animals, for assaying or screening drugs that modulate nucleic acid
CC expression, or for gene therapy in patients whose cells have aberrant
CC gene expression. This sequence corresponds to a PCR primer which
CC hybridises to the nucleic acids of the invention to amplify the SNP
CC containing region. (Note: SEQ ID NOS 1-49582 are claimed and stated as
CC being provided in the specification, however these sequences are not
CC provided in the printed specification).
XX
SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1046 CCCAACTTCCTTATCTTTC 1064
DB ||||| ||||| ||||| ||||| |||||
1 CCCAACATCCTCATCTGTC 19

RESULT 344
ADR17228/c
ID ADR17228 standard; DNA; 20 BP.
XX
AC ADR17228;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human chromosome 11 Zmax1 region reverse mapping primer #122.
XX
KW Human; high bone mass; Zmax1; ss; primer; HBM; osteoporosis; osteopathic;
KW LDL receptor; bone development; metabolic bone disease; PCR.
XX
OS Homo sapiens.
XX
PN US6780609-B1.
XX
PD 24-AUG-2004.

XX PF 05-APR-2000; 2000US-00543771.
XX PR 13-JAN-1998; 98US-0071449P.
PR 23-OCT-1998; 98US-0105511P.
PR 13-JAN-1999; 99US-00229319.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2004-623529/60.
XX New high bone mass gene of chromosome 1.1Q13.3, encoding protein useful
PT for treating, diagnosing, preventing, or screening for normal and
PT abnormal conditions of bone, including metabolic bone diseases, e.g.
PT osteoporosis.
XX Disclosure; SEQ ID NO 310; 284pp; English.
PS The invention relates to an isolated amino acid protein sequence selected
XX from an amino acid sequence appearing as ADR16922 or an amino acid
CC sequence comprising or consisting of the extracellular domain of
CC ADR16922(amino acids 23-1385). ADR16922 is encoded by the HBM (high bone
CC mass) allele of the human Zmax1 gene and has sequence similarity to LDL
CC receptors. Also disclosed are nucleic acids, proteins, cloning vectors,
CC expression vectors, transformed hosts, methods of developing
CC pharmaceutical compositions, methods of identifying molecules involved in
CC bone development, and methods of diagnosing and treating diseases
CC involved in bone development. Specifically disclosed is the Zmax1 gene
CC and the high bone mass (HBM) allele on chromosome 11q13.3 encoding
CC ADR16922. The protein is useful for treating, diagnosing, preventing, or
CC screening for normal and abnormal conditions of bone, including metabolic
CC bone diseases, e.g. osteoporosis. The present sequence is a PCR primer
CC used in the mapping of the Zmax1/HBM gene.
XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 882 AAAAGTGTGGCCACAGAC 900
Db 19 AATATTGTGGCCACACAC 1
RESULT 345
ADK67431
ID ADK67431 standard; DNA; 20 BP.
XX
AC ADK67431;
XX 18-NOV-2004 (first entry)
DT PCR primer used to amplify human ABCG2 DNA - SEQ ID 61.
XX
DE drug absorption; ABCG2; ATP-binding cassette gene; human;
KW chromosome 4q22; ss; PCR; primer.
XX
OS Homo sapiens.
XX JP2004016042-A.
PN 22-JAN-2004.
XX
PD 13-JUN-2002; 2002JP-00172759.
XX
PF 13-JUN-2002; 2002JP-00172759.
XX
PR 13-JUN-2002; 2002JP-00172759.
XX
XX (KOKU-) KOKURITSU IYAKUJIN SHOKUJIN EISEI KENKYU.
PA (IYAK-) IYAKUJIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
XX

DR WPI; 2004-113852/12.
XX Novel ABCG2 polynucleotide having a mutation at a specific position,
PT useful for gene diagnosis of abnormality of medicine absorption
PT associated with ABCG2 protein.
XX Example 1; SEQ ID NO 61; 53pp; Japanese.
PS The invention relates to a novel polynucleotide having a mutation in the
XX codon encoding a glutamine residue present at the 126 position of a 655
CC amino acid sequence. The polynucleotide of the invention may be useful
CC for the estimation or diagnosis of a condition which is associated with
CC abnormal drug absorption and in which the ABCG2 (ATP-binding cassette
CC gene) protein is associated. The current sequence is that of a PCR primr
CC which was used to amplify the human ABCG2 DNA of the invention.
XX
SQ Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 432 GAAGAGGAGATGATTTTAG 450
Db 2 GCAGAGGAGAGAGTTTAG 20
RESULT 346
ADR47879/c
ID ADR47879 standard; DNA; 20 BP.
XX
AC ADR47879;
XX 02-DEC-2004 (first entry)
DT Human chromosome 11 Zmax1 region reverse mapping primer #122.
XX
DE Human; ss; PCR; high bone mass; Zmax1; HBM; bone modulation;
KW bone development disorder; osteoporosis; chromosome 11; gene therapy;
KW primer.
XX Homo sapiens.
OS US2004176582-A1.
XX 09-SEP-2004.
PD 10-DEC-2003; 2003US-00731739.
PF 13-JAN-1998; 98US-0071449P.
XX 23-OCT-1998; 98US-0105511P.
PR 13-JAN-1999; 99US-00229319.
PR 05-APR-2000; 2000US-00544398.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
XX Carulli JP, Little RD, Recker RR, Johnson ML;
PI WPI; 2004-661408/64.
XX New nucleic acid sequence encoding high bone mass, useful in diagnosing,
XX treating and/or preventing osteoporosis.
PT Disclosure; SEQ ID NO 310; 303pp; English.
PS The invention relates to an isolated nucleic acid sequence encoding a
XX high bone mass protein (HBM). The gene exists in two alleles, Zmax1, the
CC notional wild-type (the cDNA for which appears as ADR47570 encoding
CC ADR47572) and the HBM allele (the cDNA for which appears as ADR47571
CC encoding ADR47573). The two alleles differ by a single nucleotide
CC polymorphism (G to T at position 582 of ADR47570) causing a Gly to Val
CC change at position 171 of the protein. Also included are a replicative

CC cloning vector comprising HBM/Zmax1 (and a replicon operative in an
CC isolated host cell), an expression vector comprising HBM/Zmax1 operably
CC linked to a transcription regulatory region, an isolated host cell
CC transformed with the vector(s), a method for testing a substance as a
CC therapeutic agent for bone modulation in a host, a method of identifying
CC a molecule involved in bone modulation, a method for identifying a
CC (candidate) protein involved in bone modulation, a method of testing for
CC HBM activity, a method of developing a pharmaceutical for the treatment
CC of bone development disorders, a method for treating a bone development
CC disorder in an animal, a method of altering bone development in a host, a
CC method for diagnostic screening for a genetic predisposition to a bone
CC development disorder, a diagnostic assay for bone development disorders,
CC a method of expressing the HBM protein in bone tissue, a bacterial
CC artificial chromosome comprising HBM/Zmax1 sequence (appearing as
CC ADR47574-ADR47580), a method for amplifying a nucleotide polymorphism in
CC the Zmax1 or HBM gene, a method for identifying a regulatory element of a
CC HBM gene and an isolated nucleic acid segment of at least 15 contiguous
CC nucleotides including a polymorphic site from HBM/Zmax1. The nucleic acid
CC molecule and the encoded polypeptide, composition, and methods are useful
CC in diagnosing, treating and preventing a bone development disorder, i.e.
CC osteoporosis. The gene for HBM/Zmax1 is located on chromosome 11q13.3.
CC The present sequence is a primer used in the mapping of the HBM/Zmax1
CC gene.
XX

SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 882 AAAAGTGTGGCCACAGAC 900
Db 19 AATATTGTGGCCACAC 1

RESULT 347
ADS31697

ID ADS31697 standard; DNA; 20 BP.

XX
AC ADS31697;

XX
DT 02-DEC-2004 (first entry)

DE Gene expression inhibition method erBB2 gene PCR primer #8.

XX
KW cytosstatic; gene promoter methylation inducer; cell growth inhibitor;
KW erBB2 gene expression inhibitor; DNA methylation inducer; dsRNA; CpG;
KW human; gene expression; erBB2; tumour; gene transcription; promoter;
KW small interfering RNA; siRNA; gene silencing; ss; primer.

OS Homo sapiens.
OS Synthetic.

PN WO2004076663-A1.

XX
PD 10-SEP-2004.

XX
PF 27-FEB-2004; 2004WO-JP002448.

XX
PR 27-FEB-2003; 2003US-0449860P.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX
PI Taira K, Kawasaki H;

XX
DR WPI; 2004-662014/64.

XX
PT Novel DNA methylation inducer containing double-stranded RNA targeting
PT region having CpG on DNA in mammalian cell, useful in suppressing gene
PT expression, and as cell growth inhibitor.

XX
PS Example 4; SEQ ID NO 58; 98pp; Japanese.

XX

CC The invention relates to a DNA methylation inducer (I) containing double-
CC stranded (ds)RNA that targets the region which contains CpG or CpNG (N is
CC A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having
CC DNA that codes dsRNA that targets the region which contains CpG or CpNG
CC on DNA in mammalian cell. (I) is useful in the DNA methylation process,
CC which involves introducing (I) in a mammalian cell, where the mammalian
CC cell is obtained from human. (I) is useful as gene expression inhibitor
CC or cell growth inhibitor. A gene expression inhibitor (II) is useful for
CC suppressing gene expression, where the gene is a disease related gene
CC relevant to a disease, and the expression of the gene causes the disease.
CC The gene is erBB2 and the disease is the tumour. (I) is useful for
CC controlling various biological activities in a mammal by controlling the
CC transcription level of the respective gene by methylating the respective
CC DNA. (I) or (II) enables specific methylation of the CpG island-
CC containing domain on a gene promoter of the target gene, where the
CC methylation of a promoter suppresses the expression of the target gene.
CC (I) induces sequence specific DNA methylation in a plant, and controls
CC the expression of the specific gene at the transcription level. (I)
CC enables DNA methylation in the promoter region of a gene, where the
CC methylation changes the structure of the DNA, enabling suppression of the
CC gene expression at the transcription level (DNA to mRNA). This sequence
CC corresponds to an erBB2 gene PCR primer used in the method to silence
CC gene expression in cells.
XX

SQ Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 AGCCCGGGTGGATCCCTC 858
Db 2 AGCCTGGGTGCGTCCCTC 20

RESULT 348
ADS31698/C

ID ADS31698 standard; DNA; 20 BP.

XX
AC ADS31698;

XX
DT 02-DEC-2004 (first entry)

DE Gene expression inhibition method erBB2 gene PCR primer #9.

XX
KW cytosstatic; gene promoter methylation inducer; cell growth inhibitor;
KW erBB2 gene expression inhibitor; DNA methylation inducer; dsRNA; CpG;
KW human; gene expression; erBB2; tumour; gene transcription; promoter;
KW small interfering RNA; siRNA; gene silencing; ss; primer.

OS Homo sapiens.
OS Synthetic.

PN WO2004076663-A1.

XX
PD 10-SEP-2004.

XX
PF 27-FEB-2004; 2004WO-JP002448.

XX
PR 27-FEB-2003; 2003US-0449860P.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX
PI Taira K, Kawasaki H;

XX
DR WPI; 2004-662014/64.

XX
PT Novel DNA methylation inducer containing double-stranded RNA targeting
PT region having CpG on DNA in mammalian cell, useful in suppressing gene
PT expression, and as cell growth inhibitor.

XX
PS Example 4; SEQ ID NO 59; 98pp; Japanese.

XX

CC The invention relates to a DNA methylation inducer (I) containing double-
CC stranded (ds)RNA that targets the region which contains CpG or CpNG (N is
CC A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having
CC DNA that codes dsRNA that targets the region which contains CpG or CpNG
CC on DNA in mammalian cell. (I) is useful in the DNA methylation process,
CC which involves introducing (I) in a mammalian cell, where the mammalian
CC cell is obtained from human. (I) is useful as gene expression inhibitor
CC or cell growth inhibitor. A gene expression inhibitor (II) is useful for
CC suppressing gene expression, where the gene is a disease related gene
CC relevant to a disease, and the expression of the gene causes the disease.
CC The gene is erbB2 and the disease is the tumour. (I) is useful for
CC controlling various biological activities in a mammal by controlling the
CC transcription level of the respective gene by methylating the respective
CC DNA. (I) or (II) enables specific methylation of the CpG island-
CC containing domain on a gene promoter of the target gene, where the
CC methylation of a promoter suppresses the expression of the target gene.
CC (I) induces sequence specific DNA methylation in a plant, and controls
CC the expression of the specific gene at the transcription level. (I)
CC enables DNA methylation in the promoter region of a gene, where the
CC methylation changes the structure of the DNA, enabling suppression of the
CC gene expression at the transcription level (DNA to mRNA). This sequence
CC corresponds to an erbB2 gene PCR primer used in the method to silence
CC gene expression in cells.

XX Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 AGGCGGGGTGGATCCCTC 858
||||| ||||| |||||
Db 19 AGGCCTGGGTGCGTCCCTC 1

RESULT 349
ADR27673
ID ADR27673 standard; DNA; 14 BP.

XX ADR27673;

DT 04-NOV-2004 (first entry)

XX Leptin receptor related protein, OB-RGRP, RT-PCR primer #1.

DE Osteopathic; Anorectic; Antidiabetic; Cytostatic; Antiinflammatory;
KW Immunomodulatory; Anabolic; Endocrine; Antianemic; Antiangiogenic;
KW Leptin receptor related protein; OB-RGRP; leptin receptor;
KW leptin-related disorders; osteoporosis; calcification; obesity; diabetes;
KW anorexia; sexual maturity disorder; haematopoiesis; angiogenesis;
KW thrombus formation; immunity; inflammation; fetal development; cancer;
KW human; RT-PCR; primer; ss.

XX Homo sapiens.

OS FR2850971-A1.

XX 13-AUG-2004.

XX 10-FEB-2003; 2003FR-00001543.

XX 10-FEB-2003; 2003FR-00001543.

XX (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Jockers R, Couturier C, Uhlmann E;

XX WPI; 2004-595751/58.

XX New oligonucleotides that inhibit expression of the leptin receptor
PT related protein, useful for treatment and prevention of e.g.
PT osteoporosis, obesity, diabetes, anorexia, hematopoiesis, and

PT angiogenesis.

XX Disclosure; Page 23; 104pp; French.

XX The present invention relates to a leptin receptor related protein (OB-
CC RGRP) antisense oligonucleotide (ON; ADR27653), that hybridises
CC specifically with and inhibits the expression of ADR27652. The ON
CC promotes expression of leptin receptors on the cell surface and may
CC contain phosphorothioate bonds; 2'-O-methyl nucleotides and/or a
CC triethyleneglycol residue at the 3'-end. Also claimed are interfering RNA
CC (iRNA) of 15-25 nt that hybridize specifically with ADR27672, and inhibit
CC expression of OB-RGRP. Also claimed are fusion proteins (FPs) and their
CC coding sequences comprising OB-RGRP or MYO47 (thought to be a member of
CC the OB-RGRP family, shares 68% homology with OB-RGRP), and a protein that
CC is a donor or acceptor of energy e.g. luciferase or yellow fluorescent
CC protein (YFP) for detecting compounds that modify the interaction between
CC the leptin receptor and OB-RGRP proteins, which can be used to prevent or
CC treat leptin-related disorders. ON, also related interfering RNA, are
CC used for prevention and/or treatment of leptin-related disorders, e.g.
CC osteoporosis (or other conditions involving reduced bone density);
CC calcification; obesity; diabetes; anorexia; disorders of sexual maturity,
CC haematopoiesis, angiogenesis, thrombus formation, regulation of immunity
CC and inflammation, fetal development and cancer. The present sequence is a
CC RT-PCR primer used to illustrate the invention.

XX Sequence 14 BP; 3 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CCGTGGCAGGAAGC 39
||||| ||||| |||||
Db 1 CCGTGGCAGGAAGC 14

RESULT 350

AAT54666

ID AAT54666 standard; RNA; 15 BP.

XX AAT54666;

XX 25-MAR-2003 (revised)

DT 22-APR-1997 (first entry)

XX Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1148).

DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.

XX Mus musculus.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.

XX 23-FEB-1994; 94US-00201109.

PR 29-MAR-1994; 94US-00218934.

PR 04-APR-1994; 94US-00222795.

PR 07-APR-1994; 94US-00224483.

PR 15-APR-1994; 94US-00227958.

PR 15-APR-1994; 94US-00228041.

PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 221; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
CC of the mRNA that do not form secondary folding structures and that
CC contain potential hammerhead and hairpin ribozyme cleavage sites were
CC identified by computer analysis. Ribozymes directed against these mRNA
CC sequences were designed and synthesised with modifications that improve
CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
CC and thereby inhibit IL-5 expression, making them useful for treating
CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
CC and preventing the recruitment and activation of eosinophils. The
CC ribozymes can also be used to treat eosinophilia (related to parasitic
CC infection or with pulmonary infiltration) and L-tryptophan-associated
CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 15 BP; 2 A; 2 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 123 TGACTTTTCTTATG 136
:||||:|
Db 1 UGACUUUCUUAUG 14

RESULT 351
AAZ63871
ID AAZ63871 standard; RNA; 15 BP.
XX
AC AAZ63871;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2483.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;

PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 221; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
CC of the mRNA that do not form secondary folding structures and that
CC contain potential hammerhead and hairpin ribozyme cleavage sites were
CC identified by computer analysis. Ribozymes directed against these mRNA
CC sequences were designed and synthesised with modifications that improve
CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
CC and thereby inhibit IL-5 expression, making them useful for treating
CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
CC and preventing the recruitment and activation of eosinophils. The
CC ribozymes can also be used to treat eosinophilia (related to parasitic
CC infection or with pulmonary infiltration) and L-tryptophan-associated
CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 15 BP; 2 A; 2 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 123 TGACTTTTCTTATG 136
:||||:|
Db 1 UGACUUUCUUAUG 14

RESULT 351
AAZ63871
ID AAZ63871 standard; RNA; 15 BP.
XX
AC AAZ63871;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2483.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;

KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX
DR WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 73; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 4 A; 1 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 346 TGTGATCAAAATGGG 359
:|:|:|:|:|:|
Db 2 UGUGAUCAAAUUGG 15

RESULT 352
ABX00924
ID ABX00924 standard; RNA; 15 BP.
XX
AC ABX00924;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #706 for HCV hammerhead ribozyme #706.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX

PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 41; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 15 BP; 4 A; 1 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 346 TGTGATCAATGGG 359
Db :|:|:|:|:|:|
2 UGUGAUCAAAUGGG 15

RESULT 353
ABT39781/c
ID ABT39781 standard; DNA; 17 BP.
XX
AC ABT39781;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 5418.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX

PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 667; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 8 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 ATTTTGATGAGATC 984
Db |||||
14 ATTTTGATGAGATC 1

RESULT 354
AAZ71197
ID AAZ71197 standard; DNA; 18 BP.
XX
AC AAZ71197;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5553.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1415; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ATCTCCCCCATCCC 213
| | | | | | | | | | | | | | | |
Db 5 ATCTCCCCCATCCC 18

RESULT 355
AAZ69829/C
ID AAZ69829 standard; DNA; 20 BP.
XX
AC AAZ69829;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4185.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB0000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX

DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1123; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTAATA 575
| | | | | | | | | | | | | | | |
Db 19 TGGGTTTTTTAATA 6

RESULT 356
AAZ71268
ID AAZ71268 standard; DNA; 20 BP.
XX
AC AAZ71268;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5624.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB0000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1430; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTGTTATTCTTGCT 337
Db 4 CTGTTATTCTTGCT 17

RESULT 357
AAD34452/c
ID AAD34452 standard; DNA; 20 BP.
XX
AC AAD34452;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human TREK2 cDNA specific forward PCR primer.
XX
KW Human; hTREK2 protein; cancer; diabetes; pulmonary disease; asthma;
KW cardiovascular disease; inflammatory disease; psychiatric disorder;
KW renal disease; neurodegenerative disease; neurological disorder;
KW Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma;
KW pain; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN GB2365010-A.
XX
PD 13-FEB-2002.
XX
PF 24-APR-2001; 2001GB-00010129.
XX
PR 25-APR-2000; 2000GB-00010060.
PR 01-JUN-2000; 2000GB-00013370.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Duckworth DM;
XX
XX WPI; 2002-332557/37.
DR
XX Novel human TREK2 (HTREK2) polypeptide and polynucleotide encoding it,
PT useful for identifying agonists and antagonists in the treatment of
PT diseases associated with a HTREK2 imbalance, such as diabetes, cancers or
PT asthma.
XX
XX Example 1; Page 20; 29pp; English.
PS
XX The invention relates to human HTREK2 polypeptides and nucleic acid
CC molecules encoding such polypeptides. TREK2 polypeptides are useful in
CC screening assays to identify compounds that may stimulate or inhibit
CC their function or level of expression. Sequences of the invention are
CC used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular
CC diseases, inflammatory disease, renal disease, pain, psychiatric

CC disorders including depression and schizophrenia, neurodegenerative
CC disease including Alzheimer's disease, stroke and head trauma and
CC neurological disorders. They are also used as vaccines. The present
CC sequence is human hTREK2 cDNA specific PCR primer
XX
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 CTATTGGACTGACT 127
Db 19 CTATTGGACTGACT 6

RESULT 358
ABN79739/c
ID ABN79739 standard; DNA; 20 BP.
XX
AC ABN79739;
XX
DT 29-JUL-2002 (first entry)
XX
DE Human Fas target oligonucleotide #54.
XX
KW Human; immunosuppressive; antiinflammatory; hepatotropic; cytostatic;
KW vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.
XX
OS Homo sapiens.
XX
PN US2002004490-A1.
XX
PD 10-JAN-2002.
XX
PF 09-MAR-2001; 2001US-00802669.
XX
PR 12-APR-1999; 99US-00290640.
PR 18-SEP-2000; 2000US-00665615.
XX
PA (DEAN/) DEAN N M.
PA (MARC/) MARCUSSON E G.
PA (WYAT/) WYATT J.
PA (ZHAN/) ZHANG H.
XX
PI Dean NM, Marcusson EG, Wyatt J, Zhang H;
XX
XX WPI; 2002-204886/26.
DR
XX Novel antisense compound targeted to nucleic acid encoding Fas, Fas
PT ligand or Fas associated protein-1 is useful for inhibiting expression of
PT Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating
PT hepatitis.
XX
PS Example 18; Page 24; 84pp; English.
XX
CC This invention relates to an antisense compound encoding Fas, Fas ligand,
CC or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated
CC signalling is thought to be immunosuppressive, antiinflammatory,
CC hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were
CC designed to target human Fas. Oligonucleotides were synthesised as
CC chimeric oligonucleotides and are useful for treating an animal having an
CC autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition
CC associated with apoptosis, allograft rejection, or ischemia reperfusion
CC injury. Optionally, the above mentioned conditions are prevented by
CC contacting the allograft with the antisense oligonucleotide. The
CC oligonucleotides are used in diagnostics, therapeutics, prophylaxis and
CC as research reagents and in kits. The oligonucleotides are also useful
CC for research purposes. The present nucleotide sequence is related to
CC human Fas
XX
SQ Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
| | | | | | | | | |
Db 18 AGATGAGTTTATT 5

RESULT 359
AAL42518/c
ID AAL42518 standard; DNA; 20 BP.
XX
AC AAL42518;
XX
DT 28-JUN-2002 (first entry)
XX
DE Alpha-V integrin-specific inhibitory antisense nucleic acid 7.
XX
KW Antisense nucleic acid; ss; alpha-V integrin chain; antisense inhibition;
KW cell adhesion modulation; platelet aggregation; immune function;
KW tissue repair; cell proliferation; tumour invasion; cancer; gingivitis;
KW chronic inflammatory disease; Chron's disease; rheumatoid arthritis;
KW ocular neovascular disease; diabetic retinopathy; osteoporosis;
KW excessive bone resorption; inflammatory skin disorder; psoriasis.
XX
OS Unidentified.
XX
PN EP1197553-A1.
XX
PD 17-APR-2002.
XX
PF 12-OCT-2000; 2000EP-00121394.
XX
PR 12-OCT-2000; 2000EP-00121394.
XX
PA (ATHR-) A3D GMBH ANTISENSE DESIGN & DRUG DEV.
XX
PI Kronenwett R, Graef T, Haas R, Nedbal W;
XX WPI; 2002-364499/40.
DR
XX
PT Antisense nucleic acid against alpha V integrin for use in pharmaceutical
compositions for the specific inhibition of the expression of alpha
PT integrins in mammalian cells useful.
XX
PS Claim 8; Page 3; 17pp; English.
XX

The invention comprises antisense nucleic acids that are capable of
binding to the transcription product of the gene coding for the alpha-V
integrin chain, thereby inhibiting the expression of alpha-V integrins in
mammalian cells. The antisense nucleic acids of the invention are useful
for the treatment of pathological disorders by the modulation of cell
adhesion which affects platelet aggregation, immune functions, tissue
repair, cell proliferation, tumour invasion, inflammation and inherited
diseases. Disorders which can be treated include: cancer; restenosis
(e.g. Chron's disease and rheumatoid arthritis); chronic inflammatory diseases
(e.g. Chron's disease and rheumatoid arthritis); disorders associated with excessive
bone resorption (e.g. osteoporosis); disorders of mammalian oral cavity
(e.g. gingivitis); and inflammatory skin disorders (e.g. psoriasis). The
present DNA sequence represents an antisense nucleic acid of the
invention used to inhibit alpha-V integrin expression

Sequence 20 BP; 11 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 TTTTCCTTATATT 430
| | | | | | | | | |
Db 17 TTTTCCTTATATT 4

RESULT 360
ACH00628
ID ACH00628 standard; DNA; 20 BP.
XX
AC ACH00628;
XX
DT 12-FEB-2004 (first entry)
XX
DE Mammalian inverted nipple associated microsatellite PCR primer #82.
XX
KW Inverted nipple; microsatellite; PCR; primer; ss; pig.
XX
OS Mammalia.
XX
PN WO2003066891-A2.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-EP001045.
XX
PR 05-FEB-2002; 2002EP-00002632.
XX
PA (FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE.
XX
PI Hardge T, Schellander K, Wimmers K;
XX WPI; 2003-671539/63.
DR
XX
PT Determining predisposition to inverted nipples useful e.g. for selecting
PT breeding animals comprises detecting specific microsatellite markers.
XX
PS Disclosure; Page 23; 63pp; German.
XX

The present invention relates to the use of a nucleic acid to determine
the predisposition of appearance or inheritance of inverted nipples,
where the nucleic acid is identical to the region of microsatellites
S0200, SW2443, S0097, S0007, SW1301 or S0164 on chromosomes 6, 2, 4, 14,
1 and 3, respectively, in pigs, or homologous positions in the genomes of
other mammals. The nucleic acids can be used to select pets, breeding or
farm animals that lack inverted nipples, particularly by genomic
screening of many related mammals in a population. The present sequence
is a PCR primer used in the exemplification of the invention to identify
microsatellite markers associated with the inverted nipple phenotype

Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 894 CACAGACCAAGAGC 907
| | | | | | | | | |
Db 2 CACAGACCAAGAGC 15

RESULT 361
ADH77414
ID ADH77414 standard; DNA; 20 BP.
XX
AC ADH77414;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PTPN12 antisense oligonucleotide seq id 55.
XX
KW cytosstatic; PTPN12 Inhibitor; PTPN12;
KW protein tyrosine phosphatase, non-receptor type 12;
KW hyperproliferative disorder; colon cancer; metabolic disorder;
KW antisense technology; antisense oligonucleotide; human; ss.
XX
OS Homo sapiens.

XX FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidine
FT residues are 5-methoxycytidine"
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl (2'-MOE) nucleotides"
XX US2003232434-A1.
PN 18-DEC-2003.
XX 17-JUN-2002; 2002US-00172911.
XX 17-JUN-2002; 2002US-00172911.
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Cowsert LM, Dobie KW;
PI WPI; 2004-061282/06.
XX
XX New antisense oligonucleotides targeted to a nucleic acid encoding
PT protein tyrosine phosphatase, non-receptor type 12 (PTPN12) useful for
PT treating a disease associated with PTPN12, e.g. colon cancer.
XX
XX Example 15; SEQ ID NO 55; 117pp; English.
XX
XX The invention describes a compound 8-80 nucleobases in length targeted
CC to, and which specifically hybridizes with a nucleic acid molecule
CC encoding PTPN12 (protein tyrosine phosphatase, non-receptor type 12), and
CC inhibits the expression of PTPN12. The compound, composition and methods
CC are useful for treating a disease or condition associated with PTPN12,
CC such as a hyperproliferative disorder, e.g. colon cancer, or a metabolic
CC disorder. They are also useful in research and diagnostics for modulating
CC the expression of PTPN12. This sequence represents a human protein
CC tyrosine phosphatase, non-receptor type 12 (PTPN12) antisense
CC oligonucleotide.
XX
XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 345 CTGTGATCAAAATGG 358
Db 1 CTGTGATCAAAATGG 14
RESULT 362
ADL27795/c
ID ADL27795 standard; DNA; 20 BP.
XX
AC ADL27795;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human Fas cDNA, antisense oligonucleotide #75.
XX
KW Antisense therapy; human; Fas; Fas ligand; FasL; Apo-1L; CD95L;
KW Fas associated protein 1; Fap-1; signal transduction; autoimmune disease;
KW inflammatory disease; cancer; immunosuppressive; antiinflammatory;
KW cytotstatic; phosphorothioate; ss.
XX

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 5 nucleotides in length at each
FT end. All cytidine residues are 5-methylcytidines"
XX US6653133-B1.
PN 25-NOV-2003.
XX 18-SEP-2000; 2000US-00665615.
XX 12-APR-1999; 99US-00290640.
XX (ISIS-) ISIS PHARM INC.
XX Dean NM, Marcusson EG, Wyatt J;
PI WPI; 2004-050524/05.
XX
XX New antisense oligonucleotides of 20-50 nucleobases, useful for treating
PT autoimmune or inflammatory diseases, and cancer.
XX
XX Example 18; SEQ ID NO 156; 76pp; English.
XX
XX The present invention relates to antisense compounds targeted to nucleic
CC acids encoding human Fas (also known as Apo-1 or CD95), Fas ligand (FasL,
CC also Apo-1L and CD95L), and Fas associated protein 1 (Fap-1). The
CC antisense compound comprises an antisense oligonucleotide that
CC specifically hybridises with one of the said nucleic acids and inhibits
CC Fas, FasL or Fap-1 mediated signal transduction. The antisense
CC oligonucleotide is a chimeric oligonucleotide. The antisense
CC oligonucleotide comprises at least one modified internucleoside linkage,
CC preferably a phosphorothioate linkage. It also comprises at least one
CC modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
CC moiety. The antisense oligonucleotide further comprises at least one
CC modified nucleobase, preferably a 5-methylcytosine. The antisense
CC oligonucleotides are useful for the treatment of autoimmune or
CC inflammatory diseases, and cancers associated with overexpression of or
CC constitutive activation of Fas, FasL, or Fap-1. The present sequence
CC represents an antisense oligonucleotide used in the examples of the
CC present invention.
XX
XX Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 620 AGATGAGTTTATT 633
Db 18 AGATGAGTTTATT 5
RESULT 363
ADM53567/c
ID ADM53567 standard; DNA; 20 BP.
XX
AC ADM53567;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Fas antisense oligonucleotide seqid 156.
XX
KW immunosuppressive; antiinflammatory; hepatotropic; virucide; cytotstatic;
KW antisense technology; Fas; Fas ligand; Fap-1; Fas associated disorder;
KW Fap-1 associated disorder; ischaemia reperfusion injury; apoptosis;
KW allograft; autoimmune disease; inflammatory disease; hepatitis; cancer;
KW

KW lymphoma; human; antisense oligonucleotide; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT modified_base 1. .5
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
PN US2004033979-A1.
XX
PD 19-FEB-2004.
XX
XX 14-JUL-2003; 2003US-00619220.
XX
PR 12-APR-1999; 99US-00290640.
PR 18-SEP-2000; 2000US-00665615.
PR 09-MAR-2001; 2001US-00802669.
XX
PA (DEAN/) DEAN N M.
PA (MARC/) MARCUSSEN E G.
PA (WYAT/) WYATT J.
PA (ZHAN/) ZHANG H.
XX
PI Dean NM, Marcussen EG, Wyatt J, Zhang H;
XX WPI; 2004-180091/17.
DR
XX New antisense compound targeted to nucleic acid molecule encoding Fas or
PT Fap-1, useful in diagnosing, treating or preventing autoimmune or
PT inflammatory disease, cancer, apoptosis, allograft rejection or ischemia
PT reperfusion injury.
XX
PS Example 18; SEQ ID NO 156; 83pp; English.
XX
CC The invention describes an antisense compound 8-30 or 8-50 nucleobases in
CC length targeted to the 5'-untranslated region, translational start site,
CC translational termination region or 3'-untranslated region of a nucleic
CC acid molecule encoding Fas, Fas ligand or Fap-1. Also described are: a
CC pharmaceutical composition comprising the anti-sense compound and a
CC pharmaceutical carrier or diluent; a method of inhibiting the expression
CC of Fas or Fap-1 in cells or tissues: treating an animal having a disease
CC or condition associated with Fas or Fap-1; and preventing allograft
CC rejection, ischaemia reperfusion injury or apoptosis in an allograft
CC recipient. The antisense compound and pharmaceutical composition is
CC useful in diagnosing, treating or preventing autoimmune or inflammatory
CC disease, e.g. hepatitis, cancer, e.g. cancer of the colon, liver, lung or
CC a lymphoma, apoptosis, allograft rejection, e.g. cardiac, renal, hepatic
CC or skin allograft and ischemia reperfusion injury. This sequence
CC represents a human Fas antisense oligonucleotide.
XX
SQ Sequence 20 BP; 9 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AGATGAGTTTATT 633
Db |||||
18 AGATGAGTTTATT 5

RESULT 364

AAQ40912
ID AAQ40912 standard; DNA; 17 BP.
XX
AC AAQ40912;
XX
DT 25-MAR-2003 (revised)
DT 07-SEP-1993 (first entry)
XX
DE C-erb-B2 sense oligonucleotide.
XX
KW Double; triple; helix; duplex; triplex; major groove; SKBR3 cell; ss.
XX
OS Synthetic.
XX
PN WO9309813-A1.
XX
PD 27-MAY-1993.
XX
PF 10-NOV-1992; 92WO-GB002073.
XX
PR 12-NOV-1991; 91GB-00023947.
XX
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Epenetos AA;
XX
DR WPI; 1993-182253/22.
XX
PT Cpd. comprising anti-sense oligo:nucleotide and radioactive moiety - for
PT treating viral infection, sepsis, leukaemia and tumours.
XX
PS Example 3; Page 26; 43pp; English.
XX
CC For the selective killing of SKBR3 cells the following radiolabelled c-
CC erb-B2 oligonucleotides were used: (1) the antisense oligonucleotide
CC given in AAQ40911, complementary to the non-transcribed sequence at the
CC 5' end of the gene; (2) the sense oligonucleotide given in AAQ40912,
CC complementary to the transcribed sequence at the 5' end of the gene; and
CC (3) the random sequence given in AAQ40913, having the same base compsn.
CC as the antisense oligonucleotide. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 360 GAGCCTGCGGCCTTGTG 376
Db |||||
1 GAGCTGGCGGCCTTGTG 17

RESULT 365
AAQ40911/c
ID AAQ40911 standard; DNA; 17 BP.
XX
AC AAQ40911;
XX
DT 25-MAR-2003 (revised)
DT 07-SEP-1993 (first entry)
XX
DE C-erb-B2 antisense oligonucleotide.
XX
KW Double; triple; helix; duplex; triplex; major groove; SKBR3 cell; ss.
XX
OS Synthetic.
XX
PN WO9309813-A1.
XX
PD 27-MAY-1993.
XX
PF 10-NOV-1992; 92WO-GB002073.

XX 12-NOV-1991; 91GB-00023947.
PR (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX Epenetos AA;
PA PI
XX WPI; 1993-182253/22.
DR Cpd. comprising anti-sense oligo:nucleotide and radioactive moiety - for
PT treating viral infection, sepsis, leukaemia and tumours.
XX
PS Example 3; Page 26; 43pp; English.
XX
CC For the selective killing of SKBR3 cells the following radiolabelled c-
CC erb-B2 oligonucleotides were used: (1) the antisense oligonucleotide
CC given in AAQ40911, complementary to the non-transcribed sequence at the
CC 5' end of the gene; (2) the sense oligonucleotide given in AAQ40912,
CC complementary to the transcribed sequence at the 5' end of the gene; and
CC (3) the random sequence given in AAQ40913, having the same base compsn.
CC as the antisense oligonucleotide. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 360 GAGCCTGGCGCCTTG TG 376
Db 17 GAGCTGGCGCCTTG T 1

RESULT 366
AAT05984/C
ID AAT05984 standard; DNA; 17 BP.
XX AAT05984;
AC
XX 31-MAY-1996 (first entry)
DT
XX COX II forward primer binds 60 bp upstream of COX II gene.
DE
XX Human; mitochondrial cytochrome C oxidase; COX; subunit I; subunit II;
KW subunit III; mutation; Alzheimer's disease; AD; sporadic form;
KW diabetes mellitus; IDDM; detection; PCR; amplify; primer; ss.
XX
OS Synthetic.
XX WO9526973-A1.
PN
XX 12-OCT-1995.
PD
XX 30-MAR-1995; 95WO-US004063.
PF
XX 30-MAR-1994; 94US-00219842.
PR
PR 03-MAR-1995; 95US-00397808.
XX
XX (GENE-) APPLIED GENETICS INC..
PA
XX Hernstadt C, Parker WD, Davis RE, Miller SW;
XX WPI; 1995-358577/46.
DR
XX Mutant mitochondrial cytochrome C oxidase genes - useful for generating
PT probes for diagnosing and treating e.g. Alzheimer's disease and new cell
PT lines for screening for drugs.
XX
XX Example 1; Page 78; 149pp; English.
PS
XX The sequences given in AAT05976-81 are primers which were used in the
CC amplification of the human mitochondrial cytochrome C oxidase (COX)

CC subunit I, II and III genes. These primers were targetted 100 bp upstream
CC and downstream of each gene. The amplified sequences were cloned and
CC further amplified using the primers given in AAT05982-87. COX genes from
CC normal individuals and patients with Alzheimer's disease were sequenced
CC and compared. The COX subunit I and II genes were found to be mutated in
CC patients with Alzheimer's disease (AD) and comparison between wildtype
CC and mutated sequences can lead to the identification of recurrent
CC mutations. Knowledge of these mutations allows the detection of the
CC sporadic form of AD. Mutations within the COX I and II genes have also
CC been found to segregate with diabetes mellitus. Oligomers which are
CC antisense to the positions of mutations can be used in the therapy of AD
XX
SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 367
AAA18772
ID AAA18772 standard; RNA; 17 BP.
XX
AC AAA18772;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1998.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cyostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
XX WO9950403-A2.
PN
XX
XX 07-OCT-1999.
PD
XX 24-MAR-1999; 99WO-US006507.
PF
XX 27-MAR-1998; 98US-0079678P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
PI
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PT
XX
XX Claim 56; Page 116; 305pp; English.
PS
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;

CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 7 A; 6 C; 2 G; 0 T; 2 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2e+02; Length 17;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 939 CAGAATCTGAAGCCCCCA 955
Db 1 CAGAAUCUCAAGCACCA 17

RESULT 368
AAF04220
ID AAF04220 standard; DNA; 17 BP.
XX
AC AAF04220;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1736.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
AC AAF04220;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1736.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
PS Claim 4; Page 95; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 4 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 TTTTCCTTACAATTCAA 412
Db 1 TTTTCCTTACAACCTCCA 17

RESULT 369
AAF04668
ID AAF04668 standard; DNA; 17 BP.
XX
AC AAF04668;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2184.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 4; Page 105; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 4 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 TTTTCCTTACAATTCAA 412
Db 1 TTTTCCTTACAACCTCCA 17

RESULT 370
ABK02567/c
ID ABK02567 standard; RNA; 17 BP.
XX
AC ABK02567;
XX
DT 12-MAR-2002 (first entry)
XX

DE Human NOGO Amberzyme #239.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200159103-A2.

XX

PD 16-AUG-2001.

XX

PF 09-FEB-2001; 2001WO-US004273.

XX

PR 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

PI Blatt L, Mcswiggen J, Chowrira BM;

XX

DR WPI; 2001-607195/69.

XX

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

PS Claim 88; Page 136; 200pp; English.

XX

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention

XX

SQ Sequence 17 BP; 11 A; 2 C; 2 G; 0 T; 2 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 413 GGGTTTTTCCTTATTT 429
| | | | | | | | | | | | | | | | |
Db 17 GAGTTTTTCCTTATTT 1

RESULT 371
AAF69066/c
ID AAF69066 standard; DNA; 17 BP.

XX

AC AAF69066;

XX

DT 12-APR-2001 (first entry)

XX

DE COXII PCR primer #13.

XX

KW Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer; ss.

KW

XX Homo sapiens.

OS

XX US6171859-B1.

PN

XX 09-JAN-2001.

PD

XX 30-MAR-1995; 95US-00413740.

PF

XX 30-MAR-1994; 94US-00219842.

PR

XX (MITO-) MITOKOR.

PA

XX Herrnstadt C, Parker WD;

PI

XX WPI; 2001-136875/14.

DR

XX

PT Targeting conjugate molecule to mitochondria having defective cytochrome C oxidase activity for diagnosing Alzheimer's disease, involves contacting mitochondria with a conjugate of targeting molecule and toxin.

PT

XX

PS Example 2; Col 41-42; 88pp; English.

XX

The present invention relates to a method for selectively accumulating a mitochondrial disabling or destructive amount of a conjugate molecule in mitochondria having defective cytochrome C oxidase (COX) activity or displaying increased membrane potential. The method involves contacting mitochondria with a conjugate molecule comprising a targeting molecule conjugated to a toxin, where the conjugate or targeting molecule selected accumulates in the mitochondria. The method is useful for diagnosis of Alzheimer's disease (AD), especially sporadic AD. The present sequence is a PCR primer used in the method of the present invention

XX

SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTTAATACCTT 579
| | | | | | | | | | | | | | | | |
Db 17 GGTTCCTTCTAATACCTT 1

RESULT 372
AAF69029/c
ID AAF69029 standard; DNA; 17 BP.


```
XX AAF69029;
AC
XX 12-APR-2001 (first entry)
DT
XX COXII PCR primer #5.
DE
XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
KW ss.
KW
XX Homo sapiens.
OS
XX US6171859-B1.
XX
XX 09-JAN-2001.
PD
XX 30-MAR-1995; 95US-00413740.
PF
XX 30-MAR-1994; 94US-00219842.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Parker WD;
XX
DR WPI; 2001-136875/14.
XX
XX Targeting conjugate molecule to mitochondria having defective cytochrome
PT C oxidase activity for diagnosing Alzheimer's disease, involves
PT contacting mitochondria with a conjugate of targeting molecule and toxin.
XX
XX Example 2; Col 39; 88pp; English.
XX
XX The present invention relates to a method for selectively accumulating a
CC mitochondrial disabling or destructive amount of a conjugate molecule in
CC mitochondria having defective cytochrome C oxidase (COX) activity or
CC displaying increased membrane potential. The method involves contacting
CC mitochondria with a conjugate molecule comprising a targeting molecule
CC conjugated to a toxin, where the conjugate or targeting molecule selected
CC accumulates in the mitochondria. The method is useful for diagnosis of
CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
CC a PCR primer used in the method of the present invention
XX
XX Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
PT Targeting conjugate molecule to mitochondria having defective cytochrome
PT C oxidase activity for diagnosing Alzheimer's disease, involves
PT contacting mitochondria with a conjugate of targeting molecule and toxin.
XX
XX Example 2; Col 39; 88pp; English.
XX
XX The present invention relates to a method for selectively accumulating a
CC mitochondrial disabling or destructive amount of a conjugate molecule in
CC mitochondria having defective cytochrome C oxidase (COX) activity or
CC displaying increased membrane potential. The method involves contacting
CC mitochondria with a conjugate molecule comprising a targeting molecule
CC conjugated to a toxin, where the conjugate or targeting molecule selected
CC accumulates in the mitochondria. The method is useful for diagnosis of
CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
CC a PCR primer used in the method of the present invention
XX
XX Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 562 TGGGTTTTTTAATACCT 578
DB 17 TGGTTTTTCTAATACCT 1
RESULT 373
AAF69063/C
ID AAF69063 standard; DNA; 17 BP.
XX
AC AAF69063;
XX
XX 12-APR-2001 (first entry)
DT
XX COXII PCR primer #10.
DE
XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
KW ss.
KW
XX Homo sapiens.
OS
XX US6171859-B1.
XX
XX 09-JAN-2001.
PD
XX 30-MAR-1995; 95US-00413740.
PF
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```
XX 30-MAR-1994; 94US-00219842.
PR
XX (MITO-) MITOKOR.
PA
XX Herrnstadt C, Parker WD;
XX
PI WPI; 2001-136875/14.
XX
DR Targeting conjugate molecule to mitochondria having defective cytochrome
XX C oxidase activity for diagnosing Alzheimer's disease, involves
PT contacting mitochondria with a conjugate of targeting molecule and toxin.
PT
XX Example 2; Col 41-42; 88pp; English.
XX
XX The present invention relates to a method for selectively accumulating a
CC mitochondrial disabling or destructive amount of a conjugate molecule in
CC mitochondria having defective cytochrome C oxidase (COX) activity or
CC displaying increased membrane potential. The method involves contacting
CC mitochondria with a conjugate molecule comprising a targeting molecule
CC conjugated to a toxin, where the conjugate or targeting molecule selected
CC accumulates in the mitochondria. The method is useful for diagnosis of
CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
CC a PCR primer used in the method of the present invention
XX
XX Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 562 TGGGTTTTTTAATACCT 578
DB 17 TGGTTTTTCTAATACCT 1
RESULT 374
AAF69064/C
ID AAF69064 standard; DNA; 17 BP.
XX
AC AAF69064;
XX
XX 12-APR-2001 (first entry)
DT
XX COXII PCR primer #11.
DE
XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
KW ss.
KW
XX Homo sapiens.
OS
XX US6171859-B1.
XX
XX 09-JAN-2001.
PD
XX 30-MAR-1995; 95US-00413740.
PF
XX 30-MAR-1994; 94US-00219842.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Parker WD;
XX
DR WPI; 2001-136875/14.
XX
XX Targeting conjugate molecule to mitochondria having defective cytochrome
PT C oxidase activity for diagnosing Alzheimer's disease, involves
PT contacting mitochondria with a conjugate of targeting molecule and toxin.
PT
XX Example 2; Col 41-42; 88pp; English.
XX
XX The present invention relates to a method for selectively accumulating a
CC mitochondrial disabling or destructive amount of a conjugate molecule in
CC mitochondria having defective cytochrome C oxidase (COX) activity or
CC displaying increased membrane potential. The method involves contacting
CC mitochondria with a conjugate molecule comprising a targeting molecule
CC conjugated to a toxin, where the conjugate or targeting molecule selected
CC accumulates in the mitochondria. The method is useful for diagnosis of
CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
CC a PCR primer used in the method of the present invention
XX
XX Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 562 TGGGTTTTTTAATACCT 578
DB 17 TGGTTTTTCTAATACCT 1
RESULT 374
AAF69064/C
ID AAF69064 standard; DNA; 17 BP.
XX
AC AAF69064;
XX
XX 12-APR-2001 (first entry)
DT
XX COXII PCR primer #11.
DE
XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
KW ss.
KW
XX Homo sapiens.
OS
XX US6171859-B1.
XX
XX 09-JAN-2001.
PD
XX 30-MAR-1995; 95US-00413740.
PF
XX 30-MAR-1994; 94US-00219842.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C, Parker WD;
XX
DR WPI; 2001-136875/14.
XX
XX Targeting conjugate molecule to mitochondria having defective cytochrome
PT C oxidase activity for diagnosing Alzheimer's disease, involves
PT contacting mitochondria with a conjugate of targeting molecule and toxin.
PT
XX Example 2; Col 41-42; 88pp; English.
XX
XX The present invention relates to a method for selectively accumulating a
CC mitochondrial disabling or destructive amount of a conjugate molecule in
```


CC mitochondria having defective cytochrome C oxidase (COX) activity or
CC displaying increased membrane potential. The method involves contacting
CC mitochondria with a conjugate molecule comprising a targeting molecule
CC conjugated to a toxin, where the conjugate or targeting molecule selected
CC accumulates in the mitochondria. The method is useful for diagnosis of
CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
CC a PCR primer used in the method of the present invention
XX
SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 563 GGGTTTTTTAATACCTT 579
Db 17 GGTTTTTCTAATACCTT 1

RESULT 375
AAF69018/c
ID AAF69018 standard; DNA; 17 BP.
XX
AC AAF69018;

DT 12-APR-2001 (first entry)
XX
DE COXII PCR primer #3.

XX Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
KW ss.
XX

OS Homo sapiens.
XX
PN US6171859-B1.

XX 09-JAN-2001.

XX 30-MAR-1995; 95US-00413740.

XX 30-MAR-1994; 94US-00219842.

XX (MITO-) MITOKOR.

XX Hernstadt C, Parker WD;

XX WPI; 2001-136875/14.

XX Targeting conjugate molecule to mitochondria having defective cytochrome
PT C oxidase activity for diagnosing Alzheimer's disease, involves
PT contacting mitochondria with a conjugate of targeting molecule and toxin.

XX Example 1; Col 38; 88pp; English.

XX The present invention relates to a method for selectively accumulating a
CC mitochondrial disabling or destructive amount of a conjugate molecule in
CC mitochondria having defective cytochrome C oxidase (COX) activity or
CC displaying increased membrane potential. The method involves contacting
CC mitochondria with a conjugate molecule comprising a targeting molecule
CC conjugated to a toxin, where the conjugate or targeting molecule selected
CC accumulates in the mitochondria. The method is useful for diagnosis of
CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
CC a PCR primer used in the method of the present invention
XX

SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 376
ABL46970
ID ABL46970 standard; RNA; 17 BP.
XX
AC ABL46970;

XX 27-JUN-2003 (first entry)

XX Human GRID zinzyme substrate oligonucleotide #54.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.

XX Homo sapiens.

XX WO200162911-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005957.

XX 24-FEB-2000; 2000US-0184594P.

XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 72; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 105 TCAGTGGGGCTATTGGA 121
Db 1 UCAGUGGGGCGUGGGA 17

RESULT 377
AAI65652
ID AAI65652 standard; DNA; 17 BP.
XX
AC AAI65652;

XX 03-JAN-2002 (first entry)

XX Primer for studying biallelic polymorphic markers in the IBD1 region.

XX Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox;
KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;
KW inflammatory disease; immune disease; cryptogenetic inflammation;
KW hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.

XX OS Homo sapiens.
XX PN FR2806739-A1.
XX XX
XX PD 28-SEP-2001.
XX XX
XX PF 27-MAR-2000; 2000FR-000003832.
XX XX
XX PR 27-MAR-2000; 2000FR-000003832.
XX XX
XX PA (DAUS-) FOND DAUSSET-CEPH JEAN.
XX XX
XX PI Hugot JP, Thomas G, Zouali M, Lesage S, Chamaillard M;
XX XX
XX DR WPI; 2001-608364/70.
XX XX
XX PT New human nucleic acids associated with intestinal inflammatory disease,
XX PT useful for diagnosis, prognosis and control of these diseases, also
XX PT related proteins.
XX XX
XX PS Example 4; Page 85; 97pp; French.
XX XX
XX CC Primers AAI65647-78 were used to characterise biallelic polymorphic
XX CC markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory
XX CC bowel disease 1 (IBD1) polypeptide, which is associated with intestinal
XX CC inflammatory disease. The specification also describes a polypeptide
XX CC which is in proximity to IBD1, and is designated IBD1prox. The IBD1 gene
XX CC is probably involved in regulation of apoptosis and activation of NF-
XX CC kappa B. The IBD1 and IBD1prox polynucleotides are is useful as source of
XX CC probes and primers, as source of (anti)sense oligonucleotides, for
XX CC recombinant production of polypeptides, and in screening for interactive
XX CC compounds. The polypeptides are used to raise specific antibodies which
XX CC useful for diagnostic detection or purification of IBD1 and IBD1prox, to
XX CC screen for specific binding agents, potential therapeutic agents. The
XX CC IBD1 and IBD1prox polynucleotides and polypeptides are useful for
XX CC treatment and prevention of inflammatory and/or immune diseases or
XX CC cancer, where associated with mutations in genes corresponding to IBD1
XX CC and IBD1prox, especially cryptogenetic inflammation of the intestines
XX CC (hemorrhagic rectocolitis, Crohn's disease and Blau syndrome)
XX XX
XX SQ Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 197 GCCATCTCCCCCATCCC 213
DB 1 GCCATCTCCCCAAGCCC 17

RESULT 378
ABN06757
ID ABN06757 standard; DNA; 17 BP.
XX
XX AC ABN06757;
XX XX
XX DT 29-MAY-2002 (first entry)
XX XX
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6749.
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200192524-A2.
XX XX
XX PD 06-DEC-2001.
XX XX
XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX XX
XX PA (AEOM-) AEOMICA INC.
XX XX
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX XX
XX DR WPI; 2002-179446/23.
XX XX
XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX XX
XX PS Disclosure; SEQ ID NO 6749; 214pp; English.
XX XX
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX CC nucleic acids can be used as probes to detect, characterise and quantify
XX CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMLP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMLP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX CC disorder associated with the expression of hGDMLP-1, in particular heart
XX CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX CC The present sequence represents an oligomer used in the screening of the
XX CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence
XX XX
XX SQ Sequence 17 BP; 5 A; 2 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 836 AGGAAGGCCGGGTGGA 852
DB 1 AGGAAGGCCGTGGAGGA 17

RESULT 379
ABN02571/c
ID ABN02571 standard; DNA; 17 BP.
XX
XX AC ABN02571;
XX XX
XX DT 29-MAY-2002 (first entry)
XX XX
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2563.
XX XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS
XX WO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2563; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 745 GCAGCTGCCACCTTATG 761
|||||
Db 17 GCAGCTGCCGCTTCTG 1

RESULT 380
ABN02572/c
ID ABN02572 standard; DNA; 17 BP.
XX
AC ABN02572;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2564.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX WO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2564; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence


```

XX
SQ      Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

      Query Match          1.2%;   Score 13.8;   DB 1;   Length 17;
      Best Local Similarity 88.2%;   Pred. No. 2e+02;
      Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      744 GGCAGCTGCCACCTTAT 760
      |||||
      17 GGCAGCTGCCGCCTTCT 1

RESULT 381
ABV82997
ID      ABV82997 standard; DNA; 17 BP.
XX
AC      ABV82997;
XX
DT      03-JAN-2003 (first entry)
XX
DE      Human HTPL scanning oligonucleotide SEQ ID 4243.
XX
KW      Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW      human testis expressed Patched like protein; testis; adrenal; liver;
KW      male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW      prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS      Homo sapiens.
XX
PN      EP1229046-A2.
XX
PD      07-AUG-2002.
XX
PF      28-JAN-2002; 2002EP-00001167.
XX
PR      30-JAN-2001; 2001WO-US000663.
PR      30-JAN-2001; 2001WO-US000664.
PR      30-JAN-2001; 2001WO-US000665.
PR      30-JAN-2001; 2001WO-US000667.
PR      30-JAN-2001; 2001WO-US000668.
PR      30-JAN-2001; 2001WO-US000669.
PR      23-MAY-2001; 2001US-00864761.
PR      09-OCT-2001; 2001US-0327898P.
XX
PA      (AEOM-) AEOMICA INC.
XX
PI      Zhan J;
XX
DR      WPI; 2002-676582/73.
XX
PT      Novel isolated human testis expressed Patched like protein (HTPL), useful
PT      for identifying agonist and antagonist and specific binding partners, and
PT      for treating subjects having defects in HTPL.
XX
PS      Example 2; Page 620; 718pp; English.
XX
CC      The present invention relates to human testis expressed Patched like
CC      protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC      has two isoforms, with a few single base pair differences between the
CC      two. One of the single base pair changes introduces a premature stop
CC      codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC      shares an overall structure organisation with the Patched protein. The
CC      shared structural features strongly imply that HTPL plays a role similar
CC      to that of Patched, and is a potential tumour suppressor. HTPL is
CC      important in regulating male germ cell development, and the HTPL gene was
CC      mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC      useful for diagnosing a disorder caused by mutation in HTPL, and in
CC      therapy and manufacture of a medicament for treatment or prevention of
CC      such disorder associated with decreased expression or activity of human
CC      HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC      foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC      skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC      clinically useful diagnostic markers and potential therapeutic agents for

```

CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 3 A; 1 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 673 AAATTATGTTACTTGT 689
Db 1 AGATTATGTTCTTGT 17

RESULT 382
ABK19408
ID ABK19408 standard; RNA; 17 BP.
XX
AC ABK19408;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 2055.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
OS
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
DR
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 128; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 960 GGACCCAGGACATTTTG 976
Db 1 GGACUCAGGACAUUUGG 17
||||| ||||| ||||| : : : |

RESULT 383
ABL311405
ID ABL311405 standard; DNA; 17 BP.
XX
AC ABL311405;
XX
XX 21-MAR-2002 (first entry)
DT
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 894.
DE
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
KW
XX Homo sapiens.
OS
XX
PN WO200192572-A1.
XX
XX 06-DEC-2001.
PD
XX
PF 01-JUN-2001; 2001WO-JP004662.
XX
XX 01-JUN-2000; 2000JP-00164798.
PR
XX (NISN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
PA
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
PI WPI; 2002-122074/16.
XX
DR
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
PT
XX Claim 10; Page 262; 345pp; Japanese.
PS
XX
CC The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
XX
SQ Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 404 ACAATTCAAGGGTTT 420
Db 1 ACAATTACAGGGTTT 17
||||| ||||| ||||| |||||

RESULT 384
ADA49961/C
ID ADA49961 standard; DNA; 17 BP.
XX
AC ADA49961;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human mitochondrial COX gene primer #9.
XX
KW Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
KW segregation; nootropic; neuroprotective; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003087858-A1.
XX
PD 08-MAY-2003.
XX
PF 15-OCT-2001; 2001US-00978600.
XX
PR 30-MAR-1994; 94US-00219842.
PR 30-MAR-1995; 95US-00413740.
PR 23-NOV-1999; 99US-00448312.
XX
PA (MITO-) MITOKOR.
XX
XX Herrnstadt C, Ghosh SS;
PI
XX WPI; 2003-597110/56.
DR
XX
PT Compositions and methods for the treatment and diagnosis of Alzheimer's
PT disease using nucleic acids related in sequence to (mutants of) the
PT cytochrome c oxidase gene.
XX
PS Example 1; Page 24; 93pp; English.
XX
CC The present invention relates to compositions and method for the
CC treatment and diagnosis of Alzheimer's disease (AD). The method comprises
CC the use of genetic mutations in the human mitochondrial cytochrome c
CC oxidase (COX) gene and their segregation with AD. Also disclosed are
CC antisense sequences specific to mutant human cytochrome c oxidase genes
CC that are designed to bind and inhibit transcription or translation of the
CC target mutant COX genes without inhibiting transcription or translation
CC of wild-type cytochrome c oxidase genes. Also disclosed are probes for
CC detecting a disease state associated with one or more mutations in the
CC mitochondrial COX genes, and a kit comprising a probe for detection of an
CC Alzheimer's disease genotype which is complementary to the sense or
CC antisense strands of a mitochondrial COX gene. Definitive diagnosis of
CC Alzheimer's disease can currently only be accomplished by pathological
CC examination at autopsy, the new method provides a non-invasive diagnostic
CC that is reliable at or before the earliest manifestations of AD symptoms.
CC There is at present no effective therapy for AD other than certain
CC palliative treatments. The new therapeutic compositions and methods
CC provide an effective therapy that addresses the primary cause of AD. The
CC present sequence represents a primer for the human mitochondrial COX
CC gene.
XX
SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578

```
Db      ||| ||| ||| ||| ||| ||| |||
17 TGGTTTCTTAATACCT 1

RESULT 385
ADA50007/c
ID  ADA50007 standard; DNA; 17 BP.
XX
AC  ADA50007;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human mitochondrial COX gene primer #55.
XX
KW  Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
KW  segregation; neutropic; neuroprotective; primer; ss.
XX
OS  Homo sapiens.
XX
PN  US2003087858-A1.
XX
PD  08-MAY-2003.
XX
PF  15-OCT-2001; 2001US-00978600.
XX
PR  30-MAR-1994; 94US-00219842.
XX
PR  30-MAR-1995; 95US-00413740.
XX
PR  23-NOV-1999; 99US-00448312.
XX
PA  (MITO-) MITOKOR.
XX
PI  Herrnstadt C, Ghosh SS;
XX
DR  WPI; 2003-597110/56.
XX
PT  Compositions and methods for the treatment and diagnosis of Alzheimer's
PT  disease using nucleic acids related in sequence to (mutants of) the
PT  cytochrome c oxidase gene.
XX
PS  Example 2; Page 25; 93pp; English.
XX
CC  The present invention relates to compositions and method for the
CC  treatment and diagnosis of Alzheimer's disease (AD). The method comprises
CC  the use of genetic mutations in the human mitochondrial cytochrome c
CC  oxidase (COX) gene and their segregation with AD. Also disclosed are
CC  antisense sequences specific to mutant human cytochrome c oxidase genes
CC  that are designed to bind and inhibit transcription or translation of the
CC  target mutant COX genes without inhibiting transcription or translation
CC  of wild-type cytochrome c oxidase genes. Also disclosed are probes for
CC  detecting a disease state associated with one or more mutations in the
CC  mitochondrial COX genes, and a kit comprising a probe for detection of an
CC  Alzheimer's disease genotype which is complementary to the sense or
CC  antisense strands of a mitochondrial COX gene. Definitive diagnosis of
CC  Alzheimer's disease can currently only be accomplished by pathological
CC  examination at autopsy, the new method provides a non-invasive diagnostic
CC  that is reliable at or before the earliest manifestations of AD symptoms.
CC  There is at present no effective therapy for AD other than certain
CC  palliative treatments. The new therapeutic compositions and methods
CC  provide an effective therapy that addresses the primary cause of AD. The
CC  present sequence represents a primer for the human mitochondrial COX
XX  gene.
XX  Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ  Query Match 1.2%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 2e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 563 GGGTTTTTTTAATACCTT 579
    ||| ||| ||| ||| ||| ||| |||
Db 17 GGTTTTCTTAATACCTT 1

RESULT 387
ADA50009/c
ID  ADA50009 standard; DNA; 17 BP.
XX
```

```
RESULT 386
ADA49972/c
ID  ADA49972 standard; DNA; 17 BP.
XX
AC  ADA49972;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human mitochondrial COX gene primer #20.
XX
KW  Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
KW  segregation; neutropic; neuroprotective; primer; ss.
XX
OS  Homo sapiens.
XX
PN  US2003087858-A1.
XX
PD  08-MAY-2003.
XX
PF  15-OCT-2001; 2001US-00978600.
XX
PR  30-MAR-1994; 94US-00219842.
XX
PR  30-MAR-1995; 95US-00413740.
XX
PR  23-NOV-1999; 99US-00448312.
XX
PA  (MITO-) MITOKOR.
XX
PI  Herrnstadt C, Ghosh SS;
XX
DR  WPI; 2003-597110/56.
XX
PT  Compositions and methods for the treatment and diagnosis of Alzheimer's
PT  disease using nucleic acids related in sequence to (mutants of) the
PT  cytochrome c oxidase gene.
XX
PS  Example 2; Page 24; 93pp; English.
XX
CC  The present invention relates to compositions and method for the
CC  treatment and diagnosis of Alzheimer's disease (AD). The method comprises
CC  the use of genetic mutations in the human mitochondrial cytochrome c
CC  oxidase (COX) gene and their segregation with AD. Also disclosed are
CC  antisense sequences specific to mutant human cytochrome c oxidase genes
CC  that are designed to bind and inhibit transcription or translation of the
CC  target mutant COX genes without inhibiting transcription or translation
CC  of wild-type cytochrome c oxidase genes. Also disclosed are probes for
CC  detecting a disease state associated with one or more mutations in the
CC  mitochondrial COX genes, and a kit comprising a probe for detection of an
CC  Alzheimer's disease genotype which is complementary to the sense or
CC  antisense strands of a mitochondrial COX gene. Definitive diagnosis of
CC  Alzheimer's disease can currently only be accomplished by pathological
CC  examination at autopsy, the new method provides a non-invasive diagnostic
CC  that is reliable at or before the earliest manifestations of AD symptoms.
CC  There is at present no effective therapy for AD other than certain
CC  palliative treatments. The new therapeutic compositions and methods
CC  provide an effective therapy that addresses the primary cause of AD. The
CC  present sequence represents a primer for the human mitochondrial COX
XX  gene.
XX  Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ  Query Match 1.2%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 2e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 562 TGGGTTTTTTTAATACCT 578
    ||| ||| ||| ||| ||| ||| |||
Db 17 TGGTTTCTTAATACCT 1

RESULT 387
ADA50009/c
ID  ADA50009 standard; DNA; 17 BP.
XX
```

AC ADA50009;
XX 20-NOV-2003 (first entry)
DT
XX Human mitochondrial COX gene primer #57.
DE
XX Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
KW segregation; neurotropic; neuroprotective; primer; ss.
KW
XX Homo sapiens.
OS
XX US2003087858-A1.
PN
XX 08-MAY-2003.
PD
XX 15-OCT-2001; 2001US-00978600.
PF
XX 30-MAR-1994; 94US-00219842.
PR
XX 30-MAR-1995; 95US-00413740.
PR
XX 23-NOV-1999; 99US-00448312.
XX
PA (MITO-) MITOKOR.
XX
XX Herrnstadt C, Ghosh SS;
PI
XX WPI; 2003-597110/56.
DR
XX Compositions and methods for the treatment and diagnosis of Alzheimer's
PT disease using nucleic acids related in sequence to (mutants of) the
PT cytochrome c oxidase gene.
XX
PS Example 2; Page 25; 93pp; English.
XX
CC The present invention relates to compositions and method for the
CC treatment and diagnosis of Alzheimer's disease (AD). The method comprises
CC the use of genetic mutations in the human mitochondrial cytochrome c
CC oxidase (COX) gene and their segregation with AD. Also disclosed are
CC antisense sequences specific to mutant human cytochrome c oxidase genes
CC that are designed to bind and inhibit transcription or translation of the
CC target mutant COX genes without inhibiting transcription or translation
CC of wild-type cytochrome c oxidase genes. Also disclosed are probes for
CC detecting a disease state associated with one or more mutations in the
CC mitochondrial COX genes, and a kit comprising a probe for detection of an
CC Alzheimer's disease genotype which is complementary to the sense or
CC antisense strands of a mitochondrial COX gene. Definitive diagnosis of
CC Alzheimer's disease can currently only be accomplished by pathological
CC examination at autopsy, the new method provides a non-invasive diagnostic
CC that is reliable at or before the earliest manifestations of AD symptoms.
CC There is at present no effective therapy for AD other than certain
CC palliative treatments. The new therapeutic compositions and methods
CC provide an effective therapy that addresses the primary cause of AD. The
CC present sequence represents a primer for the human mitochondrial COX
CC gene.
XX
SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 563 GGGTTTTTTAATACCTT 579
Db 17 GGGTTTTTCTAATACCTT 1

RESULT 388
ADA50006/c
ID ADA50006 standard; DNA; 17 BP.
XX
AC ADA50006;
XX
XX 20-NOV-2003 (first entry)
DT
XX

DE Human mitochondrial COX gene primer #54.
XX
KW Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
KW segregation; neurotropic; neuroprotective; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003087858-A1.
XX
PD 08-MAY-2003.
XX
PF 15-OCT-2001; 2001US-00978600.
XX
PR 30-MAR-1994; 94US-00219842.
PR 30-MAR-1995; 95US-00413740.
PR 23-NOV-1999; 99US-00448312.
XX
PA (MITO-) MITOKOR.
XX
XX Herrnstadt C, Ghosh SS;
PI
XX WPI; 2003-597110/56.
DR
XX Compositions and methods for the treatment and diagnosis of Alzheimer's
PT disease using nucleic acids related in sequence to (mutants of) the
PT cytochrome c oxidase gene.
XX
PS Example 2; Page 25; 93pp; English.
XX
CC The present invention relates to compositions and method for the
CC treatment and diagnosis of Alzheimer's disease (AD). The method comprises
CC the use of genetic mutations in the human mitochondrial cytochrome c
CC oxidase (COX) gene and their segregation with AD. Also disclosed are
CC antisense sequences specific to mutant human cytochrome c oxidase genes
CC that are designed to bind and inhibit transcription or translation of the
CC target mutant COX genes without inhibiting transcription or translation
CC of wild-type cytochrome c oxidase genes. Also disclosed are probes for
CC detecting a disease state associated with one or more mutations in the
CC mitochondrial COX genes, and a kit comprising a probe for detection of an
CC Alzheimer's disease genotype which is complementary to the sense or
CC antisense strands of a mitochondrial COX gene. Definitive diagnosis of
CC Alzheimer's disease can currently only be accomplished by pathological
CC examination at autopsy, the new method provides a non-invasive diagnostic
CC that is reliable at or before the earliest manifestations of AD symptoms.
CC There is at present no effective therapy for AD other than certain
CC palliative treatments. The new therapeutic compositions and methods
CC provide an effective therapy that addresses the primary cause of AD. The
CC present sequence represents a primer for the human mitochondrial COX
CC gene.
XX
SQ Sequence 17 BP; 9 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 562 TGGGTTTTTTAATACCT 578
Db 17 TGGTTTTTCTAATACCT 1

RESULT 389
ADA50271
ID ADA50271 standard; DNA; 17 BP.
XX
AC ADA50271;
XX
XX 20-NOV-2003 (first entry)
DT
XX
DE Human PCR primer 90835 related to abacavir hypersensitivity.
XX
KW hypersensitivity reaction; abacavir; 57.1 ancestral haplotype;
KW Major Histocompatibility Complex; MHC; human leukocyte antigen; HLA;

KW HLA-B*5701; C4A6; HLA-DR7; HLA-DQ3; Human immunodeficiency virus; HIV;
KW immune system; acquired immune deficiency syndrome; AIDS;
KW peripheral nervous system; antiviral compound; HIV replication inhibitor;
KW antiviral; nucleoside reverse transcriptase inhibitor; NRTI;
KW antiretroviral drug; abacavir; human; sequencing primer; primer; PCR; ss;
KW 90835.
XX
OS Homo sapiens.
XX
PN WO2003068985-A1.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-AU000183.
XX
PR 12-FEB-2002; 2002AU-00000464.
XX
PA (EPIP-) EPIPOP PTY LTD.
XX
XX Mallal S;
PI
XX
DR WPI; 2003-697530/66.
XX
XX Method for the identification of subjects hypersensitive to abacavir,
PT useful for excluding patients from treatment, comprises detecting the
PT presence of the 57.1 ancestral haplotype.
XX
PS Example 2; Page 21; 43pp; English.
XX
CC This invention relates to a method for determining whether a patient will
CC show a hypersensitivity, or similar, reaction to abacavir by typing the
CC patient for presence of the 57.1 ancestral haplotype of the Major
CC Histocompatibility Complex (MHC). The ancestral haplotype is defined by
CC presence of the human leukocyte antigen (HLA) subtypes HLA-B*5701, C4A6,
CC HLA-DR7 and HLA-DQ3. Human immunodeficiency virus (HIV) is the
CC aetiological agent of a complex disease that includes progressive
CC destruction of the immune system (acquired immune deficiency syndrome,
CC AIDS) and degeneration of the peripheral nervous system. It is known that
CC some antiviral compounds which act as inhibitors of HIV replication are
CC effective agents in the treatment of AIDS. Treatment with an antiviral to
CC a person with hypersensitivity may lead to a range of ailments and
CC occasionally death. Patients who have the 57.1 ancestral haplotype are at
CC a high risk of developing a hypersensitive reaction to abacavir, a
CC nucleoside reverse transcriptase inhibitor (NRTI) antiretroviral drug
CC often used to treat HIV and AIDS. The identification method of the
CC invention may be useful for identifying patients who need to be excluded
CC from treatment with abacavir. The present sequence is that of a human
CC sequencing and PCR amplification primer which was used for identifying
CC the presence or absence of the 57.1 ancestral haplotype of the MHC of the
CC invention.
XX
SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Oy 245 TCAGATGCAACCACTAG 261
||| ||||| |||
Db 1 TCAGCTGCAACCACTAG 17

RESULT 390
ADL46684/c
ID ADL46684 standard; RNA; 17 BP.
XX
AC ADL46684;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor inozyme substrate sequence #117.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;

KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor inozyme; substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 9; SEQ ID NO 217; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human NOGO
CC receptor inozyme substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 9 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Oy 15 GGCTGCCCGGCGCTGG 31
||| ||| |||||
Db 17 GGCGGCCCGAGCGCTGG 1

RESULT 391
ADM09493/c
ID ADM09493 standard; RNA; 17 BP.
XX
AC ADM09493;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor amberzyme substrate sequence #48.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;

KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor amberzyme; substrate; ss.
XX
OS Unidentified.
XX
XX WO200281628-A2.
XX
PD 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010512.
PF
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
PI
XX WPI; 2003-058513/05.
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 9; SEQ ID NO 888; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human NOGO
CC receptor amberzyme substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 AGGCTGCCCGGCCGTG 30
Db ||||| ||||| |||||
17 AGGCGGCCCGAGGCCGTG 1

RESULT 392
ADM54293
ID ADM54293 standard; mRNA; 17 BP.
XX
AC ADM54293;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human GRID mRNA substrate sequence #603.
XX
KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;

KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNAzyme; amberzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
OS Homo sapiens.
XX
PN US2003134806-A1.
XX
PD 17-JUL-2003.
XX
PF 23-FEB-2001; 2001US-00792818.
XX
PR 10-FEB-2000; 2000US-0181594P.
XX
PA (JARV/) JARVIS T.
PA (CARL/) CARLOWITZ I V.
PA (MCSW/) MCSWIGGEN J.
PA (HAMB/) HAMBLIN P A.
PA (ELLI/) ELLIS J H.
XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
DR WPI; 2003-829646/77.
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
PS Claim 4; SEQ ID NO 603; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNAzyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 105 TCAGTGGGGCTATTGGA 121
Db :|||:|||||: :|||
1 UCAGUGGGGCUGUGGGA 17

RESULT 393
ADL82299
ID ADL82299 standard; DNA; 17 BP.
XX
AC ADL82299;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ER+ breast cancer differentially expressed sequence #269.
XX
KW gene therapy; ds; breast cancer; human; ER+ breast cancer.
XX
OS Homo sapiens.
XX

PN US2003166026-A1.
PD 04-SEP-2003.
XX
PF 08-JAN-2003; 2003US-003339782.
XX
PR 09-JAN-2002; 2002US-0348053P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Goodman LJ, Bowen BA;
XX
DR WPI; 2004-069003/07.
XX
PT Vector containing nucleic acid associated with breast cancer, useful for
PT treating, diagnosing and characterizing breast cancer, also related
PT polypeptides and antibodies.
XX
PS Claim 1; SEQ ID NO 270; 61pp; English.
XX
CC The invention relates to a composition which contains at least one vector
CC (B) containing a nucleic acid (I) associated with breast cancer. The
CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
CC -specific antibodies (Ab) are used to predict characteristics (e.g.
CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
CC used to modulate characteristics of such cells; to identify breast cancer
CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
CC or its products). The present sequence represents a human ER+ breast
CC cancer differentially expressed sequence.
XX
SQ Sequence 17 BP; 7 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 898 GACCAAGAGCCTCAACA 914
DB |||||||
1 GATCAAGACCCCTCAACA 17

RESULT 394
ACN69847
ID ACN69847 standard; DNA; 17 BP.
XX
AC ACN69847;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:6749.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
DR WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 6749; 0pp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 5 A; 2 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 836 AGGAAGGCCGGGTGGA 852
DB |||||||
1 AGGAAGGCCGTGAGGA 17

RESULT 395
ACN65662/c
ID ACN65662 standard; DNA; 17 BP.
XX
AC ACN65662;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:2564.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.

```
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 2564; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 744 GGCAGCTGCCACCTTAT 760
Db 17 GGCAGCTGCCGCTTCT 1
RESULT 396
ACN65661/c
ID ACN65661 standard; DNA; 17 BP.
XX
AC ACN65661;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:2563.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
```

```
XX US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 2563; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 745 GCAGCTGCCACCTTATG 761
Db 17 GCAGCTGCCGCTTCTG 1
RESULT 397
AAV44608/c
ID AAV44608 standard; DNA; 18 BP.
XX
AC AAV44608;
XX
DT 24-NOV-1998 (first entry)
```

```
XX DE Human uncoupling protein-2 UCP2 gene reverse primer hUCP2g.e6r1.
XX KW Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
XX KW obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
XX KW hypothermia; wasting; cachexia; anorexia; inflammation; fever;
XX KW hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO98311396-A1.
XX XX 23-JUL-1998.
XX PD 22-APR-1997; 97WO-US006864.
XX PF 15-JAN-1997; 97US-0034960P.
XX XX
XX PA (UYDU-) UNIV DUKE.
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (CNRS ) CENT NAT RECH SCI.
XX XX
XX PI Surwit RS, Collins SA, Warden CH, Seldin MF, Ricquier D;
XX PI Bouillaud F;
XX XX
XX DR WPI; 1998-413823/35.
XX XX
XX PT Method for treating disease associated with altered UCP-2 expression - by
XX PT administering agent which enhances or inhibits UCP-2 activity,
XX PT effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
XX PT etc.
XX XX
XX PS Example IX; Page 47; 98pp; English.
XX XX
XX CC Primer hUCP2g.e6r1 is used with forward primer hUCPg.e6f1 (see AAV44607)
XX CC in the PCR amplification of bp 3147-3416 in exon 6 of the human
XX CC uncoupling protein-2 (UCP2) gene. Primers (see AAV44603-18) were designed
XX CC to amplify hUCP2 exons 4, 6, 7 and 8 from genomic DNA. Common amino acid
XX CC variants (see AAW69166) are present in exons 4, 6 and 8; A55V in exon 4,
XX CC N190S in exon 6, and L294M in exon 8 (see also AAV44595). Restriction
XX CC enzymes have been identified that would differentially digest each
XX CC of the alleles. The invention relates to a method for treating disease
XX CC associated with altered UCP2 expression, such as obesity, diabetes,
XX CC syndrome X, hypothermia, hyperinsulinaemia, glucose intolerance, wasting,
XX CC anorexia, inflammation, cachexia, fever or hyperthermia
XX XX
XX SQ Sequence 18 BP; 5 A; 1 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 201 TCTCCCCCATCCCCCAT 217
Db ||||| ||||| ||||| |||||
17 TCTCACCTTCCCCCAT 1

RESULT 398
AAZ00111
ID AAZ00111 standard; DNA; 18 BP.
XX AC
XX AC AAZ00111;
XX XX
XX DT 12-OCT-1999 (first entry)
XX XX
XX DE HEV US-1 amplifying primer.
XX XX
XX KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
XX KW vaccine; passive immunisation; PCR primer; ss.
XX XX
XX OS Synthetic.
XX OS Hepatitis E virus.
```

```
XX PN WO9919732-A1.
XX XX
XX PD 22-APR-1999.
XX XX
XX PF 15-OCT-1998; 98WO-US021941.
XX XX
XX PR 15-OCT-1997; 97US-0061199P.
XX XX
XX PA (ABBO ) ABBOTT LAB.
XX XX
XX PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX XX
XX DR WPI; 1999-288017/24.
XX XX
XX PT Detection of United States isolates of hepatitis E virus.
XX XX
XX PS Example 2; Page 141; 260pp; English.
XX XX
XX CC The invention provides a method for detecting a US (sub)type hepatitis E
XX CC virus (US-HEV), or its naturally occurring variants in a sample by
XX CC treatment with a binding partner specific for a marker of the virus, and
XX CC then detecting any complex formed. The method is used to diagnose
XX CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
XX CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
XX CC are useful in vaccines or for passive immunisation. The polypeptides are
XX CC also used to raise specific antibodies (useful as immunoassay reagents).
XX CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
XX CC usual hybridisation and amplification assays for detecting infection. The
XX CC present sequence represents a HEV specific primer
XX XX
XX SQ Sequence 18 BP; 6 A; 8 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1035 TAAACATCACCCCAAC 1051
Db | ||||| ||||| |||||
2 TGAACATCACGCCCAAC 18

RESULT 399
AAZ76902/C
ID AAZ76902 standard; DNA; 18 BP.
XX AC
XX AC AAZ76902;
XX XX
XX DT 17-OCT-2003 (revised)
XX DT 05-AUG-1999 (first entry)
XX XX
XX DE H2-1 Pag1 gene direct repeat sequence.
XX XX
XX KW H2-1 pag1 promoter; persistence-associated gene 1; insect cell;
XX KW constitutive expression promoter; direct repeat; ss.
XX XX
XX OS Heliothis zea virus 1.
XX XX
XX PN US5911982-A.
XX XX
XX PD 15-JUN-1999.
XX XX
XX PF 18-APR-1996; 96US-00634350.
XX XX
XX PR 06-OCT-1995; 95US-0004894P.
XX PR 11-OCT-1995; 95US-0005128P.
XX XX
XX PA (NASC-) NAT SCI COUNCIL.
XX XX
XX PI Chao Y;
XX XX
XX DR WPI; 1999-357167/30.
XX XX
```


Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 CCCCCATCCCCCATTTTC 220
Db 18 CCTCCATCCCCCATCTC 2

RESULT 402
AAZ70376/c
ID AAZ70376 standard; DNA; 18 BP.
XX
AC AAZ70376;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4732.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
DR
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1240; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 5 A; 2 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 905 AGCCTCAACATTTTCCTA 921
Db 17 AGCCTCAGCATTTTCATA 1

RESULT 403
ABL54891
ID ABL54891 standard; DNA; 18 BP.
XX
AC ABL54891;
XX
DT 31-MAY-2002 (first entry)
XX
DE PCR primer BV-b5.
XX
KW PCR primer; gap vector; Escherichia coli; stop codon assay;
KW truncating mutation; ss.
XX
OS Synthetic.
XX
PN KR2001016649-A.
XX
PD 05-MAR-2001.
XX
PF 02-AUG-1999; 99KR-00031647.
XX
PR 02-AUG-1999; 99KR-00031647.
XX
PA (KWAN-) KWANGMYUNG SUNGAB MEDICAL FOUND.
XX
DR WPI; 2001-495301/54.
XX
PT Gap vector for Escherichia coli stop codon assay used for assaying
PT heterozygous truncating mutation.
XX
PS Disclosure; Page 19; 33pp; Korean.
XX
CC This sequence represents a PCR primer used within the scope of the
CC invention. The invention relates to a gap vector (GV) for assaying
CC Escherichia coli (E.coli) stop codon. The invention also relates to a
CC method for assaying heterozygous truncating mutation using the GV
CC comprising the following steps: (1) multiplying exon fragments showing
CC truncating mutation by polymerase chain reaction (PCR) and cloning the
CC exon fragments with a plasmid for E. coli having a low copy number; (2)
CC using the plasmid having cloned exon gene as a template and performing
CC PCR with a primer having 50-200 bp of 5' and 3' terminals of the exon
CC gene to make a gap vector for E. coli stop codon assay; (3) multiplying
CC the same genetic fragment as the multiplied exon fragment through RT-PCR
CC or PCR using RNA obtained from a sample to be measured or cDNA as a
CC template; and (4) transforming the gap vector obtained from step (2) and
CC the genetic fragment obtained from step (3) into E. coli at the same time
XX
SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 CACATGAAAGTTTGAGA 1016
Db 1 CACATGCAAGTTTGAAA 17

RESULT 404
ACF63028/c
ID ACF63028 standard; DNA; 18 BP.
XX
AC ACF63028;
XX
DT 09-OCT-2003 (first entry)
XX
DE Human progesterone receptor PCR primer SEQ ID NO:277.
XX
KW Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
KW progesterone receptor; pcna; cdc2; c-erbB2; methylation; CpG;
KW characterisation; classification; diagnosis; differentiation;
KW colon cell proliferative disorder; PCR primer; ss.

XX OS Homo sapiens.
OS Synthetic.
XX PN WO2003014388-A2.
XX PD 20-FEB-2003.
XX PF 09-AUG-2002; 2002WO-EP008939.
XX PR 09-AUG-2001; 2001DE-01039283.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Distler J, Model F, Taubert H;
XX WPI; 2003-256600/25.
XX DR Determining methylation status of CpG dinucleotides using modified
XX PT genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
XX PT characterization, grading, staging and/or diagnosis of colon cancer.
XX PS Claim 26; Page 171; 219pp; English.
XX CC The present invention describes a method for determining the methylation
CC status of CpG dinucleotides within the genes for oestrogen receptor, p21,
CC p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erbB2, p53
CC and/or CEA, which comprises contacting the target nucleic acid with a
CC reagent that distinguishes between methylated and non-methylated CpG
CC dinucleotides, and determining from the methylation status of the CpG
CC positions the presence of a colon cancer. A set of oligomers or peptide
CC nucleic acid (PNA)-oligomers can be used as probes for determining the
CC cytosine methylation state and/or single nucleotide polymorphisms (SNP)
CC of a corresponding genomic DNA by analysis of a chemically pretreated
CC genomic DNA. The pretreated genomic DNA is useful for the determination
CC of the methylation status of a corresponding genomic DNA and/or detection
CC of SNPs. The methods and pretreated genomic DNA are also useful for the
CC characterisation, classification, diagnosis and differentiation of colon
CC cell proliferative disorders. ACF62752 to ACF63278 represent sequences
CC used in the exemplification of the present invention
XX SQ Sequence 18 BP; 8 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 TAGGAGATGAGTTTAT 632
Db | | | | | | | | | | | | | | | |
17 TAGGAGATGAGATTTT 1

RESULT 405
ACF63026
ID ACF63026 standard; DNA; 18 BP.
XX AC ACF63026;
XX 09-OCT-2003 (first entry)
XX DE Human progesterone receptor PCR primer SEQ ID NO:275.
XX KW Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
KW progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
KW characterisation; classification; diagnosis; differentiation;
KW colon cell proliferative disorder; PCR primer; ss.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO2003014388-A2.
XX PD 20-FEB-2003.

XX 09-AUG-2002; 2002WO-EP008939.
XX PF Synthetic.
XX PR 09-AUG-2001; 2001DE-01039283.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Distler J, Model F, Taubert H;
XX WPI; 2003-256600/25.
XX DR Determining methylation status of CpG dinucleotides using modified
XX PT genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
XX PT characterization, grading, staging and/or diagnosis of colon cancer.
XX PS Claim 26; Page 170; 219pp; English.
XX CC The present invention describes a method for determining the methylation
CC status of CpG dinucleotides within the genes for oestrogen receptor, p21,
CC p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erbB2, p53
CC and/or CEA, which comprises contacting the target nucleic acid with a
CC reagent that distinguishes between methylated and non-methylated CpG
CC dinucleotides, and determining from the methylation status of the CpG
CC positions the presence of a colon cancer. A set of oligomers or peptide
CC nucleic acid (PNA)-oligomers can be used as probes for determining the
CC cytosine methylation state and/or single nucleotide polymorphisms (SNP)
CC of a corresponding genomic DNA by analysis of a chemically pretreated
CC genomic DNA. The pretreated genomic DNA is useful for the determination
CC of the methylation status of a corresponding genomic DNA and/or detection
CC of SNPs. The methods and pretreated genomic DNA are also useful for the
CC characterisation, classification, diagnosis and differentiation of colon
CC cell proliferative disorders. ACF62752 to ACF63278 represent sequences
CC used in the exemplification of the present invention
XX SQ Sequence 18 BP; 5 A; 0 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 TAGGAGATGAGTTTAT 632
Db | | | | | | | | | | | | | | | |
2 TAGGAGATGAGATTTT 18

RESULT 406
ADM06379/c
ID ADM06379 standard; DNA; 18 BP.
XX AC ADM06379;
XX 20-MAY-2004 (first entry)
XX DE Human PCR primer SEQ ID NO:5064.
XX KW human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.
XX OS Homo sapiens.
XX PN EP1347046-A1.
XX PD 24-SEP-2003.
XX PF 12-APR-2002; 2002EP-00008400.
XX PR 22-MAR-2002; 2002JP-00137785.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX

XX WPI; 2003-723558/69.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX Example 8; SEQ ID NO 5064; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents an

CC oligonucleotide used in the invention.

XX Sequence 18 BP; 9 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

SQ Query Match 1.2%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 295 TCGAATTGTTGTTCTG 311

Db ||| ||||| |||||

18 TCGTATTGTTGTGCTG 2

RESULT 407

ADJ65208

ID ADJ65208 standard; DNA; 18 BP.

XX AC ADJ65208;

XX 20-MAY-2004 (first entry)

DE Human connexin gene 26 Cx26 235 Del mutant primer seq id 10.

XX hereditary hearing loss; connexin 26; Cx26; mitochondrial gene;

KW Cytomegalovirus gene; CMV; human; PCR; primer; ss; mutant.

XX Homo sapiens.

XX US2004038266-A1.

PN 26-FEB-2004.

XX 22-MAY-2003; 2003US-00443545.

XX 28-MAY-2002; 2002US-0370762P.

PR (DOBR/) DOBROWOLSKI S F.

PA (LINZ/) LIN Z.

XX Dobrowolski SF, Lin Z;

XX WPI; 2004-213937/20.

DR Genetically screening for detecting hereditary hearing loss by detecting

XX connexin 26, a mitochondrial or Cytomegalovirus nucleic acids by

PT hybridization and/or PCR.

XX Claim 6; SEQ ID NO 10; 22pp; English.

PS The invention describes a method of genetically screening for detecting

XX hereditary hearing loss. The method comprises detecting a nucleic acid

CC from a connexin 26 (Cx26), a mitochondrial gene and/or a Cytomegalovirus

CC (CMV) gene by hybridisation and/or PCR. The methods of the invention are

CC used for detecting causes of hereditary hearing loss. This sequence

CC represents a primer used in the isolation of DNA encoding the human

CC connexin 26 (Cx26) mutant Cx26 235 Del.

XX SQ Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCCATCC 212

Db | ||||| |||||

1 CCCCATCTCCACATCC 17

RESULT 408

ADN35818/C

ID ADN35818 standard; DNA; 18 BP.

XX AC ADN35818;

XX 01-JUL-2004 (first entry)

DE Human NSCLC gene antisense-S oligonucleotide #39.

XX ss; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC;

KW diagnosis; cancer; URLC1; antisense.

XX Homo sapiens.

OS WO2004031413-A2.

XX 15-APR-2004.

PD 22-SEP-2003; 2003WO-JP012072.

PF 30-SEP-2002; 2002US-0414673P.

PR 28-FEB-2003; 2003US-0451374P.

PR 28-APR-2003; 2003US-0466100P.

XX (ONCO-) ONCOTHERAPY SCI INC.

PA (UYTY) UNIV TOKYO.

XX Nakamura Y, Daigo Y, Nakatsuru S;

PI WPI; 2004-330206/30.

DR Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)

XX comprises determining an expression level of an NSCLC-associated gene in

PT a sample.

XX Disclosure; SEQ ID NO 499; 394pp; English.

PS The invention relates to a method of diagnosing non-small cell lung

XX cancer (NSCLC) or a predisposition to developing NSCLC in a subject by

CC determining the expression level of a NSCLC-associated gene in a

CC biological sample derived from the subject, where an increase or decrease

CC of the level compared to a normal control level of the gene indicates

CC that the subject suffers from or is at risk of developing NSCLC. The

CC method is useful in diagnosing NSCLC or a predisposition to developing

CC NSCLC in a subject. The compound, polynucleotide and the encoded

CC polypeptide and composition are useful in treating or preventing NSCLC.

CC This sequence corresponds to an antisense oligonucleotide of genes that

CC are differentially expressed in NSCLC cells.

XX Sequence 18 BP; 5 A; 7 C; 0 G; 6 T; 0 U; 0 Other;

SQ Query Match 1.2%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 432 GAAGAGGAGATGATTTT 448

Db ||| ||||| |||||

18 GAGGAGGAATGATTTT 2


```
RESULT 409
ADS90119
ID ADS90119 standard; DNA; 18 BP.
XX
AC ADS90119;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:1135.
XX
KW ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Unidentified.
XX
XX WO2004035803-A2.
PN
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
PI
XX WPI; 2004-348468/32.
DR
XX Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject..
XX
PS Disclosure; SEQ ID NO 1135; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 18 BP; 3 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 152 GAGGATTATGCGGTTTA 168
Db ||||| ||||| ||||| |||||
1 GAGGGTTATCGCGTTTA 17

RESULT 410
AAA83453/c
ID AAA83453 standard; DNA; 19 BP.
XX
AC AAA83453;
XX
DT 04-DEC-2000 (first entry)
XX
```

```
XX cdk8 ribozyme binding site #173.
DE
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KW
XX Mammalia.
OS
XX WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI
XX WPI; 2000-412314/35.
XX
DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
PT
XX Disclosure; Page 62; 109pp; English.
PS
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 10 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 415 GTTTTTCCTTATATTG 431
Db ||||| ||||| ||||| |||||
19 GTTTTCCATATACTTG 3

RESULT 411
AAA83063/c
ID AAA83063 standard; DNA; 19 BP.
XX
AC AAA83063;
XX
XX 04-DEC-2000 (first entry)
DT
XX cdk6 ribozyme binding site #123.
DE
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
KW
XX Mammalia.
OS
XX WO200032765-A2.
PN
XX 08-JUN-2000.
PD
XX 06-DEC-1999; 99WO-US028772.
PF
XX 04-DEC-1998; 98US-0110954P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
PI
XX
```

```

DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
XX
PS Disclosure; Page 56; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.2%; Score 13.8; DB 1; Length 19;
XX Best Local Similarity 88.2%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 603 AAGACTTCATAAGTAGG 619
Db ||||||| |||||||
19 AACACTTCAGAGTAGG 3
XX
XX
XX RESULT 412
XX AAH56706/c
ID AAH56706 standard; DNA; 19 BP.
XX
AC AAH56706;
XX
DT 06-SEP-2001 (first entry)
XX
DE Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:354.
XX
KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
KW antibacterial; antiviral; antiproliferative; antisense therapy;
KW microbial infection; ss.
XX
OS Streptococcus pyogenes.
XX
XX WO200136625-A2.
PN
XX
XX 25-MAY-2001.
PD
XX
XX 20-NOV-2000; 2000WO-CA001347.
PF
XX
XX 18-NOV-1999; 99US-0166249P.
PR
XX
XX (GENE-) GENESENSE TECHNOLOGIES INC.
PA
XX
XX Wright JA, Young AH, Dugourd D;
PI
XX
XX WPI; 2001-355633/37.
DR
XX
XX Novel antisense compounds targeting nucleic acid encoding groEL or groES
PT gene of microorganism, which hybridize with and inhibit expression of the
PT genes, useful to inhibit growth of microorganism having the genes.
PT
XX
PS Claim 3; Page 50; 110pp; English.
XX
XX
XX The present invention specifically claims AAH56368 to AAH56832 which are
CC antisense oligonucleotides to nucleotide sequences encoding groE. More
CC generally, antisense compounds (I) comprising antisense oligonucleotides
CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
CC microorganism, where the antisense compound is complementary to GL or GS
CC of a microorganism and specifically hybridizes with and inhibits the
CC

```

expression of GL or GS, is claimed. (I) have antibacterial, antiviral and antiproliferative activities, and can be used in antisense therapy and for inhibiting expression of GROES or groEL. (I) are useful for inhibiting expression of GL or GS in cells or tissues in vitro. (I) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterial cell or a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism, (I). (I) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism having a pathological condition mediated by microorganisms having a GL or GS gene and administering (I) such that the growth of microorganism is inhibited. The antisense compounds are utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854 represent PCR primers for groE sequences which are used in the exemplification of the present invention. AAH56855 to AAH56870 represent groE nucleotide sequence given in the present invention

Sequence 19 BP; 8 A; 2 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 567 TTTTAAATACCTTTATA 583
 ||||| |||||
 Db 18 TTTTAAACCTTTAGA 2

RESULT 413
 AAH58225/c

ID AAH58225 standard; DNA; 19 BP.
 AC AAH58225;
 XX

DT 10-SEP-2001 (first entry)
 XX
 DE Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:649.
 XX

KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulneryary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX

PF 26-OCT-2000; 2000WO-US029500.
 XX
 PR 26-OCT-1999; 99US-0161532P.
 XX

XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 PI
 XX WPI; 2001-300427/31.
 DR
 XX

PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX

PS Example 1; Page 119; 408pp; English.

XX The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnery, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX

SQ Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 603 AAGACTTCATAAGTAGG 619

Db 19 AACACTTCAGAGTAGG 3

RESULT 414

AAH58615/c

ID AAH58615 standard; DNA; 19 BP.

XX

AC AAH58615;

XX

DT 10-SEP-2001 (first entry)

XX

DE Cell-cycle dependent kinase cdk8 ribozyme binding site SEQ ID NO:1039.

XX

KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

KW recognition site; target; ribozyme binding site; eye disease; vulnery;

KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;

KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;

KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;

KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;

KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;

KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;

KW sickle cell retinopathy; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200130362-A2.

XX

PD 03-MAY-2001.

XX

PF 26-OCT-2000; 2000WO-US029500.

XX

PR 26-OCT-1999; 99US-0161532P.

XX

PA (IMMU-) IMMUSOL INC.

XX

PI Robbins JM, Tritz R;

XX

DR WPI; 2001-300427/31.

XX

PT Treating proliferative skin or eye diseases and scarring, using ribozymes

PT that cleave RNA encoding cytokines involved in inflammation, matrix

PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX

PS Example 1; Page 147; 408pp; English.

XX The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnery, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX

SQ Sequence 19 BP; 10 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 415 GTTTTTCCTTATATTG 431

Db 19 GTTTTCCATATACTTG 3

RESULT 415

AAF74684

ID AAF74684 standard; DNA; 19 BP.

XX

AC AAF74684;

XX

DT 16-MAY-2001 (first entry)

XX

DE P. furiosus thermophilic glucoamylase PCR primer SEQ ID NO:9.

XX

KW Pyrococcus furiosus; thermophilic glucoamylase; starch decomposition;

KW glucose; oligosaccharide; cyclodextrin; genetic engineering; PCR primer;

KW ss.

XX

OS Pyrococcus furiosus.

XX

PN WO200109348-A1.

XX

PD 08-FEB-2001.

XX

PF 26-JUL-2000; 2000WO-JP004956.

XX

PR 02-AUG-1999; 99JP-00218778.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

PI Koyama N, Okui T, Takakura H, Asada K, Kato I;

XX

DR WPI; 2001-168708/17.

XX

PT Polypeptides with thermophilic glucoamylase activity and high thermal

PT stability, applicable in efficient utilization of biomass e.g. in

PT decomposing starch to produce glucose or oligosaccharides or

PT cyclodextrins.

XX

PS Example 4; Page 56; 62pp; Japanese.

XX The present invention describes a protein derived from Pyrococcus

CC

CC furiousus having thermophilic glucoamylase activity. Also described are:
CC (i) a nucleic acid encoding the protein; (ii) a nucleic acid hybridisable
CC with any of the above nucleic acids under stringent conditions and
CC encoding a protein with thermophilic glucoamylase activity; (iii) a
CC recombinant DNA contains the nucleic acid; (iv) a transformant which is
CC transformed with the recombinant DNA; (v) a process for producing the
CC protein by culturing the transformant before collecting the protein that
CC has thermophilic glucoamylase activity from the cultured material; and
CC (vi) a process for producing glucose by the action of the above protein
CC on the alpha-1,4 linkage in a D-glucopyranose polymer to produce free
CC glucose, or oligosaccharides, or cyclodextrin. The proteins are
CC applicable in efficient utilisation of biomass e.g. in decomposing starch
CC to produce glucose or oligosaccharides or cyclodextrins. Such proteins
CC can be produced by genetic engineering at low cost. The present sequence
CC represents a PCR primer for a Pyrococcus furiosus protein having
CC thermophilic glucoamylase activity, which is used in an example from the
CC present invention
XX
SQ Sequence 19 BP; 3 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 857 TCTTTGTGTTGTAGTCC 873
DB 3 TCCATGTGTTGTAGTCC 19
|| |||||

RESULT 416
ADFF31834
ID ADF31834 standard; RNA; 19 BP.
XX
AC ADF31834;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IGF-1R siNA lower strand, SEQ ID NO:499.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW proliferative disease; restenosis; polycystic kidney disease;
KW inflammatory disease; allergic disease; autoimmune disease;
KW transplant rejection; cytostatic; vasotropic; nephrotropic;
KW antiinflammatory; antiallergic; immunosuppressive; human;
KW insulin-like growth factor 1 receptor; IGF-1R; ss.
XX
OS Homo sapiens.
XX
PN WO2003070911-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B;
XX
DR WPI; 2003-721691/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of cancer , downregulates expression of the insulin-like growth
PT factor-1 receptor gene.
XX
PS Example 3; SEQ ID NO 499; 147pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human insulin-like growth factor 1
CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA), double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the IGF-1R gene in cells, tissue explants or organisms
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC cancer and other proliferative diseases (e.g., restenosis and polycystic
CC kidney disease), inflammatory and/or allergic diseases, autoimmune
CC diseases and transplant rejection. . The siNAs are also useful for drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
CC represents the lower strand of a human IGF-1R-targeted double-stranded
CC siNA.
XX
SQ Sequence 19 BP; 3 A; 3 C; 11 G; 0 T; 2 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 2.1e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 22 CGGGCCGTGGCAGGAAG 38
DB 3 CGGGCAGUGGCGGCGAG 19
||| ||| |

RESULT 417
ADFF31557/c
ID ADF31557 standard; RNA; 19 BP.
XX
AC ADF31557;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IGF-1R transcript target sequence/siNA upper strand, SEQ ID NO:222.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW proliferative disease; restenosis; polycystic kidney disease;
KW inflammatory disease; allergic disease; autoimmune disease;
KW transplant rejection; cytostatic; vasotropic; nephrotropic;
KW antiinflammatory; antiallergic; immunosuppressive; human;
KW insulin-like growth factor 1 receptor; IGF-1R; target sequence; ss.
XX
OS Homo sapiens.
XX
PN WO2003070911-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005044.
XX
PR 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-0386782P.

PT infection.
XX
PS Disclosure; SEQ ID NO 63; 136pp; English.
XX
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents a PCR primer for
CC the Oryza minuta Pi9 locus.
XX
SQ Sequence 19 BP; 14 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 414 GGTTTTCCTTATATT 430
Db 19 GGTTTTCCTTGTATT 3

RESULT 420
ADN75775
ID ADN75775 standard; RNA; 19 BP.
XX
AC ADN75775;
XX
DT 01-JUL-2004 (first entry)
XX
DE TCPTP associated siRNA hTCPTP1.5 #2.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosstatic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
PR 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Claim 1; SEQ ID NO 600; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosstatic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX

SQ Sequence 19 BP; 4 A; 4 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 2.1e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 343 GGCTGTGATCAAAATGGG 359
Db 2 GACUGUGAUCAUAGGG 18

RESULT 421
ADN75774/c
ID ADN75774 standard; RNA; 19 BP.
XX
AC ADN75774;
XX
DT 01-JUL-2004 (first entry)
XX
DE TCPTP associated siRNA hTCPTP1.5 #1.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosstatic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
PR 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Claim 6; SEQ.ID NO 599; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosstatic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 19 BP; 5 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 343 GGCTGTGATCAAAATGGG 359
Db 18 GACTGTGATCATATGGG 2

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RESULT 422
ADQ27278
ID ADQ27278 standard; DNA; 19 BP.
XX
AC ADQ27278;
XX
DT 26-AUG-2004 (first entry)
XX
DE RNA interference target sequence #186.
XX
KW ss; detection; RNA interference; siRNA; gene silencing; gene expression;
KW cytotoxicity.
XX
OS Homo sapiens.
XX
PN WO2004048566-A1.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-JP014893.
XX
PR 22-NOV-2002; 2002JP-00340053.
XX
PA (NATO/) NATORI Y.
PA (SAIG/) SAIGO K.
PA (TEIK/) TEI K.
PA (NAIT/) NAITO Y.
XX
PI Saigo K, Tei K, Naito Y;
XX
DR WPI; 2004-487423/46.
XX
PT Detecting sequence of RNA interference useful for synthesizing siRNA, by
PT detecting regions in sequence fulfilling specific criteria such as base
PT at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
PT guanine or cytosine.
XX
PS Disclosure; SEQ ID NO 200; 325pp; Japanese.
XX
CC The invention relates to a method of detecting the base sequence for RNA
CC interference by detecting the regions in the DNA sequence fulfilling the
CC following requirements such as: (i) the base at 3' terminal is adenine,
CC thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine;
CC (iii) the seven base sequence at 3' terminal is rich in adenine, thymine
CC and uracil, and; (iv) there are bases in a such a number that it causes
CC RNA interference without showing cytotoxicity. The method is used for
CC designing and synthesizing siRNA causing RNA interference. This sequence
CC corresponds to an RNA interference target sequence of the invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 744 GGCAGCTGCCACCTTAT 760
Db | ||||| |||||
3 GACAGCTGCGACCTTAT 19

RESULT 423
ADP48850
ID ADP48850 standard; DNA; 19 BP.
XX
AC ADP48850;
XX
DT 09-SEP-2004 (first entry)
XX
DE Mouse Myo1c targeted short inhibitory RNA (siRNA) target DNA SeqID90.
XX
KW short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating;
KW permeabilised cell membrane; antidiabetic; anorectic; gene therapy;
KW type II diabetes; insulin resistance; obesity; Myo1c; ds; mouse; murine.
XX

RESULT 424
ADP48849
ID ADP48849 standard; DNA; 19 BP.
XX
AC ADP48849;
XX
DT 09-SEP-2004 (first entry)
XX
DE Mouse Myo1c targeted short inhibitory RNA (siRNA) target DNA SeqID89.
XX
KW short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating;
KW permeabilised cell membrane; antidiabetic; anorectic; gene therapy;
KW type II diabetes; insulin resistance; obesity; Myo1c; ds; mouse; murine.
XX
OS Mus musculus.
XX
PN WO2004053103-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039774.
XX
PR 11-DEC-2002; 2002US-0432427P.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
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XX Mus musculus.
OS
XX WO2004053103-A2.
PN
XX
XX 24-JUN-2004.
PD
XX
XX 11-DEC-2003; 2003WO-US039774.
PF
XX
XX 11-DEC-2002; 2002US-0432427P.
PR
XX
XX (UYMA-) UNIV MASSACHUSETTS.
PA
XX
XX Czech MP, Zhou Q, Jiang Z;
PI
XX WPI; 2004-468860/44.
DR
XX
XX Introducing a nucleic acid into an adipocyte, useful for treating type II
PT diabetes, obesity or insulin resistance, comprises contacting an
PT adipocyte having a cell membrane with a nucleic acid molecule, thus
PT forming a mixture.
XX
XX Disclosure; SEQ ID NO 90; 91pp; English.
PS
XX
XX This invention relates to a novel method of introducing a nucleic acid
CC into an adipocyte which comprises contacting an adipocyte having a cell
CC membrane with a nucleic acid molecule, thus forming a mixture and
CC electroporating the mixture under conditions such that the cell membrane
CC becomes permeabilised, such that the nucleic acid is introduced into the
CC adipocyte. The invention may be useful for the production of compounds
CC with an antidiabetic or anorectic activity whilst the disclosed sequences
CC may be useful for gene therapy. The methods are useful for treating type
CC II diabetes, insulin resistance or obesity. The present sequence is that
CC of a region of a gene which may be targeted by short inhibitory RNA
CC (siRNA) used with the method of the invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1097 TACCTGCTCATTGTGTTT 1113
Db ||||| ||||| |||||
2 TACCACCTCATTGTGTTT 18

RESULT 424
ADP48849
ID ADP48849 standard; DNA; 19 BP.
XX
AC ADP48849;
XX
DT 09-SEP-2004 (first entry)
XX
DE Mouse Myo1c targeted short inhibitory RNA (siRNA) target DNA SeqID89.
XX
KW short inhibitory RNA; siRNA; adipocyte; cell membrane; electroporating;
KW permeabilised cell membrane; antidiabetic; anorectic; gene therapy;
KW type II diabetes; insulin resistance; obesity; Myo1c; ds; mouse; murine.
XX
OS Mus musculus.
XX
PN WO2004053103-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039774.
XX
PR 11-DEC-2002; 2002US-0432427P.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
```


PI Czech MP, Zhou Q, Jiang Z;
XX WPI; 2004-468860/44.
XX
PT Introducing a nucleic acid into an adipocyte, useful for treating type II
PT diabetes, obesity or insulin resistance, comprises contacting an
PT adipocyte having a cell membrane with a nucleic acid molecule, thus
PT forming a mixture.
XX
PS Disclosure; SEQ ID NO 89; 91pp; English.
XX
CC This invention relates to a novel method of introducing a nucleic acid
CC into an adipocyte which comprises contacting an adipocyte having a cell
CC membrane with a nucleic acid molecule, thus forming a mixture and
CC electroporating the mixture under conditions such that the cell membrane
CC becomes permeabilised, such that the nucleic acid is introduced into the
CC adipocyte. The invention may be useful for the production of compounds
CC with an antidiabetic or anorectic activity whilst the disclosed sequences
CC may be useful for gene therapy. The methods are useful for treating type
CC II diabetes, insulin resistance or obesity. The present sequence is that
CC of a region of a gene which may be targeted by short inhibitory RNA
CC (siRNA) used with the method of the invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1097 TACCTGCTCATTTGTTT 1113
Db 3 TACCACCTCATTTGTTT 19

RESULT 425
ABK15072/c
ID ABK15072 standard; DNA; 15 BP.
XX
AC ABK15072;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human beta actin PCR primer #2.
XX
KW Human; PCR; primer; beta actin; molecular beacon;
KW target cell identification; prenatal diagnosis; cystic fibrosis;
KW chromosomal aberration; trisomy 21; Down's syndrome; ss.
XX
OS Homo sapiens.
XX
PN EP1172445-A1.
XX
PD 16-JAN-2002.
XX
PF 14-JUL-2000; 2000EP-00115268.
XX
PR 14-JUL-2000; 2000EP-00115268.
XX
PA (PRAE-) PRAENADIA GMBH.
XX
PI Wiebusch H, Schmitt-John T, Weidner J;
XX
DR WPI; 2002-156652/21.
XX
PT Identifying target cell for prenatal diagnosis, by in situ hybridizing
PT target sequence in target cell with complementary labeled sequence and
PT identifying target cell by detecting hybridized sequence by flow
PT cytometry.
XX
XX Example 2; Fig 3/4; 28pp; English.
PS
XX This invention relates to a method for identifying a target cell or for
CC allowing direct genetic analysis of target cell, the method involves in

CC situ hybridisation of a target sequence in a target cell with a
CC complementary labeled sequence, and identifying the target cell by
CC detecting the presence of a hybridised sequence by flow cytometry. The
CC method of the invention is useful for distinction of foetal and maternal
CC cells and can be used in prenatal diagnosis for the detection of cystic
CC fibrosis or chromosomal aberrations such as trisomy 21 (Down's syndrome).
CC The method is also useful for the diagnosis of diseases which are due to
CC or characterised by the transcripition of genes which are not expressed in
CC the wild type cell, or diseases characterised by the absence of altered
CC expression or expression rates of certain genes or gene fragments. This
CC method improves the identification of foetal cells within a maternal
CC blood sample, and therefore enables the distinction between maternal and
CC foetal cells. The method is less time consuming and required less
CC expertise than common practices and increases the overall sampling rate
CC of target cell within a blood sample. The method also allows simultaneous
CC detection of different cell types or lines in a fast multiplex assay
CC which can be combined with the detection of various genetic differences
CC within the cells at once. The method also allows detection of rare
CC sequences and does not rely on the availability of monoclonal antibodies.
CC The present sequence represents a human beta actin PCR primer used in
CC conjunction with the primer represented in ABK15071 as a control PCR and
CC to allow for normalisation of the number of target cells used in the
CC method of the invention
XX
SQ Sequence 15 BP; 1 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 GAAGCAGCGCGGCC 56
Db 15 GAAGCAGCGCGTGCC 1

RESULT 426
ADJ82300/c
ID ADJ82300 standard; DNA; 15 BP.
XX
AC ADJ82300;
XX
DT 06-MAY-2004 (first entry)
XX
DE KLMSY-encoding nucleotide #28.
XX
KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX
OS Synthetic.
XX
PN WO2003045973-A2.
XX
PD 05-JUN-2003.
XX
PF 30-SEP-2002; 2002WO-US031165.
XX
PR 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT) BECTON DICKINSON & CO.
PA (HAAL/) HAALAND P D.
XX
PI Dean C, Heidaran M, Spargo CA;
XX
DR WPI; 2003-505179/47.
XX
PT New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.
XX

PS Disclosure; SEQ ID NO 81; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGF-R) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-

CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell

CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,

CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,

CC muscle or bone cell. The peptides are also useful for treating fibrotic

CC disorders, myeloproliferative diseases, and blood vessel proliferative

CC (angiogenic) disorders. This sequence represents a possible nucleotide

CC encoding the P3 peptide.

XX

SQ Sequence 15 BP; 5 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 615 GTAGGAGATGAGTTT 629

Db 15 GTAGGACATGAGTTT 1

RESULT 427

ADJ82292/c

ID ADJ82292 standard; DNA; 15 BP.

XX

AC ADJ82292;

XX

DT 06-MAY-2004 (first entry)

XX

DE KLMSY-encoding nucleotide #20.

XX

XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;

KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;

KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;

KW myeloproliferative disease; blood vessel proliferative disease;

KW angiogenesis.

XX

OS Synthetic.

XX

PN WO2003045973-A2.

XX

PD 05-JUN-2003.

XX

PF 30-SEP-2002; 2002WO-US031165.

XX

PR 28-NOV-2001; 2001US-0333476P.

XX

PA (BECT) BECTON DICKINSON & CO.

PA (HAAL/) HAALAND P D.

XX

PI Dean C, Heidaran M, Spargo CA;

XX

DR WPI; 2003-505179/47.

XX

XX New peptides having growth inhibitory action, useful for inhibiting tumor

PT or cancer cell proliferation, or for treating fibrotic disorders,

PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.

XX

PS Disclosure; SEQ ID NO 73; 48pp; English.

XX

CC The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGF-R) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-

CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell

CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,

CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,

CC muscle or bone cell. The peptides are also useful for treating fibrotic

CC disorders, myeloproliferative diseases, and blood vessel proliferative

CC (angiogenic) disorders. This sequence represents a possible nucleotide

CC encoding the P3 peptide.

XX

SQ Sequence 15 BP; 6 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 615 GTAGGAGATGAGTTT 629

Db 15 GTAGGATATGAGTTT 1

RESULT 428

ADJ82304/c

ID ADJ82304 standard; DNA; 15 BP.

XX

AC ADJ82304;

XX

DT 06-MAY-2004 (first entry)

XX

DE KLMSY-encoding nucleotide #32.

XX

XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;

KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;

KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;

KW myeloproliferative disease; blood vessel proliferative disease;

KW angiogenesis.

XX

OS Synthetic.

XX

PN WO2003045973-A2.

XX

PD 05-JUN-2003.

XX

PF 30-SEP-2002; 2002WO-US031165.

XX

PR 28-NOV-2001; 2001US-0333476P.

XX

PA (BECT) BECTON DICKINSON & CO.

PA (HAAL/) HAALAND P D.

XX

PI Dean C, Heidaran M, Spargo CA;

XX

DR WPI; 2003-505179/47.

XX

XX New peptides having growth inhibitory action, useful for inhibiting tumor

PT or cancer cell proliferation, or for treating fibrotic disorders,

PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.

XX

PS Disclosure; SEQ ID NO 85; 48pp; English.

XX

CC The invention relates to an isolated peptide or polypeptide (I) of no

CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGF-R) is activated in

CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-

CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell

CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,

CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.
XX
SQ Sequence 15 BP; 5 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 615 GTAGGAGATGAGTTT 629
Db 15 GTACGAGATGAGTTT 1
RESULT 429
ADG13597/c
ID ADG13597 standard; RNA; 15 BP.
XX
AC ADG13597;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human HER1-4 hammerhead ribozyme target sequence #2.
XX
KW Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW HER4; hammerhead ribozyme; inozyme; zinzyme; DNazyme; amberzyme; cancer;
KW brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW multidrug resistant cancer.
XX
OS Homo sapiens.
XX
PN US2003186909-A1.
XX
PD 02-OCT-2003.
XX
PF 21-OCT-2002; 2002US-00277494.
XX
PR 27-JAN-1997; 97US-0036749P.
PR 04-DEC-1997; 97US-00985162.
PR 22-SEP-1999; 99US-00401063.
PR 03-MAY-2001; 2001US-00848754.
PR 25-JUL-2001; 2001US-00916466.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2004-032029/03.
XX
PT New double stranded short interfering ribonucleic acid molecule for
PT inhibiting expression of epidermal growth factor receptor gene.
XX
PS Claim 7; SEQ ID NO 24; 113pp; English.
XX
CC The invention relates to a double stranded short interfering RNA (siRNA)
CC molecule that inhibits expression of epidermal growth factor receptor
CC (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC expression vector comprising a nucleic acid sequence encoding siRNA
CC molecule(s) in a manner that allows expression of the nucleic acid
CC molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC amberzymes zinzymes and DNazymes. The invention is used for inhibiting
CC expression of EGFR. It can be used for treatment of cancer, prostate
CC cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC life in vitro , stability, and ease of introduction of oligonucleotide to

CC target site. The present sequence is an EGFR/HER1-4 target sequence for
CC an siRNA of the invention.
XX
SQ Sequence 15 BP; 1 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 380 GCAGGCAATGCAGTC 394
Db 15 GCAGGCAAGCAGTC 1
RESULT 430
AAH77878
ID AAH77878 standard; DNA; 16 BP.
XX
AC AAH77878;
XX
DT 13-NOV-2001 (first entry)
XX
DE PCR primer used to amplify cDNA encoding a human hB7-H2 polypeptide.
XX
KW hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS;
KW congenital immune deficiency; cellular immune response; PCR primer;
KW inflammatory condition; autoimmune disease; rheumatoid arthritis;
KW multiple sclerosis; insulin-dependent diabetes mellitus; ss.
XX
OS Homo sapiens.
XX
PN WO200164704-A1.
XX
PD 07-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US006769.
XX
PR 02-MAR-2000; 2000US-0186519P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Chen L;
XX
DR WPI; 2001-514837/56.
XX
PT An isolated DNA encoding a hB7-H2 polypeptide, useful for treating
PT cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, multiple
PT sclerosis or insulin-dependent diabetes mellitus).
XX
PS Example 1; Page 26; 50pp; English.
XX
CC PCR primers AAH77878-79 were used to amplify cDNA encoding a human
CC polypeptide, designated hB7-H2. The hB7-H2 polypeptide co-stimulates T
CC cells. The hB7-H2 proteins and its variants are generally useful as
CC immune response-stimulating therapeutics. For example, the polypeptides
CC can be used for treatment of disease conditions characterized by
CC immunosuppression, e.g., cancer, AIDS or AIDS-related complex, other
CC virally or environmentally-induced conditions, and certain congenital
CC immune deficiencies. They may also be employed to increase immune
CC function that has been impaired by the use of radiotherapy or
CC immunosuppressive drugs such as certain chemotherapeutic agents, and
CC therefore are particularly useful when given in conjunction with such
CC drugs or radiotherapy. The hB7-H2 nucleic acid and polypeptide can be
CC used to treat conditions involving cellular immune responses, e.g.,
CC inflammatory conditions (such as, for example, those induced by
CC infectious agents including Mycobacterium tuberculosis or M. leprae), or
CC other pathologic cell-mediated responses such as those involved in
CC autoimmune diseases (e.g. rheumatoid arthritis), multiple sclerosis, or
CC insulin-dependent diabetes mellitus)
XX
SQ Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 16;

```
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 CCGCGGCCCCAGTTC 63
Db 1 CCGCGGCCCAAGTTC 15

RESULT 431
ADO49843
ID ADO49843 standard; DNA; 16 BP.
XX
AC ADO49843;
XX
DT 29-JUL-2004 (first entry)
XX
DE H. pylori strain J99 genome fragment SEQ ID NO:466.
XX
KW ds; stroke; phosphodiesterase 4D; PDE4D.
XX
OS Helicobacter pylori.
XX
PN US2004091865-A1.
XX
PD 13-MAY-2004.
XX
PF 25-SEP-2002; 2002US-00255120.
XX
PR 19-MAR-2001; 2001US-00811352.
PR 04-FEB-2002; 2002US-00067514.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Gretarsdottir S, Jonsdottir S, Reynisdottir ST, Thorleifsson G;
XX
DR WPI; 2004-374932/35.
XX
PT Diagnosing susceptibility to a stroke in an individual comprising
PT screening for an at-risk haplotype in the phosphodiesterase 4D gene.
XX
PS Disclosure; SEQ ID NO 466; 574pp; English.
XX
CC The invention relates to a method of diagnosing susceptibility to a
CC stroke in an individual comprising screening for an at-risk haplotype in
CC the phosphodiesterase 4D (PDE4D) gene that is more frequently present in
CC an individual susceptible to stroke (affected) compared to a healthy
CC individual (control), where the at-risk haplotype increases risk of
CC stroke significantly. The composition, methods and kit are useful for
CC diagnosing, predicting of clinical course and treating stroke using
CC polymorphisms in the PDE4D gene. These may also be used in identifying
CC agents that enhance or inhibit PDE4D polypeptide expression or activity.
CC The present sequence represents a fragment of H. pylori strain J99 genome
CC which is not referred to at all in the main body of the specification.
XX
SQ Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels -0; Gaps 0;

Qy 442 TGATTTTAGCTGGGA 456
Db 1 TGGTTTAGCTGGGA 15

RESULT 432
ADO50267
ID ADO50267 standard; DNA; 16 BP.
XX
AC ADO50267;
XX
DT 29-JUL-2004 (first entry)
XX
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```
DE H. pylori strain J99 genome fragment SEQ ID NO:890.
XX
KW ds; stroke; phosphodiesterase 4D; PDE4D.
XX
OS Helicobacter pylori.
XX
PN US2004091865-A1.
XX
PD 13-MAY-2004.
XX
PF 25-SEP-2002; 2002US-00255120.
XX
PR 19-MAR-2001; 2001US-00811352.
PR 04-FEB-2002; 2002US-00067514.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Gretarsdottir S, Jonsdottir S, Reynisdottir ST, Thorleifsson G;
XX
DR WPI; 2004-374932/35.
XX
PT Diagnosing susceptibility to a stroke in an individual comprising
PT screening for an at-risk haplotype in the phosphodiesterase 4D gene.
XX
PS Disclosure; SEQ ID NO 890; 574pp; English.
XX
CC The invention relates to a method of diagnosing susceptibility to a
CC stroke in an individual comprising screening for an at-risk haplotype in
CC the phosphodiesterase 4D (PDE4D) gene that is more frequently present in
CC an individual susceptible to stroke (affected) compared to a healthy
CC individual (control), where the at-risk haplotype increases risk of
CC stroke significantly. The composition, methods and kit are useful for
CC diagnosing, predicting of clinical course and treating stroke using
CC polymorphisms in the PDE4D gene. These may also be used in identifying
CC agents that enhance or inhibit PDE4D polypeptide expression or activity.
CC The present sequence represents a fragment of H. pylori strain J99 genome
CC which is not referred to at all in the main body of the specification.
XX
SQ Sequence 16 BP; 2 A; 1 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 442 TGATTTTAGCTGGGA 456
Db 1 TGGTTTAGCTGGGA 15

RESULT 433
AAF04357
ID AAF04357 standard; DNA; 17 BP.
XX
AC AAF04357;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1873.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO2000061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
```


XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
PI WPI; 2000-647423/62.
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX Claim 4; Page 98; 164pp; English.
PS The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 851 GATCCCTCTTTGTGT 865
Db 2 GATACCTCTTTGTGT 16
RESULT 434
AAF04805
ID AAF04805 standard; DNA; 17 BP.
XX
AC AAF04805;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2321.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PP 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX Claim 4; Page 108; 164pp; English.
PS The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and

CC interferon alpha
XX
SQ Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 851 GATCCCTCTTTGTGT 865
Db 2 GATACCTCTTTGTGT 16
RESULT 435
AAF04219
ID AAF04219 standard; DNA; 17 BP.
XX
AC AAF04219;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1735.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX Claim 4; Page 95; 164pp; English.
PS The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 396 TTTTCCTTACAATTC 410
Db 2 TTTTCCTTACAATTC 16
RESULT 436
AAF04667
ID AAF04667 standard; DNA; 17 BP.
XX
AC AAF04667;

Fri Aug 19 11:00:00 2005

XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #2183.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US009721.
XX PR 12-APR-1999; 99US-0129390P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX PT interferon alpha and erythropoietin.
XX PS Claim 4; Page 105; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
XX CC Inhibition of the repressors removes prevents inhibition (and
XX CC consequently increases expression of) genes involved in the production of
XX CC erythropoietin, granulocyte colony stimulating factor protein and
XX CC interferon alpha
XX SQ Sequence 17 BP; 3 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 TTTTCCTTACAATTC 410
Db 2 TTTTCCTTACAATTC 16

RESULT 437
AAFO2422
ID AAF02422 standard; DNA; 17 BP.
AC AAF02422;
XX 16-FEB-2001 (first entry)
DE Hammerhead ribozyme substrate #717.
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US009721.
XX PR 12-APR-1999; 99US-0129390P.
XX

PA (RIBO-) RIBOZYME PHARM INC.
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX PT interferon alpha and erythropoietin.
XX PS Claim 37; Page 72; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
XX CC Inhibition of the repressors removes prevents inhibition (and
XX CC consequently increases expression of) genes involved in the production of
XX CC erythropoietin, granulocyte colony stimulating factor protein and
XX CC interferon alpha
XX SQ Sequence 17 BP; 2 A; 2 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 294 CTGGAATTGTTGTTT 308
Db 2 CTGTAATTGTTGTTT 16

RESULT 438
ABK00818
ID ABK00818 standard; RNA; 17 BP.
XX AC ABK00818;
XX DT 12-MAR-2002 (first entry)
XX DE Human NOGO Inozyme #88.
XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX OS Homo sapiens.
OS Synthetic.
XX WO200159103-A2.
PN 16-AUG-2001.
PD 09-FEB-2001; 2001WO-US004273.
XX 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX

Db 16 GTTTTCCTTATTTT 2

RESULT 440

ABK00819

ID ABK00819 standard; RNA; 17 BP.

XX

AC ABK00819;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human NOGO Inozyme #89.

XX

KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200159103-A2.

XX

PD 16-AUG-2001.

XX

XX 09-FEB-2001; 2001WO-US004273.

PF

XX 11-FEB-2000; 2000US-0181797P.

PR

PR 28-FEB-2000; 2000US-0185516P.

PR

PR 06-MAR-2000; 2000US-0187128P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX

PI Blatt L, Mcswiggen J, Chowrira BM;

XX

XX WPI; 2001-607195/69.

DR

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX

XX Claim 88; Page 79; 200pp; English.

PS

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a NYN motif) pr

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targetting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targetting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is an inozyme of the invention

XX

SQ Sequence 17 BP; 1 A; 10 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 2.3e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 49 CCGCGGCCCCCAGTTC 63

Db 1 CCGCGGCCCCCAGUGC 15

RESULT 441

ABN06296

ID ABN06296 standard; DNA; 17 BP.

XX

AC ABN06296;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6288.

XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

PR

PR 21-SEP-2000; 2000US-0234687P.

PR

PR 27-SEP-2000; 2000US-0236359P.

PR

PR 04-OCT-2000; 2000GB-00024263.

PR

PR 30-JAN-2001; 2001WO-US000661.

PR

PR 30-JAN-2001; 2001WO-US000662.

PR

PR 30-JAN-2001; 2001WO-US000663.

PR

PR 30-JAN-2001; 2001WO-US000664.

PR

PR 30-JAN-2001; 2001WO-US000665.

PR

PR 30-JAN-2001; 2001WO-US000666.

PR

PR 30-JAN-2001; 2001WO-US000667.

PR

PR 30-JAN-2001; 2001WO-US000668.

PR

PR 30-JAN-2001; 2001WO-US000669.

PR

PR 05-FEB-2001; 2001US-0266860P.

XX

XX (AEOM-) AEOMICA INC.

PA

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

PI

XX WPI; 2002-179446/23.

DR

XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

PT

XX

PS Disclosure; SEQ ID NO 6288; 214pp; English.

XX The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1

CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

CC -1 proteins, as standards in assays used to determine the concentration

CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

CC capture probes for surface-enhanced laser desorption/ionisation, as

CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPLP-1, in particular heart

CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the

CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequence

XX

SQ Sequence 17 BP; 1 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35

Db 2 CCGGGCTGTGGCAGG 16

RESULT 442

ABN06295

ID ABN06295 standard; DNA; 17 BP.

XX

AC ABN06295;

XX

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6287.

XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMPLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

PA

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX

DR WPI; 2002-179446/23.

XX

PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.

XX

PS Disclosure; SEQ ID NO 6287; 214pp; English.

XX

CC The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1

CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

CC -1 proteins, as standards in assays used to determine the concentration

CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

CC capture probes for surface-enhanced laser desorption/ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPLP-1, in particular heart

CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the

CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequence

XX

SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35

Db 3 CCGGGCTGTGGCAGG 17

RESULT 443

ABN06297

ID ABN06297 standard; DNA; 17 BP.

XX

AC ABN06297;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6289.

XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMPLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US0000661.
PR 30-JAN-2001; 2001WO-US0000662.
PR 30-JAN-2001; 2001WO-US0000663.
PR 30-JAN-2001; 2001WO-US0000664.
PR 30-JAN-2001; 2001WO-US0000665.
PR 30-JAN-2001; 2001WO-US0000666.
PR 30-JAN-2001; 2001WO-US0000667.
PR 30-JAN-2001; 2001WO-US0000668.
PR 30-JAN-2001; 2001WO-US0000669.
PR 30-JAN-2001; 2001WO-US0000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 6289; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 1 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
|||
Db 1 CCGGGCTGTGGCAGG 15

RESULT 444
ABN02575/c
ID ABN02575 standard; DNA; 17 BP.
XX
AC ABN02575;
XX
XX 29-MAY-2002 (first entry)
DT
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2567.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.

XX WO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US0000661.
PR 30-JAN-2001; 2001WO-US0000662.
PR 30-JAN-2001; 2001WO-US0000663.
PR 30-JAN-2001; 2001WO-US0000664.
PR 30-JAN-2001; 2001WO-US0000665.
PR 30-JAN-2001; 2001WO-US0000666.
PR 30-JAN-2001; 2001WO-US0000667.
PR 30-JAN-2001; 2001WO-US0000668.
PR 30-JAN-2001; 2001WO-US0000669.
PR 30-JAN-2001; 2001WO-US0000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI
XX
XX WPI; 2002-179446/23.
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2567; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCT 757
|||
Db 15 AGGCAGCTGCCGCCT 1

RESULT 445
ABV82999
ID ABV82999 standard; DNA; 17 BP.
XX

```
AC  ABV82999;
XX
DT  03-JAN-2003  (first entry)
XX
DE  Human HTPL scanning oligonucleotide SEQ ID 4245.
XX
KW  Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW  human testis expressed Patched like protein; testis; adrenal; liver;
KW  male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW  prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS  Homo sapiens.
XX
PN  EP1229046-A2.
XX
PD  07-AUG-2002.
XX
PF  28-JAN-2002; 2002EP-00001167.
XX
PR  30-JAN-2001; 2001WO-US000663.
PR  30-JAN-2001; 2001WO-US000664.
PR  30-JAN-2001; 2001WO-US000665.
PR  30-JAN-2001; 2001WO-US000667.
PR  30-JAN-2001; 2001WO-US000668.
PR  30-JAN-2001; 2001WO-US000669.
PR  23-MAY-2001; 2001US-00864761.
PR  09-OCT-2001; 2001US-0327898P.
XX
PA  (AEOM-) AEOMICA INC.
XX
PI  Zhan J;
XX
DR  WPI; 2002-676582/73.
XX
PT  Novel isolated human testis expressed Patched like protein (HTPL), useful
PT  for identifying agonist and antagonist and specific binding partners, and
PT  for treating subjects having defects in HTPL.
XX
PS  Example 2; Page 620; 718pp; English.
XX
CC  The present invention relates to human testis expressed Patched like
CC  protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC  has two isoforms, with a few single base pair differences between the
CC  two. One of the single base pair changes introduces a premature stop
CC  codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC  shares an overall structure organisation with the Patched protein. The
CC  shared structural features strongly imply that HTPL plays a role similar
CC  to that of Patched, and is a potential tumour suppressor. HTPL is
CC  important in regulating male germ cell development, and the HTPL gene was
CC  mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC  useful for diagnosing a disorder caused by mutation in HTPL, and in
CC  therapy and manufacture of a medicament for treatment or prevention of
CC  such disorder associated with decreased expression or activity of human
CC  HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC  foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC  skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC  clinically useful diagnostic markers and potential therapeutic agents for
CC  male infertility and cancer. The present oligonucleotide was used in an
CC  example from the invention
XX
SQ  Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match          1.2%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity 93.3%;  Pred. No. 2.3e+02;
  Matches 14;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      675 ATTATGTTACTTGT 689
      ||||| ||||| |||||
DB      1 ATTATGTTCTTGT 15

RESULT 446
ABV82998
```

```
ID  ABV82998 standard; DNA; 17 BP.
XX
AC  ABV82998;
XX
DT  03-JAN-2003  (first entry)
XX
DE  Human HTPL scanning oligonucleotide SEQ ID 4244.
XX
KW  Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW  human testis expressed Patched like protein; testis; adrenal; liver;
KW  male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW  prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS  Homo sapiens.
XX
PN  EP1229046-A2.
XX
PD  07-AUG-2002.
XX
PF  28-JAN-2002; 2002EP-00001167.
XX
PR  30-JAN-2001; 2001WO-US000663.
PR  30-JAN-2001; 2001WO-US000664.
PR  30-JAN-2001; 2001WO-US000665.
PR  30-JAN-2001; 2001WO-US000667.
PR  30-JAN-2001; 2001WO-US000668.
PR  30-JAN-2001; 2001WO-US000669.
PR  23-MAY-2001; 2001US-00864761.
PR  09-OCT-2001; 2001US-0327898P.
XX
PA  (AEOM-) AEOMICA INC.
XX
PI  Zhan J;
XX
DR  WPI; 2002-676582/73.
XX
PT  Novel isolated human testis expressed Patched like protein (HTPL), useful
PT  for identifying agonist and antagonist and specific binding partners, and
PT  for treating subjects having defects in HTPL.
XX
PS  Example 2; Page 620; 718pp; English.
XX
CC  The present invention relates to human testis expressed Patched like
CC  protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC  has two isoforms, with a few single base pair differences between the
CC  two. One of the single base pair changes introduces a premature stop
CC  codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC  shares an overall structure organisation with the Patched protein. The
CC  shared structural features strongly imply that HTPL plays a role similar
CC  to that of Patched, and is a potential tumour suppressor. HTPL is
CC  important in regulating male germ cell development, and the HTPL gene was
CC  mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC  useful for diagnosing a disorder caused by mutation in HTPL, and in
CC  therapy and manufacture of a medicament for treatment or prevention of
CC  such disorder associated with decreased expression or activity of human
CC  HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC  foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC  skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC  clinically useful diagnostic markers and potential therapeutic agents for
CC  male infertility and cancer. The present oligonucleotide was used in an
CC  example from the invention
XX
SQ  Sequence 17 BP; 3 A; 1 C; 3 G; 10 T; 0 U; 0 Other;

  Query Match          1.2%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity 93.3%;  Pred. No. 2.3e+02;
  Matches 14;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      675 ATTATGTTACTTGT 689
      ||||| ||||| |||||
DB      2 ATTATGTTCTTGT 16
```

RESULT 447
ABK18400
ID ABK18400 standard; RNA; 17 BP.
XX
AC ABK18400;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 1047.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
XX WPI; 2002-082995/11.
DR
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 77; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 958 CTGGACCCAGGACAT 972
|:|||||
Db 3 CUGGACUCAGGACAU 17
RESULT 448
ABT39733/C
ID ABT39733 standard; DNA; 17 BP.
XX
AC ABT39733;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 5370.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 661; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
|||||
Db 17 ATGTTCACTTGAAGA 3

RESULT 449
ABT35826
ID ABT35826 standard; DNA; 17 BP.
XX
AC ABT35826;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 1463.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 204; 720pp; French.
XX

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SQ Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 513 ATCTGTATACATGTG 527
|||||
||

Db 2 ATCTGTATACATATG 16

RESULT 450
ADA99777
ID ADA99777 standard; DNA; 17 BP.
XX
AC ADA99777;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 766.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX

PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 766; 103pp; English.
XX

CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX

SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 892 CCCACAGACCAAGAG 906
|||||
Db 3 CCCAGAGACCAAGAG 17

RESULT 451
ADA99778
ID ADA99778 standard; DNA; 17 BP.
XX
AC ADA99778;

XX 20-NOV-2003 (first entry)
DT
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 767.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX EP1281758-A2.
PN
PD 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
PR 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI WPI; 2003-423107/40.
XX
DR New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
PT
XX Example 8; SEQ ID NO 767; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 892 CCCACAGACCAAGAG 906
Db 2 CCCAGAGACCAAGAG 16
||| |||||

RESULT 452
ADA99779
ID ADA99779 standard; DNA; 17 BP.
XX
XX
AC ADA99779;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 768.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KW developmental disorder; ss.
XX
OS Homo sapiens.
XX EP1281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI WPI; 2003-423107/40.
XX
DR New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
PT
XX Example 8; SEQ ID NO 768; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 892 CCCACAGACCAAGAG 906
Db 1 CCCAGAGACCAAGAG 15
||| |||||

RESULT 453
ACD52118
ID ACD52118 standard; RNA; 17 BP.
XX
XX
AC ACD52118;
XX
DT 24-SEP-2003 (first entry)
XX
DE HBV inozyme substrate sequence #248.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX

| | | | |
|------------|---|-----------------------|---|
| PN | WO200281494-A1. | KW | Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; |
| XX | | KW | RNA stability; RNA expression; RNA synthesis; antisense; |
| PD | 17-OCT-2002. | KW | enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme; |
| XX | | KW | amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; |
| PF | 26-MAR-2002; 2002WO-US009187. | KW | HBV reverse transcriptase; Enhancer I region; viral replication; |
| XX | | KW | degenerative; disease state; HBV infection; HCV infection; cirrhosis; |
| PR | 26-MAR-2001; 2001US-00817879. | KW | liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; |
| PR | 08-JUN-2001; 2001US-00877478. | XX | virucide; antiinflammatory; substrate; ss. |
| PR | 08-JUN-2001; 2001US-0296876P. | OS | Hepatitis B virus. |
| PR | 24-OCT-2001; 2001US-0335059P. | XX | |
| PR | 05-DEC-2001; 2001US-0337055P. | PN | WO200281494-A1. |
| XX | | XX | 17-OCT-2002. |
| PA | (RIBO-) RIBOZYME PHARM INC. | XX | 26-MAR-2002; 2002WO-US009187. |
| PA | (BLAT/) BLATT L. | PR | 26-MAR-2001; 2001US-00817879. |
| PA | (MACE/) MACEJAK D. | PR | 08-JUN-2001; 2001US-00877478. |
| PA | (MCSW/) MCSWIGGEN J. | PR | 08-JUN-2001; 2001US-0296876P. |
| PA | (MORR/) MORRISSEY D. | PR | 24-OCT-2001; 2001US-0335059P. |
| PA | (PAVC/) PAVCO P. | PR | 05-DEC-2001; 2001US-0337055P. |
| PA | (LEEP/) LEE P. | XX | |
| PA | (DRAP/) DRAPER K. | PA | (RIBO-) RIBOZYME PHARM INC. |
| PA | (ROBE/) ROBERTS E. | PA | (BLAT/) BLATT L. |
| XX | | PA | (MACE/) MACEJAK D. |
| PI | Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P; | PA | (MCSW/) MCSWIGGEN J. |
| PI | Draper K, Roberts E; | PA | (MORR/) MORRISSEY D. |
| XX | | PA | (PAVC/) PAVCO P. |
| DR | WPI; 2003-229207/22. | PA | (LEEP/) LEE P. |
| XX | | PA | (DRAP/) DRAPER K. |
| XX | | PA | (ROBE/) ROBERTS E. |
| CC | Novel compound useful for treating cirrhosis, liver failure, | XX | |
| CC | hepatocellular carcinoma, or condition associated with hepatitis C virus | PI | Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P; |
| CC | infection. | PI | Draper K, Roberts E; |
| PS | Example 1; Page 154; 387pp; English. | XX | |
| XX | | XX | WPI; 2003-229207/22. |
| CC | The present invention relates to nucleic acid molecules which modulate | PT | Novel compound useful for treating cirrhosis, liver failure, |
| CC | the synthesis, expression and/or stability of Hepatitis C virus (HCV) or | PT | hepatocellular carcinoma, or condition associated with hepatitis C virus |
| CC | Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense | PT | infection. |
| CC | and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes, | XX | |
| CC | inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed | PS | Example 1; Page 165; 387pp; English. |
| CC | are nucleic acid decoy molecules and aptamers that bind to HBV reverse | XX | |
| CC | transcriptase and/or HBV reverse transcriptase primer sequences, as well | CC | The present invention relates to nucleic acid molecules which modulate |
| CC | as oligonucleotides that specifically bind the Enhancer I region of HBV | CC | the synthesis, expression and/or stability of Hepatitis C virus (HCV) or |
| CC | DNA. The nucleic acids may be used to modulate the expression of HBV | CC | Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense |
| CC | genes and HBV viral replication. Also disclosed is a method for screening | CC | and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes, |
| CC | compounds and/or potential therapies directed against HBV, and compounds | CC | inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed |
| CC | that modulate the expression and/or replication of HCV. The compounds and | CC | are nucleic acid decoy molecules and aptamers that bind to HBV reverse |
| CC | methods of the invention are useful for the treatment of degenerative and | CC | transcriptase and/or HBV reverse transcriptase primer sequences, as well |
| CC | disease states related to HBV and HCV infection, replication and gene | CC | as oligonucleotides that specifically bind the Enhancer I region of HBV |
| CC | expression such as cirrhosis, liver failure, and hepatocellular | CC | DNA. The nucleic acids may be used to modulate the expression of HBV |
| CC | carcinoma. The present sequence represents a substrate for one of the HBV | CC | genes and HBV viral replication. Also disclosed is a method for screening |
| CC | ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences | CC | compounds and/or potential therapies directed against HBV, and compounds |
| CC | disclosed in the present invention | CC | that modulate the expression and/or replication of HCV. The compounds and |
| XX | | CC | methods of the invention are useful for the treatment of degenerative and |
| SQ | Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other; | CC | disease states related to HBV and HCV infection, replication and gene |
| | | CC | expression such as cirrhosis, liver failure, and hepatocellular |
| | | CC | carcinoma. The present sequence represents a substrate for one of the HBV |
| | | CC | ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences |
| | | CC | disclosed in the present invention |
| | | XX | |
| | | Query Match | 1.2%; Score 13.4; DB 1; Length 17; |
| | | Best Local Similarity | 40.0%; Pred. No. 2.3e+02; |
| | | Matches | 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0; |
| QY | 570 TTAATACCTTTATAT 584 | | |
| DB | :: : :: :: : | | |
| | 1 UUAAGGCCUUUAU 15 | | |
| | | | |
| RESULT 454 | | | |
| ACD53199 | | | |
| ID | ACD53199 standard; RNA; 17 BP. | | |
| XX | | | |
| AC | ACD53199; | | |
| XX | | | |
| DT | 24-SEP-2003 (first entry) | | |
| XX | | | |
| DE | HBV G-cleaver substrate sequence #36. | | |
| XX | | | |
| | | Query Match | 1.2%; Score 13.4; DB 1; Length 17; |
| | | Best Local Similarity | 40.0%; Pred. No. 2.3e+02; |
| | | Matches | 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0; |
| | | | |
| | | QY | 569 TTTAATACCTTTATA 583 |
| | | DB | :: : :: :: : |
| | | | 3 UUAAGGCCUUUAU 17 |

XX Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 420; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
Db 17 ATGTTCACTTGAAGA 3

RESULT 458
ADC38464/c
ID ADC38464 standard; DNA; 17 BP.
XX
AC ADC38464;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:813.
XX
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1b; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX

PT New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 813; 172pp; English.
XX
CC The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1b, which is used in an example from the
CC present invention.
XX
SQ Sequence 17 BP; 8 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCATTTTCCTTACAA 407
Db 16 TCATTTTCCTTCA 2

RESULT 459
ADC38465/c
ID ADC38465 standard; DNA; 17 BP.
XX
AC ADC38465;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:814.
XX
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1b; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX
PT New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 814; 172pp; English.
XX
CC The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1b, which is used in an example from the
CC present invention.
XX
SQ Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 393 TCATTTTCCTTACAA 407
Db 15 TCATTTTCCTTTCAA 1

RESULT 460
ADC38463/c
ID ADC38463 standard; DNA; 17 BP.
XX
AC ADC38463;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:812.
XX
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1b; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
PI WPI; 2003-430501/40.
DR
XX
PT New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 812; 172pp; English.
XX
CC The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1b, which is used in an example from the
CC present invention.
XX
SQ Sequence 17 BP; 8 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 393 TCATTTTCCTTACAA 407
Db 17 TCATTTTCCTTTCAA 3

RESULT 461
ADB45002
ID ADB45002 standard; DNA; 17 BP.
XX
AC ADB45002;
XX
DT 18-DEC-2003 (first entry)
XX

DE Tumour suppression/reversion associated nucleotide #5325.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
PS Disclosure; Page 654; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 851 GATCCCTCTTTGGT 865
Db 1 GATCCCTCTTTGGT 15

RESULT 462
ADI51662/c
ID ADI51662 standard; DNA; 17 BP.
XX
AC ADI51662;
XX
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID4165.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;

KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 4165; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
DB |||||
17 ATGTTCACTTGAAGA 3

RESULT 463
ADI49509
ID ADI49509 standard; DNA; 17 BP.
XX
AC ADI49509;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID2012.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.
PF
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313354/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; SEQ ID NO 2012; 30pp; French.
XX
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 1 A; 2 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 ATATGCTGGGTTTTT 570
DB |||||
2 ATCTGCTGGGTTTTT 16

RESULT 464
ACC54318/c
ID ACC54318 standard; DNA; 17 BP.
XX
AC ACC54318;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #3085.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX

DR WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

PS Claim 1; Page 752; 798pp; French.

XX

CC This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. The invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration

XX

SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
|||||

Db 17 ATGTTCACTTGAAGA 3

RESULT 465

ADL82512/c

ID ADL82512 standard; DNA; 17 BP.

XX

AC ADL82512;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human ER+ breast cancer differentially expressed sequence #482.

XX

XW gene therapy; ds; breast cancer; human; ER+ breast cancer.

XX

OS Homo sapiens.

XX

OS US2003166026-A1.

PN

XX

XX 04-SEP-2003.

XX

PF 08-JAN-2003; 2003US-00339782.

XX

PR 09-JAN-2002; 2002US-0348053P.

XX

PA (LYNX-) LYNX THERAPEUTICS INC.

XX

PI Goodman LJ, Bowen BA;

XX

DR WPI; 2004-069003/07.

XX

PT Vector containing nucleic acid associated with breast cancer, useful for treating, diagnosing and characterizing breast cancer, also related polypeptides and antibodies.

PT

XX

PS Claim 1; SEQ ID NO 483; 61pp; English.

XX

CC The invention relates to a composition which contains at least one vector (B) containing a nucleic acid (I) associated with breast cancer. The vector (B), also polypeptides (II) encoded by (I), are used for treatment of breast cancer. Arrays based on (I), (II), or their fragments, and (II) -specific antibodies (Ab) are used to predict characteristics (e.g. invasiveness or stage) of breast cancer, and (I), or its fragments, are used to modulate characteristics of such cells; to identify breast cancer genes and to detect breast cancer (by detecting polymorphic nucleic acid or its products). The present sequence represents a human ER+ breast cancer differentially expressed sequence.

CC

XX

SQ Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 588 ATGTTCACTTTAAGA 602
|||||

Db 17 ATGTTCACTTGAAGA 3

RESULT 466

ADM59349

ID ADM59349 standard; RNA; 17 BP.

XX

AC ADM59349;

XX

DT 03-JUN-2004 (first entry)

XX

DE Hepatitis B virus (HBV) RNA target sequence #1483.

XX

XW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocellular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; cytostatic.

XX

OS Hepatitis B virus.

XX

PN US2004054156-A1.

XX

PD 18-MAR-2004.

XX

PF 15-JAN-2003; 2003US-00342902.

XX

PR 14-MAY-1992; 92US-00882712.

PR 07-FEB-1994; 94US-00193627.

PR 08-NOV-1999; 99US-00436430.

PR 20-MAR-2000; 2000US-00531025.

PR 09-AUG-2000; 2000US-00636385.

PR 24-OCT-2000; 2000US-00696347.

PR 08-JUN-2001; 2001US-00877478.

XX

PA (DRAP/) DRAPER K.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PA (MORR/) MORRISSEY D.

XX

PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;

XX

DR WPI; 2004-247781/23.

XX

PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.

PT

XX

PS Disclosure; SEQ ID NO 1483; 122pp; English.

XX

CC The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2'-OH group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, hepatocellular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an HBV RNA target sequence, used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 569 TTTAATACCTTTATA 583
::||: ||::||:
Db 3 UUUAAUGCCUUUAU 17

RESULT 467
ADM58815
ID ADM58815 standard; RNA; 17 BP.
XX
AC ADM58815;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #949.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 949; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 570 TTAATACCTTTATAT 584
::||: ||::||:
Db 1 UUA AUGCCUUUAU 15

RESULT 468
ACN69387
ID ACN69387 standard; DNA; 17 BP.
XX
AC ACN69387;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPLP-1 probe SEQ ID NO:6289.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
DR WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 6289; 0pp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (SI) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (SI), 95% deviation from (SI) which are conservative substitutions, and
CC 65% identity to (SI). A polypeptide of the invention acts as a agonist. or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 1 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
||||| |||||||
Db 1 CCGGCTGTGGCAGG 15

RESULT 469
ACN69386
ID ACN69386 standard; DNA; 17 BP.
XX
AC ACN69386;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:6288.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
DR
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 6288; opp; English.

XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 1 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35
||||| |||||||
Db 2 CCGGCTGTGGCAGG 16

RESULT 470
ACN69385
ID ACN69385 standard; DNA; 17 BP.
XX
AC ACN69385;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:6287.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX

DR WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder

PT associated with decreased expression or activity of human genome-derived

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle

PT function.

XX Disclosure; SEQ ID NO 6287; Opp; English.

PS

XX The invention relates to a novel polypeptide (I) comprising a sequence

CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully

CC defined in the specification, a fragment of at least 8 amino acids of

CC (S1), 95% deviation from (S1) which are conservative substitutions, and

CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or

CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A

CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of

CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.

CC The present sequence represents a 17-mer nucleotide, used in the

CC invention for scanning the sequence represented in ACN63103

XX

SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 CCGGGCCGTGGCAGG 35

|||||

Db 3 CCGGGCTGTGGCAGG 17

RESULT 471

ACN65665/c

ID ACN65665 standard; DNA; 17 BP.

XX

AC ACN65665;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human GDMLP-1 probe SEQ ID NO:2567.

XX

KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;

KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;

KW skeletal muscle function.

XX

OS Homo sapiens.

XX

PN US2004137589-A1.

XX

PD 15-JUL-2004.

XX

PF 26-NOV-2003; 2003US-00723361.

XX

PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001US-0266860P.

PR 25-MAY-2001; 2001US-00866108.

XX

XX (GUY/) GU Y.

PA (JIY/) JI Y.

PA (PENN/) PENN S G.

PA (HANK/) HANZEL D K.

PA (RANK/) RANK D.

PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.

XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX WPI; 2004-533378/51.

DR

XX Novel myosin-like protein-1, useful for treating or preventing disorder

PT associated with decreased expression or activity of human genome-derived

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle

PT function.

XX Disclosure; SEQ ID NO 2567; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence

CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully

CC defined in the specification, a fragment of at least 8 amino acids of

CC (S1), 95% deviation from (S1) which are conservative substitutions, and

CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or

CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A

CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of

CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.

CC The present sequence represents a 17-mer nucleotide, used in the

CC invention for scanning the sequence represented in ACN63102

XX

SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 743 AGGCAGCTGCCACCT 757

|||||

Db 15 AGGCAGCTGCCGCCT 1

RESULT 472

AAZ90709

ID AAZ90709 standard; DNA; 18 BP.

XX

AC AAZ90709;

XX

DT 19-JUN-2000 (first entry)

XX

DE Forward primer for amplifying human KVLQT1 exon 1.

XX

KW KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;

KW antiarrhythmic; gene therapy; human; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200006600-A1.

XX

PD 10-FEB-2000.

XX

PF 06-OCT-1998; 98WO-US017838.

XX

PR 29-JUL-1998; 98US-0094477P.

PR 17-AUG-1998; 98US-00135020.

XX

PA (UTAH) UNIV UTAH RES FOUND.

XX

PI Keating MT, Sanguinetti MC, Splawski I;

XX

DR WPI; 2000-195262/17.

XX

PT Mutant forms of genes encoding minK protein and KVLQT1 protein involved

PT in cardiac potassium channel formation useful for screening drugs, for

PT preventing and treating cardiac arrhythmia.

XX Example 11; Page 70; 167pp; English.

PS The invention relates to KVLQT1 and KCNE1 genes, associated with long QT

XX (LQT) syndrome. It provides a minK protein comprising a mutation which

CC substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and

CC Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening

CC KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and

CC treating LQT. The ability to predict LQT enables physicians to prevent

CC the diseases with medical therapy such as beta blocking agents and opts

CC for better treatments. Sequences AAZ90707-Z90740 represent PCR primers

CC for amplifying human KVLQT1 exons

XX

SQ Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 GCCGCGCCCCCAGTT 62

Db 2 GCCGCGCCCCCAGTT 16

RESULT 473

AAZ71388

ID AAZ71388 standard; DNA; 18 BP.

XX

AC AAZ71388;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human biallelic marker upstream amplification primer SEQ ID NO:5744.

XX

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO9954500-A2.

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX

PS Claim 8; Page 1455; 2745pp; English.

XX

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX

SQ Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX

SQ Sequence 18 BP; 7 A; 0 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 612 TAAAGTAGGAGATGAG 626

Db 3 TAAAGTAAGAGATGAG 17

RESULT 474

AAZ71139/c

ID AAZ71139 standard; DNA; 18 BP.

XX

AC AAZ71139;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human biallelic marker upstream amplification primer SEQ ID NO:5495.

XX

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO9954500-A2.

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX

PS Claim 8; Page 1402; 2745pp; English.

XX

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX

SQ Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 2.4e+02; Mismatches 14; Conservative 0; Indels 1; Gaps 0;

QY 1060 CTTTCCAGTGGCTAA 1074
Db 18 CTTACCAGTGGCTAA 4

RESULT 475
AAZ98939
ID AAZ98939 standard; DNA; 18 BP.
XX
AC AAZ98939;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human long QT syndrome-associated KVLQT1 exon 1 forward primer #2.
XX
KW KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss;
KW cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
KW chromosome 11p15.5; PCR primer.
XX
OS Homo sapiens.
XX
PN WO200006199-A1.
XX
PD 10-FEB-2000.
XX
PF 12-MAY-1999; 99WO-US010260.
XX
PR 29-JUL-1998; 98US-0094477P.
PR 17-AUG-1998; 98US-00135010.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (GENZ) GENZYME CORP.
XX
PI Keating MT, Sanguinetti MC, Curran ME, Landes GM, Connors TD;
PI Burn TC, Splawski I;
XX
DR WPI; 2000-195199/17.
XX
PT New isolated mutant KVLQT1 nucleic acids, useful for developing products
PT for the diagnosis, prevention and treatment of long QT syndrome.
XX
PS Claim 27; Page 73; 178pp; English.
XX
CC The invention relates to KVLQT1 nucleic acids which have a mutation
CC compared to wild-type KVLQT1 (AAZ98901) The KVLQT1 gene encodes a protein
CC of 676 amino acids which forms a cardiac I(ks) potassium channel with the
CC KCNE1 protein (AAY80563). The KVLQT1 gene contains 15 introns and encodes
CC a protein containing 6 putative transmembrane segments and a pore forming
CC region. The gene has been mapped to the chromosomal location 11p15.5. The
CC sequences AAZ98937-298970 represent primers used to PCR amplify the
CC KVLQT1 exon sequences. Mutations in the KVLQT1 or KCNE1 genes result in
CC cardiac arrhythmias observed as a prolonged QT curve in
CC electrocardiograms (Long QT syndrome). The genes and proteins can be used
CC for the diagnosis of subjects with long QT syndrome. They can also be
CC used to screen for drugs which can be used for treating or preventing
CC long QT syndrome. The KVLQT1 nucleic acids can be used for gene therapy,
CC and KVLQT1 peptides can be used for peptide therapy
XX
SQ Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GCGCGGCCCCCAGTT 62
Db 2 GCGCGGCCCCCAGTT 16

RESULT 476

AAA66260/C
ID AAA66260 standard; DNA; 18 BP.
XX
AC AAA66260;
XX
DT 09-OCT-2000 (first entry)
XX
DE Dog genomic marker oligonucleotide sequence SEQ ID NO:122.
XX
KW Dog; genome; genomic marker; radiation hybrid map; identification;
KW chromosome location; gene marker; polymorphic microsatellite marker;
KW phenotype; behaviour; pedigree; ss.
XX
OS Canis familiaris.
XX
PN WO200029615-A2.
XX
PD 25-MAY-2000.
XX
PF 15-NOV-1999; 99WO-IB001907.
XX
PR 13-NOV-1998; 98US-0108193P.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Galibert F, Andre C;
XX
DR WPI; 2000-387821/33.
XX
PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral traits
PT or in genetic diseases and for studying dog pedigrees.
XX
PS Claim 1; Page 58; 87pp; English.
XX
CC The present invention describes a radiation hybrid map of the dog (Canine
CC familiaris) genome comprising the genome location of a marker selected
CC from AAA66139 to AAA66942. The radiation hybrid map is useful for
CC identifying and localising dog genes, since it covers approximately 80 %
CC of the dog genome and provides a dense map integrating different types
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC (or complementary sequences) are especially useful to identify genes
CC responsible for phenotypic and behavioural traits in dogs, to identify
CC morbid genes, to analyse diseases and identify implicated genes in such
CC diseases and their alleles, and to study dog pedigrees. They may also be
CC useful for isolating corresponding human gene sequences e.g. genes
CC involved in genetic diseases
XX
SQ Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 523 ATGTGCACATGCGGC 537
Db 17 ATGTGCACTTGCGGC 3

RESULT 477
AAC89949
ID AAC89949 standard; DNA; 18 BP.
XX
AC AAC89949;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human KVLQT1 exon 1 PCR primer #3.
XX
KW Human; KVLQT1; antiarrhythmic; cardiac; gene therapy; PCR primer;
KW cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW chromosome 11p15.5; long QT syndrome; ss.
XX

OS Homo sapiens.
XX US6150104-A.
PN
XX 21-NOV-2000.
PD
XX
XX 17-AUG-1998; 98US-00135021.
PF
XX
XX 13-JUN-1997; 97US-00874655.
PR
XX 29-JUL-1998; 98US-0094477P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
PA
XX
XX Keating MT, Splawski I;
PI
XX WPI; 2001-060013/07.
DR
XX
XX DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT or diagnosing or prognosing JLN.
PT
XX
XX Example 5; Col 45-46; 58pp; English.
PS
XX KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to chromosome
CC 11p15.5. The present invention relates to a mutant KVLQT1 coding sequence
CC (see AAC89914). The mutant KVLQT1 coding sequence is useful in the
CC diagnosis of long QT syndrome and in screening humans for the presence of
CC KVLQT1 gene variants which cause JLN syndrome. The present sequence is a
CC PCR primer used to amplify a KVLQT1 exon
XX
XX Sequence 18 BP; 1 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 48 GCCGCGGCCCCAGTT 62
Db
2 GCCGCGGCCCCAGTT 16
RESULT 478
AAS05095/c
ID AAS05095 standard; DNA; 18 BP.
XX
AC AAS05095;
XX
XX 07-SEP-2001 (first entry)
DT
XX Neurofibromatosis (NF1) HA PCR primer #15.
DE
XX Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
KW Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA;
KW frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
KW sequencing primer.
XX
XX Homo sapiens.
OS
XX WO200129251-A2.
PN
XX 26-APR-2001.
PD
XX 18-OCT-2000; 2000WO-EP010255.
PF
XX 18-OCT-1999; 99EP-00870216.
XX
PR 05-JUN-2000; 2000EP-00870122.
PR
XX (UYGE-) UNIV GENT.
PA
XX Messiaen L, Callens T;
XX WPI; 2001-300341/31.
XX
DR Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid

XX Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
PT cell lines formed with lymphocytes of patient with protein synthesis
PT inhibitor, and obtaining peptides by translating amplified RNA from cell
PT line.
XX
XX Claim 9; Page 70; 102pp; English.
PS
XX The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A
CC method for mutation analysis of the NF1 gene involves isolating
CC peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-
CC Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated
CC PBL, or short-term culturing of PBL by phytohaemagglutinin (PHA)
CC stimulation, treating the cell line or short-term culture with protein
CC synthesis inhibitor and immediately extracting RNA from the cultures. The
CC RNA is then amplified and peptide fragments are obtained by in vitro
CC transcription/translation of amplified fragments. Mutation analysis of
CC NF1 is used for detection of frame shift, mis-sense and silent mutations
CC in various exons of the gene. This is useful in screening for NF1
CC mutations in young children who are often oligosymptomatic. Efficacy of a
CC drug or agent can be identified by a screening process in which the
CC modulation is monitored in vitro using cell systems in which the
CC defective NF1 gene is expressed. The sequences can be used to design
CC drugs which modulate NF1 activity, by using knowledge of the structure of
CC the NF1 protein and of specific defects of the various NF1 mutant
CC proteins. The method allows for reliable analysis of mutations that are
CC difficult to detect due to unstable or wrong-spliced transcripts
XX
XX Sequence 18 BP; 10 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 416 TTTTTCCTTATATTT 430
Db 18 TTTTTCCTTATAGTT 4
RESULT 479
AAS05039/c
ID AAS05039 standard; DNA; 18 BP.
XX
AC AAS05039;
XX
XX 07-SEP-2001 (first entry)
DT
XX Neurofibromatosis (NF1) genomic DNA sequencing primer #91.
DE
XX Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
KW Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA;
KW frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
KW sequencing primer.
XX
XX Homo sapiens.
OS
XX WO200129251-A2.
PN
XX 26-APR-2001.
PD
XX 18-OCT-2000; 2000WO-EP010255.
PF
XX 18-OCT-1999; 99EP-00870216.
PR
XX 05-JUN-2000; 2000EP-00870122.
PR
XX (UYGE-) UNIV GENT.
PA
XX Messiaen L, Callens T;
XX WPI; 2001-300341/31.
XX
DR Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid
XX
PT

PT cell lines formed with lymphocytes of patient with protein synthesis
PT inhibitor, and obtaining peptides by translating amplified RNA from cell
XX line.
PS Claim 9; Page 64; 102pp; English.
XX
CC The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A
CC method for mutation analysis of the NF1 gene involves isolating
CC peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-
CC Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated
CC PBL, or short-term culturing of PBL by phytohaemagglutinin (PHA)
CC stimulation, treating the cell line or short-term culture with protein
CC synthesis inhibitor and immediately extracting RNA from the cultures. The
CC RNA is then amplified and peptide fragments are obtained by in vitro
CC transcription/translation of amplified fragments. Mutation analysis of
CC NF1 is used for detection of frame shift, mis-sense and silent mutations
CC in various exons of the gene. This is useful in screening for NF1
CC mutations in young children who are often oligosymptomatic. Efficacy of a
CC drug or agent can be identified by a screening process in which the
CC modulation is monitored in vitro using cell systems in which the
CC defective NF1 gene is expressed. The sequences can be used to design
CC drugs which modulate NF1 activity, by using knowledge of the structure of
CC the NF1 protein and of specific defects of the various NF1 mutant
CC proteins. The method allows for reliable analysis of mutations that are
CC difficult to detect due to unstable or wrong-spliced transcripts
XX
SQ Sequence 18 BP; 10 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 416 TTTTTCCTTATATT 430
Db 18 TTTTTCCTTAGTT 4

RESULT 480
ABV72174
ID ABV72174 standard; DNA; 18 BP.
XX
AC ABV72174;
XX
DT 05-DEC-2002 (first entry)
XX
DE PCR primer used to amplify Heartbreaker (Hbr) loci from maize.
XX
KW Heartbreaker; Hbr; DNA fingerprint; phenotype; polymorphism;
KW miniature inverted repeat transposable element; MITE; molecular marker;
KW PCR; primer; ss.
XX
OS Zea mays.
XX
PN US6420117-B1.
XX
PD 16-JUL-2002.
XX
PF 14-SEP-2000; 2000US-00662402.
XX
PR 14-SEP-1999; 99US-0153812P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI Wessler SR, Casa AM;
XX
DR WPI; 2002-654638/70.
XX
PT Producing a DNA fingerprint of an individual by amplifying fragments
PT containing a miniature inverted repeat transposable element is useful to
PT detect polymorphisms and correlate genotype with phenotype particularly
PT in maize.
XX

PS Example 1; Col 17; 37pp; English.
XX
CC PCR primers ABV72171-90 were used to amplify Heartbreaker (Hbr) loci from
CC maize genomic DNA. The Hbr family of miniature inverted repeat
CC transposable elements (MITEs) is useful to demonstrate the method of the
CC invention. The specification describes a method for producing a DNA
CC fingerprint of an individual. The method comprises generating restriction
CC fragments to which an adaptor is ligated, amplifying fragments containing
CC a MITE and resolving the amplified fragments. The presence of a certain
CC amplified fragment is correlated to a phenotype. The method is used to
CC characterize the DNA of an individual, to detect polymorphisms, to
CC correlate presence of an amplified fragment with phenotype and to
CC generate a set of molecular markers
XX
SQ Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 909 TCAACATTTTCCTAGA 923
Db 1 TCAACGTTTCCTAGA 15

RESULT 481
ABV76827
ID ABV76827 standard; DNA; 18 BP.
XX
AC ABV76827;
XX
DT 12-FEB-2003 (first entry)
XX
DE PCR primer used to amplify a CD21L gene fragment.
XX
KW Arthritic condition; CD21L; lymphotoxin-beta polypeptide;
KW chemoattractant; arthritis; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200280010-A1.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-US008856.
XX
PR 23-MAR-2001; 2001US-00816814.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Goronzy JJ, Weyand CM;
XX
DR WPI; 2003-058450/05.
XX
PT Determining the severity of arthritic conditions, e.g. rheumatoid
PT arthritis, in a mammal or human by detecting whether a sample contains
PT elevated levels of marker(s), e.g. CD21L polypeptides or lymphotoxin-beta
PT polypeptides.
XX
PS Example 2; Page 13; 27pp; English.
XX
CC The specification describes a method for determining the severity of an
CC arthritic condition in a mammal. The method comprises determining whether
CC or not a sample from the mammal contains at least 1 marker (e.g. an
CC elevated level of a CD21L polypeptide, an elevated level of a lymphotoxin
CC -beta polypeptide, or an elevated level of a chemoattractant
CC polypeptide). The presence of the marker indicates that the arthritis
CC condition is severe. The method is useful for diagnosing the severity of
CC an arthritis condition (e.g. rheumatoid arthritis) in a mammal,
CC particularly a human. PCR primers ABV76826-27 were used to amplify a
CC CD21L gene fragment from a synovial tissue sample. The primers were used
CC in the method of the invention
XX

```
SQ      Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match          1.2%;   Score 13.4;  DB 1;   Length 18;
  Best Local Similarity 93.3%;   Pred. No. 2.4e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      277 GGCATATTTCTTCAC 291
Db      1 GGCATGTTTCTTCAC 15

RESULT 482
ADK13869/c
ID      ADK13869 standard; DNA; 18 BP.
XX
AC      ADK13869;
XX
DT      06-MAY-2004 (first entry)
XX
DE      PCR primer used to amplify human PSK cDNA - SEQ ID 16.
XX
KW      inhibitor; cancer; cytostatic; antiinflammatory; solid lung tumour;
KW      colon; breast; prostate; ovary; pancreas; leukaemia; lymphoma;
KW      inflammatory disorder; gene therapy; antisense; RNA interference; PCR;
KW      primer; ss; human; PSK; prostate-derived STE20-like kinase.
XX
OS      Homo sapiens.
XX
PN      WO2004012817-A2.
XX
PD      12-FEB-2004.
XX
PF      31-JUL-2003; 2003WO-BP008470.
XX
PR      31-JUL-2002; 2002EP-00078143.
PR      19-AUG-2002; 2002US-00224524.
XX
PA      (KYL1-) KYLIX BV.
XX
PI      Van Lohuizen MMS, Berns AJM, Martins CP, Mikkers HMM, Lenz JR;
PI      Lund AH, De Koning JP;
XX
WPI; 2004-157022/15.
XX
Inhibitor compounds of expressed proteins of murine genes and/or their
human orthologs, useful for treating inflammatory diseases and cancer
disorders such as solid tumors, leukemias and lymphomas.
XX
Example 4; SEQ ID NO 16; 280pp; English.
XX
The invention relates to a novel inhibitor compound directed against the
expressed proteins or the transcription product (mRNA) of a murine gene
and/or its human orthologue and useful in the treatment of cancer. The
compound of the invention demonstrates cytostatic and antiinflammatory
activities and may be useful for the preparation of a therapeutic
composition for the treatment of cancer, in particular for the treatment
of solid tumours of the lung, colon, breast, prostate, ovary and
pancreas, as well as leukaemia and lymphoma. Furthermore, the methods of
the invention may be utilised to treat inflammatory disorders, as well as
during gene therapy, antisense therapy and RNA interference procedures.
The current sequence is that of the PCR primer of the invention which was
used to amplify human PSK (prostate-derived STE20-like kinase) cDNA.
XX
SQ      Sequence 18 BP; 1 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match          1.2%;   Score 13.4;  DB 1;   Length 18;
  Best Local Similarity 93.3%;   Pred. No. 2.4e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      896 CAGACCAAGAGCCTC 910
Db      15 CAGCCCAAGAGCCTC 1

SQ      Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match          1.2%;   Score 13.4;  DB 1;   Length 18;
  Best Local Similarity 93.3%;   Pred. No. 2.4e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      277 GGCATATTTCTTCAC 291
Db      1 GGCATGTTTCTTCAC 15

RESULT 482
ADK13869/c
ID      ADK13869 standard; DNA; 18 BP.
XX
AC      ADK13869;
XX
DT      06-MAY-2004 (first entry)
XX
DE      PCR primer used to amplify human PSK cDNA - SEQ ID 16.
XX
KW      inhibitor; cancer; cytostatic; antiinflammatory; solid lung tumour;
KW      colon; breast; prostate; ovary; pancreas; leukaemia; lymphoma;
KW      inflammatory disorder; gene therapy; antisense; RNA interference; PCR;
KW      primer; ss; human; PSK; prostate-derived STE20-like kinase.
XX
OS      Homo sapiens.
XX
PN      WO2004012817-A2.
XX
PD      12-FEB-2004.
XX
PF      31-JUL-2003; 2003WO-BP008470.
XX
PR      31-JUL-2002; 2002EP-00078143.
PR      19-AUG-2002; 2002US-00224524.
XX
PA      (KYL1-) KYLIX BV.
XX
PI      Van Lohuizen MMS, Berns AJM, Martins CP, Mikkers HMM, Lenz JR;
PI      Lund AH, De Koning JP;
XX
WPI; 2004-157022/15.
XX
Inhibitor compounds of expressed proteins of murine genes and/or their
human orthologs, useful for treating inflammatory diseases and cancer
disorders such as solid tumors, leukemias and lymphomas.
XX
Example 4; SEQ ID NO 16; 280pp; English.
XX
The invention relates to a novel inhibitor compound directed against the
expressed proteins or the transcription product (mRNA) of a murine gene
and/or its human orthologue and useful in the treatment of cancer. The
compound of the invention demonstrates cytostatic and antiinflammatory
activities and may be useful for the preparation of a therapeutic
composition for the treatment of cancer, in particular for the treatment
of solid tumours of the lung, colon, breast, prostate, ovary and
pancreas, as well as leukaemia and lymphoma. Furthermore, the methods of
the invention may be utilised to treat inflammatory disorders, as well as
during gene therapy, antisense therapy and RNA interference procedures.
The current sequence is that of the PCR primer of the invention which was
used to amplify human PSK (prostate-derived STE20-like kinase) cDNA.
XX
SQ      Sequence 18 BP; 1 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match          1.2%;   Score 13.4;  DB 1;   Length 18;
  Best Local Similarity 93.3%;   Pred. No. 2.4e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      896 CAGACCAAGAGCCTC 910
Db      15 CAGCCCAAGAGCCTC 1

SQ      Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match          1.2%;   Score 13.4;  DB 1;   Length 18;
  Best Local Similarity 93.3%;   Pred. No. 2.4e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      277 GGCATATTTCTTCAC 291
Db      1 GGCATGTTTCTTCAC 15

RESULT 483
ADN35810/c
ID      ADN35810 standard; DNA; 18 BP.
XX
AC      ADN35810;
XX
DT      01-JUL-2004 (first entry)
XX
DE      Human NSCLC gene antisense-S oligonucleotide #35.
XX
KW      ss; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC;
KW      diagnosis; cancer; URLC1; antisense.
XX
OS      Homo sapiens.
XX
PN      WO2004031413-A2.
XX
PD      15-APR-2004.
XX
PF      22-SEP-2003; 2003WO-JP012072.
XX
PR      30-SEP-2002; 2002US-0414673P.
PR      28-FEB-2003; 2003US-0451374P.
PR      28-APR-2003; 2003US-0466100P.
XX
PA      (ONCO-) ONCOTHERAPY SCI INC.
PA      (UYTY ) UNIV TOKYO.
XX
PI      Nakamura Y, Daigo Y, Nakatsuru S;
XX
WPI; 2004-330206/30.
XX
Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)
comprises determining an expression level of an NSCLC-associated gene in
a sample.
XX
Disclosure; SEQ ID NO 491; 394pp; English.
XX
The invention relates to a method of diagnosing non-small cell lung
cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
determining the expression level of a NSCLC-associated gene in a
biological sample derived from the subject, where an increase or decrease
of the level compared to a normal control level of the gene indicates
that the subject suffers from or is at risk of developing NSCLC. The
method is useful in diagnosing NSCLC or a predisposition to developing
NSCLC in a subject. The compound, polynucleotide and the encoded
polypeptide and composition are useful in treating or preventing NSCLC.
This sequence corresponds to an antisense oligonucleotide of genes that
are differentially expressed in NSCLC cells.
XX
SQ      Sequence 18 BP; 4 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match          1.2%;   Score 13.4;  DB 1;   Length 18;
  Best Local Similarity 93.3%;   Pred. No. 2.4e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      196 CGCCATCTCCCCCAT 210
Db      16 CGCCATCTCCACCAT 2

RESULT 484
ADO56517/c
ID      ADO56517 standard; DNA; 18 BP.
XX
AC      ADO56517;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #42.
XX
KW      gene therapy; human; ss; melanoma;
```


KW melanoma associated polymorphic variation; SNP;
KW single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
XX
OS Homo sapiens.
XX
PN WO2004044164-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035879.
XX
PR 06-NOV-2002; 2002US-0424475P.
PR 23-JUL-2003; 2003US-0489703P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM;
XX WPI; 2004-411721/38.
DR
XX
PT Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.
XX
PS Example 5; Page 84; 295pp; English.
XX
CC The invention relates to a method of identifying a subject at risk of
CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
XX
SQ Sequence 18 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 702 TAGTCACGGTGCTCT 716
Db ||||| ||||| |||||
16 TAGTCACGGTGCTCT 2

RESULT 485
ADR05071
ID ADR05071 standard; DNA; 18 BP.
XX
AC ADR05071;
XX
DT 21-OCT-2004 (first entry)
XX
DE PCR primer 2 used to amplify human Bcl2 cDNA.
XX
KW apoptosis; cytostatic; antiinflammatory; antiasthmatic; respiratory;
KW antirheumatic; antiarthritic; gynaecological; cardiant; vasotropic;
KW antipsoriatic; antiulcer; gastrointestinal; immunosuppressive;
KW neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory;
KW asthma; chronic obstructive pulmonary disease; cystic fibrosis;
KW rheumatoid arthritis; acute respiratory distress syndrome; preeclampsia;
KW myocardial ischaemia; reperfusion injury; psoriasis; bronchiolitis;
KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; ss;
KW quantitative PCR; QPCR; primer; human; Bcl2.
XX
OS Homo sapiens.
XX

PN WO2004065959-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-GB000271.
XX
PR 23-JAN-2003; 2003GB-00001566.
PR 25-MAR-2003; 2003US-0457533P.
XX
PA (EIRX-) EIRX THERAPEUTICS LTD.
XX
PI Seery L, Hayes I, Murphy F;
XX WPI; 2004-593556/57.
DR
XX
PT Identifying a modulator of apoptosis-associated polypeptide function,
PT useful for treating e.g., cancer, comprises incubating a sample
PT containing an apoptosis-associated polypeptide and a candidate agent to
PT permit binding.
XX
PS Example 3; Page 219; 230pp; English.
XX
CC The invention relates to a novel method for identifying an agent that
CC modulates the function of an apoptosis-associated polypeptide,
CC particularly a kinase or GPCR (G-protein-coupled receptor). The method
CC comprises providing a sample containing an apoptosis-associated
CC polypeptide and a candidate agent and incubating under conditions to
CC permit binding of the candidate agent to the polypeptide, measuring the
CC binding and comparing it with the binding of the polypeptide to a control
CC agent known not to bind to the polypeptide. The method of the invention
CC has cytostatic, antiinflammatory, antiasthmatic, respiratory,
CC antirheumatic, antiarthritic, gynaecological, cardiant, vasotropic,
CC antipsoriatic, antiulcer, gastrointestinal, immunosuppressive and
CC neuroprotective applications. The method and molecules may be useful for
CC treating a disease or condition characterised by abnormal apoptosis in
CC mammalian tissue, particularly cancer, such as small cell lung cancer,
CC cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast,
CC leukaemias, sarcomas and myelomas. Furthermore, autoimmune,
CC neurodegenerative and inflammatory conditions may be treated, including
CC asthma, chronic obstructive pulmonary disease, cystic fibrosis,
CC rheumatoid arthritis, acute respiratory distress syndrome, preeclampsia,
CC myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis,
CC Crohn's disease, ulcerative colitis and inflammatory bowel disease. The
CC current sequence is that of a QPCR (quantitative PCR) primer of the
CC invention which was used to analyse human apoptosis-associated sequence
CC expression in the presence or absence of siRNAs (small interfering RNAs).
XX
SQ Sequence 18 BP; 4 A; 10 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 199 CATCTCCCCCATCCC 213
Db ||||| ||||| |||||
3 CATCTCCCGCATCCC 17

RESULT 486
ADS90284
ID ADS90284 standard; DNA; 18 BP.
XX
AC ADS90284;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:1300.
XX
KW ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Unidentified.
XX

PN WO2004035803-A2.
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
DR WPI; 2004-348468/32.
XX
PT Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
PS Disclosure; SEQ ID NO 1300; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 18 BP; 5 A; 0 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 TAGGAGATGAGTTT 630
Db | | | | | | | | | |
3 TAGGAGATGAGATT 17

RESULT 487
AAV23538
ID AAV23538 standard; DNA; 19 BP.
XX
AC AAV23538;
XX
DT 04-AUG-1998 (first entry)
XX
DE Mouse beta defensin-1 gene specific forward primer 2.
XX
KW antimicrobial peptide; cystic fibrosis; RT-PCR; emphysema; PCR;
KW beta defensin-1; mbD-1; primer; amplification; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9807833-A1.
XX
PD 26-FEB-1998.
XX
PF 20-AUG-1997; 97WO-US014639.
XX

PR 22-AUG-1996; 96US-0023424P.
PR 01-OCT-1996; 96US-0027334P.
PR 18-FEB-1997; 97US-0038685P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
PA (NAGA-) MAGAININ PHARM INC.
XX
PI Wilson JM, Goldman M, Bals R, Stolzenberg ED, Anderson M;
PI Zasloff M;
XX
DR WPI; 1998-179058/16.
XX
PT New isolated mammalian beta defensin-1 gene(s) - used to develop products
PT for treating microbial infections, e.g. respiratory conditions
PT susceptible to microbial infection such as cystic fibrosis.
XX
PS Disclosure; Page 43; 79pp; English.
XX
CC The mouse beta defensin-1 (mbD-1) gene specific forward primer 2 was used
CC with reverse primer 1 (AAV23539) or 2 (AAV23540) in a PCR reaction where
CC mbD-1 cDNA (AAV23528) served as a template. The PCR product was used as a
CC probe to isolate the mbD-1 genomic sequence from a mouse genomic library.
CC The mbD-1 cDNA encodes for the mouse beta defensin-1 (AAW53857) peptide.
CC The mbD-1 peptide was found to be highly salt sensitive and have
CC antimicrobial properties. Expression of mbD-1 and its biological activity
CC renders the mouse as at useful model to investigate the role of
CC antimicrobial peptides in pulmonary microbial infections and in
CC respiratory diseases
XX
SQ Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 954 CACTCTGGACCCAGG 968
Db | | | | | | | | | |
3 CACTCTGGACCCCTGG 17

RESULT 488
AAZ01215/c
ID AAZ01215 standard; DNA; 19 BP.
XX
AC AAZ01215;
XX
DT 27-SEP-1999 (first entry)
XX
DE PCR primer for PG1 biallelic marker 99-1481-285.
XX
KW PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW PSA; human; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9932644-A2.
XX
PD 01-JUL-1999.
XX
PF 22-DEC-1998; 98WO-IB002133.
XX
PR 22-DEC-1997; 97US-00996306.
PR 09-SEP-1998; 98US-0099658P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;
XX
DR WPI; 1999-405178/34.
XX
PT Use of a prostate cancer associated gene and biallelic markers derived

PT from it.
XX
PS Claim 4; Page 351; 385pp; English.
XX
CC The invention relates to a mammalian PGI gene and protein, and a set of
CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
CC used in a hybridisation assay, a sequencing assay, or in an allele-
CC specific amplification assay for determining the identity of a nucleotide
CC at a PGI-related biallelic marker. The methods can be used to detect and
CC to assess the risk of developing cancer or prostate cancer. Early-stage
CC diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC dosage. However, the effectiveness of this is limited due to its
CC inability to discriminate between malignant and non-malignant affections
CC of the organ. A need exists for both a reliable diagnostic procedure
CC which would enable early-stage diagnosis, and for preventative and
CC curative treatments of the disease. The PGI gene can be used for
CC detection of prostate cancer, and the risk of developing it in the
CC future, and can also be used to determine therapies for the disease
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAATGGGGAGCCT 365
Db 15 TCAAAGGGGAGCCT 1

RESULT 489
AAA86085
ID AAA86085 standard; DNA; 19 BP.
XX
AC AAA86085;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cdc 25 hs ribozyme binding site #193.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 102; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX

SQ Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 238 CTATGACTCAGATGC 252
Db 2 CTATCACTCAGATGC 16

RESULT 490
AAZ70031/C
ID AAZ70031 standard; DNA; 19 BP.
XX
AC AAZ70031;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4387.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1166; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 TCAAATGGGGAGCCT 365
||||| |||||||||

Db 15 TCAAAAGGGGAGCCT 1

RESULT 491
AAZ76970
ID AAZ76970 standard; DNA; 19 BP.
XX
AC AAZ76970;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11326.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB0000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 2645; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 19 BP; 4 A; 6 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 CATTTCCTTACAAT 408
|||||
Db 4 CATTGCCTTACAAT 18

RESULT 492
ABA95463/C
ID ABA95463 standard; DNA; 19 BP.
XX
AC ABA95463;

XX 11-MAR-2002 (first entry)
DT
XX
DE Thermus thermophilus dnaQ gene PCR primer P133-A1237.
XX
KW DNA polymerase III; holoenzyme; enzyme; thermophilic; replicase;
KW PCR primer; ss.
XX
OS Thermus thermophilus.
XX
PN WO200173052-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-US009950.
XX
PR 28-MAR-2000; 2000US-0192736P.
XX
PA (MCHE/) MCHENRY C S.
XX
PI Mchenry CS;
XX
DR WPI; 2001-611633/70.
XX
PT Isolated DNA polymerase III holoenzyme subunits and accessory proteins
PT useful for synthesizing DNA, e.g. in the polymerase chain reaction.
XX
PS Example 14; Page 171; 249pp; English.
XX
CC The present invention relates to DNA polymerase III holoenzyme subunits
CC and accessory proteins and their coding sequences from Thermus
CC thermophilus. The various subunits may be useful in PCR assays and for
CC synthesising DNA, since the subunits provide a thermophilic replicase
CC capable of rapid replication and highly processive properties at elevated
CC temperatures compared to the prior art that is limited by relatively non-
CC processive repair-like DNA polymerases. The present sequence is a PCR
CC primer, which was used in an example from the present invention
XX
SQ Sequence 19 BP; 3 A; 10 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CAGGAAGGCCGGGT 849
|||||
Db 15 CTGGAAGGCCGGGT 1

RESULT 493
AAH61247
ID AAH61247 standard; DNA; 19 BP.
XX
AC AAH61247;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3671.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnarary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 339; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 238 CTATGACTCAGATGC 252
Db ||||| ||||| |||||
2 CTATGACTCAGATGC 16

RESULT 494
ABL43540/c
ID ABL43540 standard; DNA; 19 BP.
XX
AC ABL43540;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:584.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.

XX (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 16; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 19 BP; 8 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 406 AATTCAAGGGTTT 420
Db ||||| ||||| |||||
16 AATTCAAGGGTTATT 2

RESULT 495
ADF85077
ID ADF85077 standard; RNA; 19 BP.
XX
AC ADF85077;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human ERG2-targeted siRNA - SEQ ID 1371.
XX
KW short interfering nucleic acid; siNA; breakpoint cluster region;
KW v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL;
KW cytostatic; leukaemia; lymphoma; human; ss; siRNA; ERG2;
KW v-ets erythroblastosis virus E26 oncogene like (avian).
XX
OS Homo sapiens.
XX
PN WO2003070972-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005234.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 15-AUG-2002; 2002US-0404039P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 14-JAN-2003; 2003US-0439922P.
PR 15-JAN-2003; 2003US-0440129P.
XX (RIBO-) RIBOZYME PHARM INC.
PA Mcswiggen J, Beigelman L, Chowrira B;
XX WPI; 2003-679889/64.
DR
XX
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
PT and diagnosis of leukemia and lymphoma, downregulates the breakpoint
PT cluster region-Abelson (BCR-ABL) gene.
XX
XX Example 7; SEQ ID NO 1371; 197pp; English.
PS
XX The invention relates to a novel double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of the breakpoint
CC cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1
CC (BCR-ABL) gene. The siRNA of the invention demonstrates cytostatic
CC activity and may be useful for modulating expression of the BCR-ABL gene,
CC as well as for treating leukaemia or lymphoma and in diagnosis, drug
CC screening, target identification and validation, genetic engineering,
CC gene function studies and gene mapping. The current sequence is that of
CC the human ERG2 (v-ets erythroblastosis virus E26 oncogene like (avian))-
CC targeted siRNA of the invention.
XX
SQ Sequence 19 BP; 7 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 958 CTGGACCCAGGACAT 972
Db 5 CUGGACUCAGGACAU 19
RESULT 496
ADF85253/c
ID ADF85253 standard; RNA; 19 BP.
XX ADF85253;
AC
XX 26-FEB-2004 (first entry)
DT
XX Human ERG2-targeted siRNA - SEQ ID 1547.
DE
XX short interfering nucleic acid; siNA; breakpoint cluster region;
KW v-abl Abelson murine leukaemia viral oncogene homologue 1; BCR-ABL;
KW cytostatic; leukaemia; lymphoma; human; ss; siRNA; ERG2;
KW v-ets erythroblastosis virus E26 oncogene like (avian).
XX
XX Homo sapiens.
OS
XX WO2003070972-A2.
PN
XX 28-AUG-2003.
PD
XX 20-FEB-2003; 2003WO-US005234.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 15-AUG-2002; 2002US-0404039P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 14-JAN-2003; 2003US-0439922P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA Mcswiggen J, Beigelman L, Chowrira B;
PI

XX WPI; 2003-679889/64.
DR
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
PT and diagnosis of leukemia and lymphoma, downregulates the breakpoint
PT cluster region-Abelson (BCR-ABL) gene.
XX
XX Example 7; SEQ ID NO 1547; 197pp; English.
PS
XX The invention relates to a novel double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of the breakpoint
CC cluster region-v-abl Abelson murine leukaemia viral oncogene homologue 1
CC (BCR-ABL) gene. The siRNA of the invention demonstrates cytostatic
CC activity and may be useful for modulating expression of the BCR-ABL gene,
CC as well as for treating leukaemia or lymphoma and in diagnosis, drug
CC screening, target identification and validation, genetic engineering,
CC gene function studies and gene mapping. The current sequence is that of
CC the human ERG2 (v-ets erythroblastosis virus E26 oncogene like (avian))-
CC targeted siRNA of the invention.
XX
SQ Sequence 19 BP; 3 A; 5 C; 4 G; 0 T; 7 U; 0 Other;
Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 958 CTGGACCCAGGACAT 972
Db 15 CTGGACTCAGGACAT 1
RESULT 497
ADN75949/c
ID ADN75949 standard; RNA; 19 BP.
XX AC ADN75949;
AC
XX 01-JUL-2004 (first entry)
DT
XX TCPTP2 siRNA #1.
DE
XX small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytostatic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
XX Homo sapiens.
OS
XX WO2004016735-A2.
PN
XX 26-FEB-2004.
PD
XX 23-MAY-2003; 2003WO-US016632.
PF
XX 23-MAY-2002; 2002US-0383249P.
PR 14-APR-2003; 2003US-0462942P.
PR
XX (CEPT-) CEPTYR INC.
PA (COLD-) COLD SPRING HARBOR LAB.
PA
XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;
PI
XX WPI; 2004-203773/19.
XX
XX New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, inflammation,
PT diabetes and obesity.
PT
XX Disclosure; SEQ ID NO 774; 392pp; English.
PS
XX This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide

CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosolic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 19 BP; 7 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 345 CTGTGATCAAAATGGG 359
Db 18 CTGTGATCATATGGG 4

RESULT 498
ADN75950
ID ADN75950 standard; RNA; 19 BP.
XX
AC ADN75950;
XX
DT 01-JUL-2004 (first entry)
XX
DE TCPTP2 siRNA #2.
XX
KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
KW inflammation; diabetes; obesity; RNA interference; gene silencing; ss.
XX
OS Homo sapiens.
XX
PN WO2004016735-A2.
XX
PD 26-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016632.
XX
PR 23-MAY-2002; 2002US-0383249P.
PR 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Klinghoffer R, Lewis SP, Tonks NK, Meng T;
XX
DR WPI; 2004-203773/19.
XX
PT New isolated small interfering RNA (siRNA) polynucleotide useful for
PT treating diseases with aberrant activity of the protein tyrosine
PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
PT diabetes and obesity.
XX
PS Disclosure; SEQ ID NO 775; 392pp; English.
XX
CC This invention describes novel small interfering RNA (siRNA)
CC polynucleotides capable of interfering with expression of a polypeptide
CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
CC invention have cytosolic, immunomodulator, antimicrobial,
CC antiinflammatory, antidiabetic and anorectic activity. The methods and
CC compositions of the present invention are useful for treating diseases or
CC conditions associated with aberrant expression or activity of the protein
CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
CC inflammation, diabetes and obesity. This sequence represents a siRNA
CC directed against dual specificity phosphatase (DSP) expression.
XX
SQ Sequence 19 BP; 4 A; 3 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 345 CTGTGATCAAAATGGG 359
Db 2 CUGUGAUCUAUGGG 16

RESULT 499
ADO18480
ID ADO18480 standard; DNA; 19 BP.
XX
AC ADO18480;
XX
DT 15-JUL-2004 (first entry)
XX
DE Analytical probe chip of the invention #239.
XX
KW analytical chip; bacterial 16S-rRNA; genotypic characterization; probe;
KW ss.
XX
OS Synthetic.
XX
PN WO2004033720-A2.
XX
PD 22-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP010626.
XX
PR 09-OCT-2002; 2002EP-00022631.
XX
PA (UYGE-) UNIV GENEVE HOPITAUX.
XX
PI Schrenzel J, Francois P, Charbonnier Y, Jacquet JG, Uttinger D;
PI Kresbach GM, Abel A, Ehrat M;
XX
DR WPI; 2004-375537/35.
XX
PT Analytical chip useful for simultaneous determination of one or more
PT different bacterial 16S-rRNA in liquid sample, comprising evanescent
PT field measurement platform as solid carrier and several specific
PT recognition elements.
XX
PS Claim 1; SEQ ID NO 239; 82pp; English.
XX
CC The present invention relates to an analytical chip for simultaneous
CC determination of one or more different bacterial 16S-rRNA in liquid
CC sample. The chip is useful for detecting one or more bacterial 16S-rRNA,
CC derived from bacteria such as Achromobacter xylosoxidans , Acinetobacter
CC baumannii , Actinomyces israelii , Aerococcus viridans , Aeromonas
CC hydrophilia , Agrobacterium radiobacter , Bacillus sp. , Bacteroides
CC ovatus , Campylobacter fetus , Citrobacter freundii , Enterococcus avium
CC , Eubacterium lentum , Escherichia coli , Flavobacterium breve ,
CC Fusobacterium nucleatum , Gemella morbillorum , Gardnerella vaginalis ,
CC Haemophilus influenzae , Hafnia alvei , Kingella sp. , Klebsiella oxytoca
CC , Lactobacillus acidophilus , Legionella pneumophila , Moraxella
CC catarrhalis , Mycobacterium avium , Neisseria cinerea , Nocardia sp. ,
CC Ochrobactrum anthropi , Pasteurella multocida , Peptostreptococcus magnus
CC , Salmonella typhi , Shigella sonnei , Veillonella parvula , Veillonella
CC sp. Or Versinia enterocolitica . The chip is useful for detecting
CC clinically relevant bacteria. The chip enables determination of one or
CC more different bacterial 16S-rRNA in a liquid sample, simultaneously and
CC enables rapid, accurate, easy and reliable identification of bacteria by
CC genotypic characterization in a provided sample and also enables
CC identification of a bacterium even in a complex biological sample. The
CC chip which is produced at reduced cost, enables determination of 16S-rRNA
CC in a sample with reduced experimental error and variation. The present
CC sequence represents a probe of the invention used as an analytical chip.
XX
SQ Sequence 19 BP; 4 A; 4 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;

Fri Aug 19 11:00:00 2005

Best Local Similarity 93.3%; Pred. No. 2.4e+02; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 466 GCACTTTATTCTGAT 480
| | | | | | | | | | | | | | | | | |
Db 3 GCACTTTATTCTTAT 17

RESULT 500
ADR79444
ID ADR79444 standard; DNA; 19 BP.
XX
AC ADR79444;
XX
DT 15-JUL-2004 (first entry)
XX
DE Analytical probe chip of the invention #332.
XX
KW analytical chip; bacterial 16S-rRNA; genotypic characterization; probe;
KW ss.
XX
OS Synthetic.
XX
PN WO2004033720-A2.
XX
PD 22-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP010626.
XX
PR 09-OCT-2002; 2002EP-00022631.
XX
PA (UYGE-) UNIV GENEVE HOPITAUX.
XX
PI Schrenzel J, Francois P, Charbonnier Y, Jacquet JG, Uttinger D;
PI Kresbach GM, Abel A, Ehrat M;
XX
DR WPI; 2004-375537/35.
XX
PT Analytical chip useful for simultaneous determination of one or more
PT different bacterial 16S-rRNA in liquid sample, comprising evanescent
PT field measurement platform as solid carrier and several specific
PT recognition elements.
XX
PS Claim 45; SEQ ID NO 332; 82pp; English.
XX
CC The present invention relates to an analytical chip for simultaneous
CC determination of one or more different bacterial 16S-rRNA in liquid
CC sample. The chip is useful for detecting one or more bacterial 16S-rRNA,
CC derived from bacteria such as Achromobacter xylosoxidans , Acinetobacter
CC baumannii , Actinomyces israelii , Aerococcus viridans , Aeromonas
CC hydrophilia , Agrobacterium radiobacter , Bacillus sp. , Bacteroides
CC ovatus , Campylobacter fetus , Citrobacter freundii , Enterococcus avium
CC , Eubacterium lentum , Escherichia coli , Flavobacterium breve ,
CC Fusobacterium nucleatum , Gemella morbillorum , Gardnerella vaginalis ,
CC Haemophilus influenzae , Hafnia alvei , Kingella sp. , Klebsiella oxytoca
CC , Lactobacillus acidophilus , Legionella pneumophila , Moraxella
CC catarrhalis , Mycobacterium avium , Neisseria cinerea , Nocardia sp. ,
CC Ochrobactrum anthropi , Pasteurella multocida , Peptostreptococcus magnus
CC , Salmonella typhi , Shigella sonnei , Veillonella parvula , Veillonella
CC sp. or Yersinia enterocolitica . The chip is useful for detecting
CC clinically relevant bacteria. The chip enables determination of one or
CC more different bacterial 16S-rRNA in a liquid sample, simultaneously and
CC enables rapid, accurate, easy and reliable identification of bacteria by
CC genotypic characterization in a provided sample and also enables
CC identification of a bacterium even in a complex biological sample. The
CC chip which is produced at reduced cost, enables determination of 16S-rRNA
CC in a sample with reduced experimental error and variation. The present
CC sequence represents a probe of the invention used as an analytical chip.
XX
SQ Sequence 19 BP; 4 A; 4 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 466 GCACTTTATTCTGAT 480
| | | | | | | | | | | | | | | | | |
Db 3 GCACTTTATTCTTAT 17

RESULT 501
ADR79444
ID ADR79444 standard; DNA; 19 BP.
XX
AC ADR79444;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human apolipoprotein B (ApoB) oligonucleotide seqid 3929.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytostatic; anticonvulsant; nootropic; muscular; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS Homo sapiens.
XX
PN WO2004080406-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US007070.
XX
PR 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Bumcrot D;
XX
DR WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
PS Example 5; SEQ ID NO 3929; 378pp; English.
XX
CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its

CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholesterolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.

XX
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 830 TGACCCAGGAAGGCC 844
|||||
Db 2 TGACTCAGGAAGGCC 16

RESULT 502

ADR77809
ID ADR77809 standard; DNA; 19 BP.

XX
AC ADR77809;

XX
DT 16-DEC-2004 (first entry)

XX
DE Human apolipoprotein B (ApoB) oligonucleotide seqid 2294.

XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cyostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.

XX
OS Homo sapiens.

XX
PN WO2004080406-A2.

XX
PD 23-SEP-2004.

XX
PF 08-MAR-2004; 2004WO-US007070.

XX
PR 07-MAR-2003; 2003US-0452682P.

PR 12-MAR-2003; 2003US-0454265P.

PR 13-MAR-2003; 2003US-0454962P.

PR 13-MAR-2003; 2003US-0455050P.

PR 14-APR-2003; 2003US-0462894P.

PR 17-APR-2003; 2003US-0463772P.

PR 25-APR-2003; 2003US-0465665P.

PR 25-APR-2003; 2003US-0465802P.

PR 09-MAY-2003; 2003US-0469612P.

PR 08-AUG-2003; 2003US-0493986P.

PR 11-AUG-2003; 2003US-0494597P.

PR 26-SEP-2003; 2003US-0506341P.

PR 09-OCT-2003; 2003US-0510246P.

PR 10-OCT-2003; 2003US-0510318P.

PR 07-NOV-2003; 2003US-0518453P.

XX
PA (ALNY-) ALNYLAM PHARM.

XX
PI Manoharan M, Bumcrot D;

XX
WPI; 2004-677362/66.

XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.

XX
PS Example 5; SEQ ID NO 2294; 378pp; English.

XX
CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholesterolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.

XX
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 830 TGACCCAGGAAGGCC 844
|||||
Db 2 TGACTCAGGAAGGCC 16

RESULT 503

AAQ91053/c

ID AAQ91053 standard; DNA; 18 BP.

XX
AC AAQ91053;

XX
DT 30-JAN-1996 (first entry)

XX
DE HHV-6 associated MS genetic marker 38E internal primer 38E6.

XX
KW Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; 38E;
KW internal primer 38E6; diagnosis; ss.

XX
OS Synthetic.

XX
PN WO9512313-A1.

XX
PD 11-MAY-1995.

XX
PF 04-NOV-1994; 94WO-US012655.

XX 05-NOV-1993; 93US-00149176.
PR 24-MAR-1994; 94US-00218029.
PR 05-AUG-1994; 94US-00287942.
PR 04-NOV-1994; 94US-00334482.
XX (PATH-) PATHOGENESIS CORP.
PA
XX Burmer GC, Challoner PB, Smith KT, Brown JP, Parker JD;
PI Nowinski RC;
XX WPI; 1995-215032/28.
DR
XX Treatment of human herpes-virus-6-associated multiple sclerosis - using
PT an antiviral agent, e.g. a nucleoside analogue, administered to the
PT cerebrospinal fluid.
XX
PS Disclosure; Page 35; 116pp; English.
XX
CC AAQ91052 and AAQ91053 are an internal primer pair for the human herpes
CC virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, 38E
CC (AAQ91054). The primers can be used in the diagnosis of MS
XX
SQ Sequence 18 BP; 7 A; 6 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GCTATTGGACTGACTTTT 130
Db 18 GCTGTGGACTGGCATT 1

RESULT 504
AAT60161/c
ID AAT60161 standard; DNA; 18 BP.
XX
AC AAT60161;
XX
DT 01-DEC-1997 (first entry)
XX
DE Collagen gene promoter region binding oligomer Oligo 158 APS.
XX
KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..18
FT /*tag= a
FT /note= "Phosphorothioate linkages"
XX
PN WO9710254-A1.
XX
PD 20-MAR-1997.
XX
PF 12-SEP-1996; 96WO-US014640.
XX
PR 15-SEP-1995; 95US-00528836.
PR 11-SEP-1996; 96US-00712357.
XX
PA (GUNT/) GUNTAKA R V.
XX
PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX
XX WPI; 1997-202172/18.
DR
XX Triplex forming oligomer binds to collagen gene promoter region - used to
PT impede pathological fibrosis etc.

XX Claim 18; Page 36; 52pp; English.
PS
XX An oligomer has been produced which is capable of inhibiting expression
CC of a collagen gene. The present sequence represents a specifically
CC claimed oligomer Oligo 158 APS, which binds to the polypurine-
CC polypyrimidine region of the rat alpha(I) collagen gene promoter region.
CC The oligomer may be used to impede pathological fibrosis which is
CC associated with myocardial fibrosis in hypertensive heart diseases,
CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
CC fibrosis found in scleroderma, in hypertrophic scars and in skin
CC following burn injury. The oligomer inhibits expression of a collagen
CC gene after insertion into a cell by causing an intracellular reaction
CC which inhibits gene expression. The oligomer is preferably a triplex
CC forming oligomer (TFO) which is targeted to a 30-mer polypurine
CC oligonucleotide corresponding to the noncoding strand of the promoter
CC between -170 and -140. This section was chosen due to its binding
CC stability at physiological pH
XX
SQ Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 202 CTCCTCCCATCCCCCATTT 219
Db 18 CTCCTCCCATCTCTCCCTTT 1

RESULT 505
AAV48417/c
ID AAV48417 standard; DNA; 18 BP.
XX
AC AAV48417;
XX
DT 15-OCT-1998 (first entry)
XX
DE Transforming growth factor beta-1 antisense oligonucleotide N5.
XX
KW Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
KW modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-00101531.
XX
PR 31-JAN-1997; 97EP-00101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen K, Brysch W;
XX
DR WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of residues
PT able to form two or three hydrogen bonds, have greater activity and
PT reduced toxicity, used therapeutically or to modulate growth of cells in
PT culture.
XX
PS Example 1; Fig 3a; 286pp; English.
XX
CC AAV48412-84 represent antisense oligonucleotides directed against
CC transforming growth factor beta-1 (TGF beta-1). The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four

CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in cases
CC of cancer or (targeting TGF) for stimulating the immune system
XX
SQ Sequence 18 BP; 2 A; 3 C; 12 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 196 CGCCATCTCCCCCATCCC 213
||| ||||| ||||| ||
Db 18 CGCGGCTCCCCCATGCC 1

RESULT 506
AAX76549
ID AAX76549 standard; DNA; 18 BP.
XX
AC AAX76549;
XX
DT 06-AUG-1999 (first entry)
XX
DE Human WISP-2 PCR primer SEQ ID NO:131.
XX
KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;
KW tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
KW connective tissue disorder; catabolic state; inflammation;
KW testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9921998-A1.
XX
PD 06-MAY-1999.
XX
PF 29-OCT-1998; 98WO-US022991.
XX
PR 29-OCT-1997; 97US-0063704P.
PR 03-FEB-1998; 98US-0073612P.
PR 14-APR-1998; 98US-0081695P.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein DA, Cohen RL, Gurney AL, Hillan K, Lawrence DA;
PI Levine AJ, Pennica D, Roy MA, Goddard A, Wood WI;
XX
DR WPI; 1999-337420/28.
XX
PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3.
XX
PS Example 11; Page 272; 284pp; English.
XX

CC The present invention describes Wnt-1 induced secreted polypeptides, WISP
CC -1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2 and
CC WISP-3 have homology to connective tissue growth factor (CTGF). Products
CC from the present invention can be used to treat WISP-related disorders
CC such as breast, ovarian, and colon cancer or melanoma. The products can
CC be used to treat arteriosclerosis. The products can also be used to treat
CC other diseases e.g. benign and malignant tumours, leukaemia and lymphoid

CC malignancies, neuronal, glial, astrocytal, hypothalamic and other
CC glandular, macrophagal, epithelial, stromal, and blastocoelic disorders,
CC haematopoiesis-related disorders, tissue-growth disorders, skin
CC disorders, desmoplasia, fibrotic lesions, kidney disorders, bone-related
CC disorders, such as osteoporosis, trauma such as burns, incisions, and
CC other wounds, connective tissue disorders, catabolic states, testicular-
CC related disorders, and inflammatory, angiogenic and immunologic disorders
CC including arteriosclerosis. The products can also be used for detection
CC and diagnosis especially of individuals with neoplastic cell growth or
CC proliferation. The products can be used in the production of transgenic
CC or knock-out animals. Antibodies can be used to induce death in WISP-1, 2
CC or 3 overexpressing cells
XX
SQ Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 897 AGACCAAGAGCCTCAACA 914
||| ||||| ||||| ||
Db 1 AGTCCAAGAGTCTCAGCA 18

RESULT 507
AAZ22179/c
ID AAZ22179 standard; DNA; 18 BP.
XX
AC AAZ22179;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human c-IAP-1 mRNA inhibiting antisense oligo ISIS #23361.
XX
KW Cellular Inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5958772-A.
XX
PD 28-SEP-1999.
XX
PF 03-DEC-1998; 98US-00205204.
XX
PR 03-DEC-1998; 98US-00205204.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM, Ackermann EJ;
XX
DR WPI; 1999-561047/47.
XX
PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1
PT useful for e.g. diagnostics, therapeutics, and as research reagents.
XX

PS Claim 3; Col 39; 32pp; English.
XX
CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-
CC 1). The antisense compounds may be used for diagnostics, therapeutics
CC (for modulating the expression of c-IAP-1), prophylaxis (e.g. to prevent
CC or delay infection, inflammation, or tumor formation), as research
CC reagents (e.g. to distinguish between members of a biological pathway)
CC and in kits. Sequences AAZ22150-189 represent phosphorothioate
CC oligonucleotides used for antisense inhibition of cellular inhibitor of
CC apoptosis-1
XX

SQ Sequence 18 BP; 6 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;

| | | | | | | | | | |
|--|--|------------------------|-----|------------|----|--------|----|------|----|
| Matches | 15; | Conservative | 0; | Mismatches | 3; | Indels | 0; | Gaps | 0; |
| QY | 974 | TTGATGAGATCCAAAGGA | 991 | | | | | | |
| | | | | | | | | | |
| Db | 18 | TTGATGAGATTCAGGTA | 1 | | | | | | |
| RESULT 508 | | | | | | | | | |
| AAX22147 | | | | | | | | | |
| ID | AAX22147 | standard; tRNA; 18 BP. | | | | | | | |
| XX | | | | | | | | | |
| AC | AAX22147; | | | | | | | | |
| XX | | | | | | | | | |
| DT | 20-MAR-2003 | (revised) | | | | | | | |
| DT | 26-MAY-1999 | (first entry) | | | | | | | |
| XX | | | | | | | | | |
| DE | Murine tRNA gene fragment. | | | | | | | | |
| XX | | | | | | | | | |
| KW | Murine Leukaemia virus; MLV; retroviral transfer vector; retrovirus; | | | | | | | | |
| KW | modified tRNA primer; antiviral agent; pathogenic; virus; HIV-1; HTLV-1; | | | | | | | | |
| KW | cellular tropism; murine; ss. | | | | | | | | |
| XX | | | | | | | | | |
| OS | Mus musculus. | | | | | | | | |
| XX | | | | | | | | | |
| PN | US5886166-A. | | | | | | | | |
| XX | | | | | | | | | |
| PD | 23-MAR-1999. | | | | | | | | |
| XX | | | | | | | | | |
| PF | 15-NOV-1996; | 96US-00749495. | | | | | | | |
| XX | | | | | | | | | |
| PR | 08-SEP-1995; | 95US-00525849. | | | | | | | |
| XX | | | | | | | | | |
| PA | (LUND/) LUND A H. | | | | | | | | |
| PA | (PEDE/) PEDERSEN F S. | | | | | | | | |
| PA | (JORG/) JORGENSEN P. | | | | | | | | |
| PA | (LOVM/) LOVMAND J. | | | | | | | | |
| PA | (DUCH/) DUCH M. | | | | | | | | |
| XX | | | | | | | | | |
| PI | Pedersen FS, Jorgensen P, Lovmand J, Lund AH, Duch M; | | | | | | | | |
| XX | | | | | | | | | |
| DR | WPI; 1999-228613/19. | | | | | | | | |
| XX | | | | | | | | | |
| PT | Murine leukaemia virus retroviral vector - whose transfer is dependent on | | | | | | | | |
| PT | the presence of specific tRNA-like primer. | | | | | | | | |
| XX | | | | | | | | | |
| PS | Disclosure; Col 10; 26pp; English. | | | | | | | | |
| XX | | | | | | | | | |
| CC | The invention relates to a modified tRNA primer for reverse transcription | | | | | | | | |
| CC | of a Murine Leukaemia virus (MLV) retroviral transfer vector. The vector | | | | | | | | |
| CC | comprises (i) a retrovirus in which at least part of the genomic RNA | | | | | | | | |
| CC | sequences carrying information for the production of viral proteins have | | | | | | | | |
| CC | been replaced by one or more sequences carrying information to be | | | | | | | | |
| CC | introduced in a target cell chromosome; (ii) a primer binding site (PBS) | | | | | | | | |
| CC | which has been modified to a sequence that does not allow strong base | | | | | | | | |
| CC | pairing with the 3' end of any naturally occurring tRNA, and the three 5' | | | | | | | | |
| CC | nucleotides of the PBS are UGG, where the modified tRNA primer has been | | | | | | | | |
| CC | modified to allow strong base pairing with the PBS of the transfer | | | | | | | | |
| CC | vector. The retroviral vectors can be used as antiviral agents. Such vectors | | | | | | | | |
| CC | can be directed against pathogenic viruses, e.g. HIV-1 or HTLV-1, related | | | | | | | | |
| CC | to the type used for construction of the vector, thus having the same | | | | | | | | |
| CC | host range and cellular tropism. The use of a modified tRNA primer | | | | | | | | |
| CC | reduces the risk of uncontrolled regeneration of complete virus, or of | | | | | | | | |
| CC | virus spread. Only specialised packaging cells provided with appropriate | | | | | | | | |
| CC | artificial primers allow vector propagation. Sequences AAX22147-167 | | | | | | | | |
| CC | represent published murine tRNA sequences based on which the modified | | | | | | | | |
| CC | tRNA primer is synthesised. (Updated on 20-MAR-2003 to correct PF field.) | | | | | | | | |
| XX | | | | | | | | | |
| SQ | Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other; | | | | | | | | |
| Query Match 1.2%; Score 13.2; DB 1; Length 18; | | | | | | | | | |
| Best Local Similarity 66.7%; Pred. No. 2.6e+02; | | | | | | | | | |
| Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0 | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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|------------|-----------|------------------------|-----|
| QY | 192 | TCCACGCCATCTCCCCCA | 209 |
| Db | 1 | UCCCCGGCAUCUCCACCA | 18 |
| RESULT 510 | | | |
| AA | C66251 | | |
| ID | AAC66251 | standard; tRNA; 18 BP. | |
| XX | AAC66251; | | |
| AC | AAC66251; | | |
| XX | | | |

DT 20-FEB-2001 (first entry)
XX Murine Ala tRNA 3' nucleotide sequence.
DE tRNA primer; retroviral transfer vector; primer binding site; ss.
XX Mus sp.
XX US6107478-A.
PN 22-AUG-2000.
XX 09-OCT-1998; 98US-00169248.
PF 08-SEP-1995; 95US-00525849.
XX 15-NOV-1996; 96US-00749495.
PR (LOVM/) LOVMAND J.
XX (PEDE/) PEDERSEN F S.
PA (LUND/) LUND A H.
PA (JORG/) JORGENSEN P.
PA (DUCH/) DUCH M.
XX Duch M, Lovmand J, Lund AH, Pedersen FS, Jorgensen P;
PI WPI; 2000-586220/55.
XX New modified tRNA primer for reverse transcribing a retroviral transfer
PT vector comprising a primer binding site modified to a sequence which does
PT not allow strong base pairing with the 3' end in any occurring tRNA.
XX Disclosure; Col 10; 27pp; English.
PS This invention relates to a new tRNA primer for reverse transcribing a
XX retroviral transfer vector comprising a primer binding site (PBS) that
CC has been modified to a sequence that does not allow strong base pairing
CC with the 3' end of any naturally occurring tRNA and comprises three 5'
CC nucleotides of UGG. The new tRNA primer is modified to allow strong base
CC pairing with the modified PBS of a transfer vector; reverse transcribes
CC the retroviral transfer vector which comprises a retrovirus in which at
CC least part of the genomic RNA sequences necessary for production of viral
CC proteins required in for retroviral replication have been replaced by
CC sequences to be introduced in a target cell chromosome; and has a PBS
CC that has been modified to a sequence that does not allow strong base
CC pairing with the 3' end of any naturally occurring tRNA and the three 5'
CC nucleotides are UGG. The primer is used for reverse transcribing the
CC retroviral vector comprising a retrovirus with infectivity for birds
CC and/or mammals in which a part of the genomic RNA sequences necessary for
CC production of viral proteins required in trans for retroviral replication
CC have been replaced by sequences to be introduced in a target cell
CC chromosome. The present sequence represents a murine tRNA sequence used
CC in the design of the primer of the invention
XX Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;
SQ Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 192 TCCACGCCATCTCCCCCA 209
Db :|||:|||:|||||
1 UCCCCGGCAUCCUCCACCA 18
RESULT 511
AAA35959/c
ID AAA35959 standard; DNA; 18 BP.
XX AAA35959;
AC AAA35959;
XX 26-JUL-2000 (first entry)
DT Human genomic SNP allele specific oligonucleotide SEQ ID NO:16.
DE

XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW genomic classification; identification; DNA fingerprinting;
KW tumour characterisation; hybridisation; ss.
XX Homo sapiens.
XX WO200018960-A2.
PN 06-APR-2000.
XX 24-SEP-1999; 99WO-US022283.
PF 25-SEP-1998; 98US-0101757P.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA Landers JE, Jordan B, Housman DE, Charest A;
XX WPI; 2000-293181/25.
DR Detection of single nucleotide polymorphisms in genomes by preparation
XX and analysis of reduced complexity genomes, useful for genotyping,
PT fingerprinting and determining allele frequency of SNPs.
PT Disclosure; Page 53; 111pp; English.
XX A method has been developed for detecting the presence or absence of a
CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC method comprises preparing a reduced complexity genome (RCG) from the
CC genomic sample and analysing the RCG for the presence or absence of a SNP
CC allele. The method can be used to characterise a tumour, to generate a
CC genomic pattern for an individual genome or to generate a genomic
CC classification code for a genome. The method can be used to assess
CC whether a subject is at risk for developing a disease or to identify a
CC set of SNP alleles associated with a disease. The method can also be used
CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences
CC used in the exemplification of the present invention. AAA35948 to
CC AAA36632 represent nucleotide sequences containing SNPs
XX Sequence 18 BP; 9 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 568 TTTTAATACCTTTATATA 585
Db |||||:|||:|||||
18 TTTTATACCTTCATAAA 1
RESULT 512
AAZ98709/c
ID AAZ98709 standard; DNA; 18 BP.
XX AAZ98709;
AC AAZ98709;
XX 20-JUN-2000 (first entry)
DT Collagen promoter inhibitory oligonucleotide Oligo Col 158 APS.
XX Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
DE atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
XX peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
OS Rattus sp.
XX WO200008213-A1.
PN 17-FEB-2000.
XX 06-AUG-1999; 99WO-US017824.
PF

XX 07-AUG-1998; 98US-00130888.
PR (GUNT/) GUNTAKA R V.
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 2000-205739/18.
DR Inhibitors of collagen gene useful for treating fibrosis associated with
XX atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
XX comprises oligomers capable of inhibiting collagen gene.
XX Claim 19; Fig 8; 77pp; English.
XX This sequence represents an oligomer which is capable of inhibiting the
XX expression of the collagen gene. The oligomer is capable of binding to
XX the promoter region of the collagen gene. Collagen is a family of fibrous
XX proteins, and is the major element of skin, bone, tendon, cartilage,
XX blood vessels and teeth. The oligomers are useful for inhibiting
XX expression of the collagen gene, comprising inserting the oligomers into
XX a cell and causing an intracellular reaction to inhibit the gene
XX expression. The collagen inhibitory oligomers of the invention are useful
XX for treating pathological fibrosis associated with myocardial fibrosis in
XX hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
XX lung fibrosis, peritoneal fibrosis and skin fibrosis found in
XX scleroderma, hypertrophic scars and burn injury
XX
SQ Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 202 CTCCCCCATCCCCCATTT 219
Db ||||| ||||| |||||
18 CTCCCCCTCTCCCTTT 1

RESULT 513
AAA97374
ID AAA97374 standard; DNA; 18 BP.
XX
AC AAA97374;
XX
DT 29-JAN-2001 (first entry)
XX
DE CMV GlyB detection oligonucleotide SA-B1.
XX
KW Cytomegalovirus GlyB gene; detection oligonucleotide; detection;
KW target-associated detectable structure; signal amplification; ss.
XX
OS Human herpesvirus 5.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "Biotinylated"
XX
XX WO200055365-A1.
PN
XX
PD 21-SEP-2000.
XX
XX 13-MAR-2000; 2000WO-GB000921.
PF
XX 12-MAR-1999; 99GB-00005580.
XX
XX (TEPN-) TEPNEL MEDICAL LTD.
PA
XX
XX Mulrooney C, Oultram JD;
PI
XX WPI; 2000-638207/61.
DR

XX Detecting a target molecule by enzymatically catalyzed amplification of
PT target associated detectable structures comprises contacting a sample
PT with a locator probe, amplifying the structure bound and detecting bound
PT locator probes.
XX
PS Example 5; Page 72; 75pp; English.
XX
CC The invention relates to a novel method of detecting a target nucleic
CC acid molecule. The method involves contacting a sample with a locator
CC probe comprising a binding moiety specific for the target molecule and an
CC amplification nucleic acid sequence. An amplification structure which is
CC bound to the target molecule-locator probe complex is produced via
CC amplification of the sample and locator probe using a single stranded
CC amplification template (comprising, in the 5' to 3' direction, an
CC extension nucleic acid sequence, a hybridisation nucleic acid sequence
CC and an amplification moiety); a polymerase; and a separating agent
CC capable of removing sufficient of the extension nucleic acid sequence of
CC the amplification template when hybridised to the complementary strand to
CC allow subsequent hybridisation of the hybridisation nucleic acid sequence
CC of the amplification template to the complementary strand. After
CC optionally repeating amplification of this structure, any additional
CC locator probes or amplification template is detected, and the result is
CC correlated with the presence of a target molecules. The method is used to
CC detect target molecules in a sample by using an enzymatically catalysed
CC amplification of the target-associated detectable structures. As a small
CC number of inexpensive components are utilised, the new method is more
CC economical than previous methods. The method utilises signal
CC amplification rather than target amplification, thus overcoming
CC contamination problems. It is an enzymatically catalysed process that
CC actively assembles the signal generating structure rather than relying on
CC the passive hybridisation-based methods of non-enzymatic methods such as
CC bDNA. Unlike prior art techniques such as polymerase chain reaction
CC (PCR), the method has the ability to address RNA and DNA targets with
CC equal efficiency without pretreatments. The present sequence represents a
CC detection oligonucleotide, SA-B1, used with amplification template SA-EX1
CC (AAA97373) in an exemplification of the invention to detect the CMV GlyB
CC target oligonucleotide CMV-002 (AAA97372)
XX
SQ Sequence 18 BP; 2 A; 6 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1056 TTATCTTCCAGTGGCTA 1073
Db ||||| ||||| |||||
1 TTCTCCTTCCAGTTGCTA 18

RESULT 514
AAA08213
ID AAA08213 standard; tRNA; 18 BP.
XX
AC AAA08213;
XX
DT 28-JUN-2000 (first entry)
XX
DE Murine tRNA oligonucleotide sequence SEQ ID NO:3.
XX
KW Retroviral vector; antiviral; retrovirus; infection; primer binding site;
KW PBS; human immunodeficiency virus; human T-cell lymphotropic virus-1;
KW HIV; ss.
XX
OS Mus musculus.
XX
PN US6037172-A.
XX
PD 14-MAR-2000.
XX
PF 09-OCT-1998; 98US-00169078.
XX
PR 08-SEP-1995; 95US-00525849.

XX (PEDE/) PEDERSEN F S.
PA (LUND/) LUND A H.
PA (LOVM/) LOVMAND J.
PA (JORG/) JORGENSEN P.
XX (DUCH/) DUCH M.
XX
PI Lund AH, Lovmand J, Pedersen FS, Duch M, Jorgensen P;
XX WPI; 2000-282226/24.
DR
XX
XX Retroviral vector for gene transfer, useful as antiviral agent, has a
PT primer binding site modified to prevent base pairing with natural
PT transfer RNA.
XX
XX Disclosure; Col 10; 27pp; English.
XX
XX The present invention describes a retroviral vector (I) comprising a
CC retrovirus in which at least part of the genomic RNA sequences carrying
CC information for the production of viral proteins required in trans for
CC retroviral replication have been replaced by one or more sequences
CC carrying information to be introduced in a target cell chromosome, where
CC the primer binding site (PBS) has been modified to a sequence that does
CC not allow strong base pairing with the 3'-end of any naturally occurring
CC tRNA, and where the three 5'-nucleotides of the PBS are UGG. (I) are
CC potentially useful as antiviral agents, e.g. against human immuno-
CC deficiency virus or human T-cell lymphotropic virus-1. (I) depends on a
CC specifically engineered tRNA-like primer for reverse transcription, so
CC only special packaging cells, containing an artificial primer, can
CC support vector propagation. This reduces the risk of uncontrolled
CC regeneration of complete virus if (I) interacts with engineered or
CC endogenous cis- or trans-acting components, particularly transfection
CC efficiency is reduced by a factor of 100000 in normal packaging cells.
CC (I) can be derived from pathogenic viruses of the same type as used for
CC vector construction, i.e. they have the same host range and cell tropism,
CC but the modified PBS means that antiviral activity would not be directed
CC against the vector's own cis-acting elements. The present sequence
CC represents a murine tRNA sequence, which is used in the exemplification
CC of the present invention
XX
SQ Sequence 18 BP; 3 A; 10 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 192 TCCACGCCATCTCCCCCA 209
Db :|||:|||:|:|:|
1 UCCCCGGCAUCUCCACCA 18

RESULT 515
AAZ71352
ID AAZ71352 standard; DNA; 18 BP.
XX
AC AAZ71352;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5708.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.

PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P;
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
DR
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 1448; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 871 TCCATGCTATTAAAGTG 888
Db :|||:|||:|:|:|
1 TCCATGCTCTTACCAGTG 18

RESULT 516
AAZ75603
ID AAZ75603 standard; DNA; 18 BP.
XX
AC AAZ75603;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9959.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX Claim 8; Page 2354; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX Sequence 18 BP; 2 A; 8 C; 0 G; 8 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 209 ATCCCCCATTTCATTGCC 226

Db 1 ATCCCCCTCTTCATTTC 18

RESULT 517

AAA91755

ID AAA91755 standard; DNA; 18 BP.

XX AAA91755;

AC

XX 02-JAN-2001 (first entry)

DT

XX TM7XN1 cDNA antisense PCR primer.

DE

XX Tumour; TM7XN1; metastatis; melanoma; seven transmembrane protein;

KW secretin family; G-protein-coupled peptide hormone receptor; cancer;

KW chromosome 16q13; tumour supressor; cyl1d1; cylindromatosis; PCR primer;

KW human; ss.

XX Homo sapiens.

OS

XX AU200013568-A.

PN

XX 03-AUG-2000.

PD

XX 25-JAN-2000; 2000AU-00013568.

PX

XX 29-JAN-1999; 99EP-00101925.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA F Hoffmann- La Roche Ag;

XX WPI; 2000-572508/54.

DR

XX Nucleic acid molecule down-regulated during tumor progression and/or

PT metastasis as prognostic markers in diagnosis of metastatic and

PT progression potential of tumor cells, and for treating cancer.

XX Disclosure; Page 17; 48pp; English.

PS

XX The present invention relates to a novel human integral seven

CC

CC transmembrane protein with a long N-terminal extracellular domain: TM7XN1

CC (see AAA91751 and AAB21700) . Based on homology comparison, TM7XN1 can be

CC placed in the secretin family of G-protein-coupled peptide hormone

CC receptors. TM7XN1 gene expression is down-regulated in metastatic human

CC melanoma cells, and is down-regulated during tumour progression and/or

CC metastasis. Therefore, TM7XN1 may be involved in metastasis due to its

CC down-regulation in melanoma cells. The TM7XN1 gene is localised on

CC chromosome 16q13, and is therefore a candidate gene for the tumour

CC suppressor gene cyl1d1, which is involved in cylindromatosis. The present

CC sequence is a PCR primer for the coding sequence of TM7XN1. This sequence

CC was used during the study of mRNA expression of TM7XN1 in various human

CC cell types

XX Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

SQ

Query Match 1.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 349 GATCAAAATGGGGAGCCTG 366

Db 1 GAGCTGATGGGGAGCCTG 18

RESULT 518

AAA75986/C

ID AAA75986 standard; DNA; 18 BP.

XX AAA75986;

AC

XX 08-FEB-2001 (first entry)

DT

XX PCR primer used to amplify a human PREB gene fragment.

DE

XX Prolactin regulatory element binding protein; PREB protein;

KW kinase-mediated hormonal regulator; transcription factor; 1P element;

KW prolactin promoter; osteoporosis; cancer; autoimmune disease;

KW graft-versus-host disease; trisomy 2p; probe; PCR primer; ds.

XX Homo sapiens.

OS

XX WO200056756-A2.

PN

XX 28-SEP-2000.

PD

XX 23-MAR-2000; 2000WO-US007642.

PX

XX 23-MAR-1999; 99US-0125728P.

PR

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

PA

XX Bancroft CF, Fliss M, Clelland CL;

PI

XX WPI; 2000-638247/61.

DR

XX New polynucleotide encoding prolactin regulatory element binding protein

PT useful for treating osteoporosis, cancer and autoimmune diseases.

PX

PS Example; Page 57; 87pp; English.

XX

CC The specification describes a prolactin regulatory element binding (PREB)

CC protein. The protein is a kinase-mediated hormonal regulator of prolactin

CC gene expression, i.e. a transcription factor. The protein binds to the 1P

CC element pf the prolactin promoter. PREB proteins are useful for treating

CC osteoporosis. PREB modulators are useful for treating cancer, autoimmune

CC diseases by inhibiting the expression of prolactin. PREB antisense

CC sequences are also useful for treating a development defect. Inhibition

CC of prolactin gene expression is useful for inhibiting graft-versus-host

CC diseases in transplantations. PREB polynucleotides are useful as a probe

CC for diagnosing trisomy 2p in a subject. PCR primers AAA75984-87 were used

CC to amplify a human PREB gene fragment

XX

SQ Sequence 18 BP; 8 A; 2 C; 6 G; 2 T; 0 U; 0 Other;


```

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      279 CATATTTCTTCACTACTG 296
Db      18 CACATTTCTTCTCTGCTG 1

RESULT 519
AAC73454/c
ID      AAC73454 standard; DNA; 18 BP.
XX
AC      AAC73454;
XX
DT      02-FEB-2001 (first entry)
XX
DE      Reverse primer #96 used in multiplexing PCR/SBE assay.
XX
KW      Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW      PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS      Unidentified.
XX
PN      WO200058516-A2.
XX
PD      05-OCT-2000.
XX
PF      27-MAR-2000; 2000WO-US008069.
XX
PR      26-MAR-1999; 99US-0126473P.
XX      23-JUN-1999; 99US-0140359P.
XX
PA      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA      (AFFY-) AFFYMETRIX INC.
XX
PI      Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI      Ryder T, Sklar P;
XX
DR      WPI; 2000-656171/63.
XX
PT      Universal array of oligonucleotides tags attached to a solid substrate
PT      along with locus-specific tagged oligonucleotides useful in genotyping
PT      using single base extension reactions.
XX
PS      Example 7; Page 58; 70pp; English.
XX
CC      The present invention relates to an oligonucleotide array comprising
CC      oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC      array is useful for genotyping a nucleic acid sample at one or more loci
CC      via single base extension (SBE) reactions. A pair of primers is used to
CC      amplify a polymorphic locus in a sample e.g. a single nucleotide
CC      polymorphism (SNP). The present sequence is one of the primers used in
CC      the method of the present invention to amplify a polymorphic sample. The
CC      amplified nucleic acid product is then used as a template in a SBE
CC      reaction with an extension primer. The SBE reaction products are used to
CC      form the oligonucleotide array
XX
SQ      Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      93 TGGCATTATCCTTCAGTG 110
Db      18 TGGCCTTCTCCCTCAGTG 1

RESULT 520
AAF56336/c
ID      AAF56336 standard; DNA; 18 BP.
```

```

XX      AAF56336;
XX      19-APR-2001 (first entry)
XX      Human mGluR1beta GB-PR2:HUMMGLUB antisense oligonucleotide #7.
XX      Antisense; metabotropic glutamate receptor type 1; mGluR1; pain;
KW      inflammation; arthritis; opioid analgesic; glutamate; neurotoxicity;
KW      tumour; human; ss.
XX
OS      Homo sapiens.
XX
PN      WO200105963-A2.
XX
PD      25-JAN-2001.
XX
PF      17-JUL-2000; 2000WO-CA000824.
XX
PR      15-JUL-1999; 99US-0144004P.
XX      (UYMC-) UNIV MCGILL.
XX
PI      Fundytus ME, Coderre TJ, Cohen SR, Henry JL, Vainio A;
XX      WPI; 2001-159534/16.
XX
PT      New antisense oligonucleotides to metabotropic glutamate receptor type 1
PT      gene, which specifically hybridize to mRNA expressed from the gene useful
PT      for treating disorders related to elevated glutamate level such as pain.
XX
PS      Claim 2; Page 19; 97pp; English.
XX
CC      The present invention relates to an antisense oligonucleotide derived
CC      from the sequence of metabotropic glutamate receptor type 1 (mGluR1)
CC      gene. The antisense oligonucleotide binds to a portion of mRNA expressed
CC      from the gene or its splice variant. The binding of the oligonucleotide
CC      to the mRNA is effective in decreasing the translation of the mRNA in a
CC      host cell expressing the gene. The oligonucleotides are useful for
CC      treating chronic pain caused by injury or inflammation of a nerve caused
CC      by arthritis. The oligonucleotides may be used with an opioid analgesic.
CC      They are also useful for minimizing glutamate neurotoxicity and/or
CC      excitotoxicity associated with stroke, ischemia, CNS trauma,
CC      neurodegenerative disorders, gastrointestinal disorders or to inhibit
CC      tumour formation
XX
SQ      Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      901 CAAGAGCCTCAACATTTC 918
Db      18 CAAGAGCCTGACCTTTTC 1

RESULT 521
AAD29760
ID      AAD29760 standard; DNA; 18 BP.
XX
AC      AAD29760;
XX
DT      17-MAY-2002 (first entry)
XX
DE      Human HCN1 DNA amplifying antisense primer.
XX
KW      Human; hyperpolarisation-activated cyclic nucleotide-gated channel; HCN;
KW      therapy; stroke; ischaemia; head injury; epilepsy; Alzheimer's disease;
KW      Parkinson's disease; learning disorder; memory; attention disorder; pain;
KW      gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic;
KW      neuroprotective; cerebroprotective; antiinflammatory; anticonvulsant;
KW      tranquilliser; vasotropic; reverse transcription; RT; PCR primer; ss.
```


XX OS Homo sapiens.
XX PN WO200202630-A2.
XX PD 10-JAN-2002.
XX PF 03-JUL-2001; 2001WO-GB002959.
XX PR 03-JUL-2000; 2000GB-00016360.
XX PR 03-NOV-2000; 2000GB-00026946.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Strijbos PJLM, Bates S, Gloger I, Davies C;
XX WPI; 2002-188422/24.
XX
XX New HCN channel polypeptides and polynucleotides which encode the
PT polypeptides, for the manufacture of compositions to treat stroke,
PT ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's
PT disease.
XX
XX Example 1; Page 21; 68pp; English.
XX
XX The invention relates to new uses of human hyperpolarisation-activated,
CC cyclic nucleotide-gated (HCN) channel polypeptides and their
CC polynucleotides. The HCN channel polypeptides and polynucleotides can be
CC used in the manufacture of medicaments to treat stroke, ischaemia, head
CC injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or
CC memory and attention disorders. These compounds may also be used in
CC treating pain, gut disorders, in particular Irritable bowel syndrome
CC (IBS) or sleep disorders. HCN polynucleotides and polypeptides may also
CC be employed as diagnostic reagents for detection of mutations in the
CC above stated diseases. The present sequence is a reverse transcription
CC (RT)-PCR primer used to amplify human HCN1 channel DNA and it is used in
CC the tissue localisation of HCN1 mRNA
XX
XX Sequence 18 BP; 2 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 144 GTGCCCTTAGCGATTATG 161
Db 1 GTGCCCTTCGGGATGATG 18
RESULT 522
ACA96836/c
ID ACA96836 standard; DNA; 18 BP.
XX
XX ACA96836;
XX
XX 24-JUL-2003 (first entry)
XX
XX Human glial cell derived neurotrophic factor (GDNF) PCR primer #30.
DE
XX Human glial cell derived neurotrophic factor; GDNF; PCR; primer; ss;
KW Human; glial cell derived neurotrophic factor; GDNF; PCR; primer; ss;
KW nervous system disease.
XX
XX Homo sapiens.
XX
XX CN1364812-A.
XX
XX 21-AUG-2002.
PD
XX
XX 11-JAN-2001; 2001CN-00107450.
PF
XX
XX 11-JAN-2001; 2001CN-00107450.
PR
XX (YISH-) YISHENG BIOLOGICAL PHARM CO LTD SHUHA1. PA

XX Zhou S, Zheng Z, Feng H;
PI WPI; 2003-000523/01.
XX
XX Human glial cell derived neurotrophic factor and its derivatives and use.
PT
XX
XX Claim 6; Page 3 (Claims); 28pp; Chinese.
PS
XX The invention relates to the human glial cell derived neurotrophic factor
CC (GDNF) and its derivatives and use. The invention also relates to a
CC method of obtaining DNA encoding human glial cell derived neurotrophic
CC factor or its active segments and a method of purifying and fining coarse
CC GDNF. A composition comprising human glial cell derived neurotrophic
CC factor and a medicinal acceptable carrier can be used in the treatment of
CC nervous system diseases. Sequences ACA96807-ACA96859 represent PCR
CC primers used to amplify human GDNF cDNA
XX
XX Sequence 18 BP; 8 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 645 GACCTGTCAAATTAGAT 662
Db 18 GACCTGTCTGTTTTAGAT 1
RESULT 523
ABZ10992/c
ID ABZ10992 standard; DNA; 18 BP.
XX
XX ABZ10992;
AC
XX 16-JAN-2003 (first entry)
DT
XX Haematopoietic cell proliferation disorder related oligonucleotide #1132.
DE
XX
XX Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200277272-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 26-MAR-2002; 2002WO-EP003401.
XX
XX 26-MAR-2001; 2001US-0278333P.
PR
XX
XX (EP1G-) EPIGENOMICS AG.
PA
XX
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
XX WPI; 2003-018942/01.
DR
XX
XX Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 15; Page 74; 117pp; English.
PS
XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a

CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 2 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1071 CTAACACCACTTAACCTCT 1088
Db 18 CAAAACCACTAACCCT 1

RESULT 524
ABZ10991/c
ID ABZ10991 standard; DNA; 18 BP.
XX
AC ABZ10991;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #1131.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 15; Page 74; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a

CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 2 A; 1 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1071 CTAACACCACTTAACCTCT 1088
Db 18 CAAAACCACTAACCCT 1

RESULT 525
ABX14077/c
ID ABX14077 standard; DNA; 18 BP.
XX
AC ABX14077;
XX
DT 20-MAR-2003 (first entry)
XX
DE DNA fragment B amplification primer B1.
XX
KW vaccine; attenuated virus; recombinant virus; cancer; neoplasm; tumour;
KW replication-competent virus; carcinoma; viral infection; HIV; rotavirus;
KW respiratory syncytial virus (RSV); Hepatitis A virus; poliovirus; primer;
KW papilloma virus; measles virus; influenza virus; bacterial disease; PCR;
KW Vibrio cholerae; enterotoxigenic Escherichia coli; Shigella; Listeria;
KW Streptococcus; Salmonella; parasite; Plasmodium falciparum; trypanosome;
ss.
XX
OS Poliovirus.
OS Synthetic.
XX
PN WO200278621-A2.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-US008908.
XX
PR 28-MAR-2001; 2001US-0279553P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Andino-Pavlovsky R, Crotty S;
XX
DR WPI; 2003-103236/09.
XX
PT New population of live attenuated recombinant replication-competent
PT viruses (e.g. poliovirus, HIV or influenza virus), useful as a vaccine,
PT particularly for treating or inhibiting cancer, neoplasm, tumor or
PT carcinoma.
XX
PS Example 1; Page 32; 70pp; English.
XX

CC The invention relates to a population of live attenuated recombinant
CC replication-competent viruses, which comprise at least two member
CC viruses. Each of the member viruses comprises a nucleotide sequence
CC encoding a different antigenic polypeptide from a pathogenic organism
CC other than a parent virus from which the recombinant virus was derived,
CC and which is capable of being expressed in a eukaryotic cell. The
CC replication-competent virus population is useful in a method of inducing
CC an immune response in a subject. This comprises administering a first
CC population of replication-competent viruses in a first strain of the
CC replication-competent viruses; and after a time, administering a second
CC population in a second strain of the replication-competent viruses. The
CC second strain is a different strain from the first strain. The population
CC of live attenuated recombinant replication-competent viruses is useful as
CC a vaccine, particularly for eliciting an immune response in a subject. In
CC particular, the population of live attenuated recombinant replication-
CC competent viruses is useful for treating or inhibiting cancer, neoplasm,
CC tumour or carcinoma. Also for preventing, reducing, treating, inhibiting
CC viral infection such as HIV, rotavirus, papilloma virus, measles virus and
CC (RSV), Hepatitis A virus, poliovirus, papilloma virus, measles virus and
CC influenza virus; bacterial diseases caused by e.g. Vibrio cholerae,
CC enterotoxigenic Escherichia coli, Shigella, Listeria, Streptococcus,
CC Salmonella; parasites such as Plasmodium falciparum, trypanosomes. The
CC present sequence represents the DNA fragment B amplification primer B1
XX
SQ Sequence 18 BP; 6 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 650 GTCAATTTAGATTATGT 667
Db 18 GTCAATCTCGAATATGT 1

RESULT 526
AAL55147/c
ID AAL55147 standard; DNA; 18 BP.
XX
AC AAL55147;
XX
DT 24-APR-2003 (first entry)
XX
DE PGC-1 mutational analysis PCR primer #8.
XX
KW Peroxisome proliferator-activated receptor-gamma coactivator-1; PGC-1;
KW type 2 diabetes; antidiabetic; enzyme; PCR; primer; ss.
XX
OS Unidentified.
XX
FN WO2002100894-A2.
XX
PD 19-DEC-2002.
XX
PF 06-JUN-2002; 2002WO-DK000382.
XX
PR 08-JUN-2001; 2001EP-00610061.
PR 10-JUL-2001; 2001DK-00001080.
XX
PA (NOVO) NOVO NORDISK AS.
XX
PI Andersen G, Ek J, Hansen T, Pedersen OB;
XX
DR WPI; 2003-156949/15.
XX
PT Novel mutant DNA sequence encoding peroxisome proliferator-activated
PT receptor coactivator useful for identifying subjects who are at increased
PT risk of developing type 2 diabetes.
XX
PS Example 1; Page 26; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide molecule comprising a
CC nucleotide sequence encoding peroxisome proliferator-activated receptor-

CC gamma coactivator-1 (PGC-1), containing a mutation associated with type 2
CC diabetes of at least one nucleotide, or comprising a fragment of the
CC nucleotide sequence including the mutation. The isolated polynucleotide
CC is useful for detecting the presence of a mutation in the gene encoding the
CC PGC-1, by obtaining a biological sample from a subject and analysing the
CC sample for a mutation associated with type 2 diabetes of the nucleotides
CC in PGC-1 sequence. The biological sample is obtained from a subject, DNA
CC is isolated from the sample, DNA is amplified and hybridised to the
CC isolated polynucleotide which contains a mutation associated with type 2
CC diabetes of at least one nucleotide or comprising a fragment of the
CC nucleotide sequence including the mutation to be detected, and
CC the amplified DNA is hybridised to a second labelled polynucleotide
CC comprising a DNA sequence corresponding to a part of the wild-type gene
CC encoding PGC-1 and hybridisation of the second labelled polynucleotide to
CC the amplified DNA is determined. The substance with which the labelled
CC polynucleotide carrying the mutation is labelled is different from the
CC label substance with which the second labelled polynucleotide
CC corresponding to a part of the wild-type DNA is labelled. This method is
CC useful for determining predisposition to type 2 diabetes in a subject.
CC The polynucleotide of the invention is useful for identifying subjects
CC who are at an increased risk of developing type 2 diabetes and to
CC identify subjects with variable response to drugs which act by the
CC peroxisome proliferator-activated receptor-gamma and for tailoring
CC antidiabetic medication. This polynucleotide sequence represents a PCR
CC primer used for mutational analysis of the peroxisome proliferator-
CC activated receptor-gamma coactivator-1 (PGC-1) of the invention
XX
SQ Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 443 GATTTTAGCTGGGAGCAG 460
Db 18 GATTTGGCTTGAAGCAG 1

RESULT 527
ADA41736/c
ID ADA41736 standard; DNA; 18 BP.
XX
AC ADA41736;
XX
DT 20-NOV-2003 (first entry)
XX
DE TCV RdRP mutagenic PCR primer i120.
XX
KW RNA-dependent RNA polymerase; RdRP; plant virus; amplification system;
KW ss; primer; PCR.
XX
OS Synthetic.
OS Turnip crinkle virus.
XX
PN WO2003014366-A2.
XX
PD 20-FEB-2003.
XX
PF 29-JUL-2002; 2002WO-DE002863.
XX
PR 30-JUL-2001; 2001DE-01037444.
XX
PA (PROB-) PROBIOGEN AG.
XX
PI Sandig V, Jordan I;
XX
DR WPI; 2003-248302/24.
XX
PT Amplifying nucleic acid in animal cells, useful e.g. for gene therapy or
PT vaccination, uses an RNA-dependent, RNA-polymerase of a plant virus.
XX
PS Example 1; Page 17; 39pp; German.

XX This invention describes a novel method for amplifying nucleic acid in
CC animal cells by introducing an RNA-dependent RNA polymerase (RdRP) and
CC it's associated promoters and cis-acting signals from a plant virus into
CC the cells. RdRP is normally active in plant cells and the gene that
CC encodes it can be recovered from such cells. Both the RdRP and the
CC promoter are from plant viruses, particularly turnip crinkle virus and
CC the amplified RNA is a modified satellite or genomic RNA of this virus.
CC The method is particularly used for amplification of RNA (which may be
CC mRNA for protein synthesis; an effector, e.g. antisense RNA or ribozyme,
CC or genomic RNA) in animal cells, for (i) control of gene expression or
CC (ii) for gene therapy or vaccination. When the system includes an
CC inducible promoter, it permits strong and rapid expression of reporter
CC genes in response to a test substance, especially where the promoter
CC responds to the human immune deficiency virus or heavy metals, to produce
CC a diagnostic system or biosensor, respectively. The method of the
CC invention provides an inducible or constitutive, autonomous RNA-dependent
CC RNA amplification system for animal cells that requires only one
CC polymerase and does not use any viral structural genes or helper viruses.
CC Amplification takes place in the cytoplasm without using any components
CC potentially infectious for the host cells. Human 293 cells were
CC transformed with (i) pIJO-39, expressing a turnip crinkle virus 88 kD
CC protein; (ii) pIJO-60, expressed satellite RNA-C of the same virus in the
CC sense orientation and a fusion of internal ribosome entry site and green
CC fluorescent protein in the antisense orientation, and (iii) an expression
CC vector for T7 RNA polymerase under control of the cytomegalovirus
CC promoter. Expression of the reporter gene was detected by fluorescence
CC microscopy. This sequence represents a mutagenic PCR primer, il20, used
CC to clone the turnip crinkle virus (TCV) RdRP gene into pIJO-39.
XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 CCGAAGCAGCCGCGCC 56
DB 18 CCGAAGCAGCCGCGGAC 1

RESULT 528
ADB17690
ID ADB17690 standard; DNA; 18 BP.

XX ADB17690;
AC ADB17690;
XX 20-NOV-2003 (first entry)
DT 20-NOV-2003 (first entry)
DE Xenopus axis duplication assay PCR primer #3.
XX Wnt-1 induced secreted protein; WISP; Wnt-1 induced gene; WIG; WISP-1;
KW WISP-2; WISP-3; connective tissue growth factor; CTGF; tumour cell;
KW cell death; atherosclerosis; malignant disorder; breast cancer;
KW ovarian cancer; colon cancer; melanoma; antiarteriosclerotic; cytostatic;
KW PCR; primer; ss.
XX Xenopus laevis.
OS US2003068678-A1.
XX 10-APR-2003.
PN 27-MAR-2002; 2002US-00112267.
XX 29-OCT-1997; 97US-0063704P.
PR 04-FEB-1998; 98US-0073612P.
PR 14-APR-1998; 98US-0081695P.
PR 29-OCT-1998; 98US-00182145.
XX (GETH) GENENTECH INC.
PA Levine AJ, Pennica D;
PI

XX WPI; 2003-596689/56.
DR New nucleic acid encoding Wnt-1-Induced Secreted Protein, useful for
XX preparing a composition for treating a WISP-related disorder in a mammal
PT comprising atherosclerosis or malignant disorder, e.g., breast, ovarian
PT or colon cancer.
XX Example 11; Page 39; 205pp; English.
PS The present invention relates to the isolation of novel Wnt-1 induced
XX secreted proteins (WISPs, previously known as Wnt-1 induced gene (WIG)
CC polypeptides), and the polynucleotide sequences encoding them. The novel
CC WISP proteins (WISP-1, WISP-2, WISP-3) show homology to connective tissue
CC growth factor (CTGF). Also disclosed are vectors and host cells
CC comprising WISP polynucleotides, chimeric polypeptides comprising WISP
CC polypeptides fused to heterologous polypeptides, antibodies which bind
CC WISP polypeptides, and methods for producing the polypeptides. The
CC antibody may be used in a composition to inhibit the growth of tumour
CC cells by inducing death of the cells which are overexpressing the WISP
CC polypeptides. The WISP polynucleotide sequences are useful for preparing
CC a composition for treating WISP-related disorders such as atherosclerosis
CC and malignant disorders (e.g. breast, ovarian or colon cancer or
CC melanoma) in a mammal. The present sequence represents a PCR primer used
CC in the examples of the present invention.
XX Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 897 AGACCAAGAGCCTCAACA 914
DB 1 AGTCCAAGAGTCTCAGCA 18

RESULT 529
ACH00636
ID ACH00636 standard; DNA; 18 BP.

XX ACH00636;
AC ACH00636;
XX 12-FEB-2004 (first entry)
DT Mammalian inverted nipple associated microsatellite PCR primer #90.
DE Inverted nipple; microsatellite; PCR; primer; ss; pig.
XX Mammalia.
OS WO2003066891-A2.
XX 14-AUG-2003.
PD 03-FEB-2003; 2003WO-EP001045.
XX 05-FEB-2002; 2002EP-00002632.
PR (FOER-) FOERDERVEREIN BIOTECHNOLOGIEFORSCHUNG DE.
PA Hardge T, Schellander K, Wimmers K;
XX WPI; 2003-671539/63.
DR Determining predisposition to inverted nipples useful e.g. for selecting
XX breeding animals comprises detecting specific microsatellite markers.
PT Disclosure; Page 23; 63pp; German.
PS The present invention relates to the use of a nucleic acid to determine
XX the predisposition of appearance or inheritance of inverted nipples,
CC where the nucleic acid is identical to the region of microsatellites

CC S0200, SW2443, S0097, S0007, SW1301 or S0164 on chromosomes 6, 2, 4, 14,
CC 1 and 3, respectively, in pigs, or homologous positions in the genomes of
CC other mammals. The nucleic acids can be used to select pets, breeding or
CC farm animals that lack inverted nipples, particularly by genomic
CC screening of many related mammals in a population. The present sequence
CC is a PCR primer used in the exemplification of the invention to identify
CC microsatellite markers associated with the inverted nipple phenotype
XX
SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 300 TTGTTGTTTCTGCCTTTG 317
||| ||| ||| ||| ||| ||| |||
Db 1 TTGCTGCTTGTGCCTTTG 18

RESULT 530
ADM06240/c
ID ADM06240 standard; DNA; 18 BP.
XX
AC ADM06240;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PCR primer SEQ ID NO:4925.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.
XX
OS Homo sapiens.
XX
PN EF1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Example 8; SEQ ID NO 4925; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents an
CC oligonucleotide used in the invention.
XX
SQ Sequence 18 BP; 9 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 314 TTGGATTTCCTGTTATT 331

Db 18 TCTGGAGTTGCTGTATT 1
||| ||| ||| ||| ||| ||| |||

RESULT 531
ADM96453/c
ID ADM96453 standard; DNA; 18 BP.
XX
AC ADM96453;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CIAP-1 DNA antisense oligonucleotide #30.
XX
KW Human; cellular inhibitor of apoptosis-1; CIAP-1; ss; cellular apoptosis;
KW cancer; antisense oligonucleotide;
KW phosphorothioate internucleoside linkage; 2'-O-methoxyethyl sugar moiety;
KW 5-methylcytosine; autoimmune disorder; viral infection; cytostatic;
KW immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
PN US2004009599-A1.
XX
PD 15-JAN-2004.
XX
PF 18-JUN-2003; 2003US-00464158.
XX
PR 03-DEC-1998; 98US-00205204.
PR 16-JUN-1999; 99WO-US013624.
PR 24-SEP-2001; 2001US-00857278.
XX
PA (BENN/) BENNETT C F.
PA (ACKE/) ACKERMANN E J.
XX
PI Bennett CF, Ackermann EJ;
XX
WPI; 2004-090476/09.
DR
XX
PT Inducing cellular apoptosis by administering an antisense modulating the
PT human Cellular Inhibitor of Apoptosis-1, useful in preventing or treating
PT cancer, autoimmune disorders and viral infections.
XX
PS Example 15; SEQ ID NO 37; 25pp; English.
XX
CC The invention relates to a method of inducing cellular apoptosis
CC comprising administering to a cell an effective amount of an antisense
CC compound targeted to a nucleic acid molecule encoding human cellular
CC inhibitor of apoptosis-1 (ciAP-1), so that expression of ciAP-1 is
CC inhibited and apoptosis is induced. The cell used in the method is a
CC cancer cell. The antisense compound is an antisense oligonucleotide that
CC comprises at least one modification of the internucleoside linkage, sugar
CC moiety or nucleobase, wherein the modification is a phosphorothioate
CC internucleoside linkage, a 2'-O-methoxyethyl sugar moiety or a 5-
CC methylcytosine nucleobase. The antisense oligonucleotide is a chimeric
CC oligonucleotide. The methods and compositions are useful for the
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of human CIAP-1, such as cancer,
CC autoimmune disorders and viral infections. This sequence represents a
CC human CIAP-1 DNA antisense oligonucleotide of the invention.
XX
SQ Sequence 18 BP; 6 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 974 TTGATGAGATCCAAAGGA 991
||| ||| ||| ||| ||| ||| |||
Db 18 TTGATGAGATTC AAGGTA 1

RESULT 532

ADP81767/c
ID ADP81767 standard; DNA; 18 BP.
XX
AC ADP81767;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human MD-1 RP105-associated DNA amplifying reverse PCR primer.
XX
KW MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
KW human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2004110146-A1.
XX
PD 10-JUN-2004.
XX
PF 09-DEC-2002; 2002US-00316242.
XX
PR 09-DEC-2002; 2002US-00316242.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW;
XX
DR WPI; 2004-440335/41.
XX
PT New oligonucleotide compound that inhibits expression of MD-1 RP105-associated, useful for preparing a composition for treating autoimmune disorder.
PT
XX
PS Claim 21; SEQ ID NO 6; 63pp; English.
XX
CC The invention relates to compounds, compositions and methods for modulating the expression of MD-1 RP105-associated (also called as MD-1 and MD1) DNA. The composition comprise antisense oligonucleotides targeted to MD-1 RP105-associated DNA. The compound is useful for preparing a composition for treating autoimmune disorder. It is also useful in gene therapy. The present sequence is a PCR primer used for amplifying human MD-1 RP105-associated DNA. This sequence is used to illustrate the method of the invention.
XX
SQ Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 883 AAAGTGTGGCCACAGAC 900
Db 18 AAAGCCTGGCCACACAC 1

RESULT 533
ADO80001/c
ID ADO80001 standard; DNA; 18 BP.
XX
AC ADO80001;
XX
DT 26-AUG-2004 (first entry)
XX
DE CENPC1 extend primer #52.
XX
KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;
KW CENPC1; SNP; single nucleotide polymorphism; centromere protein C1;
KW Centromere autoantigen C1; chromosome 4ql2-q13.3; extend; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2004047514-A2.
XX
PD 10-JUN-2004.

XX
PF 25-NOV-2003; 2003WO-US037943.
XX
PR 25-NOV-2002; 2002US-0429136P.
PR 24-JUL-2003; 2003US-0490234P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
DR WPI; 2004-441037/41.
XX
PT Identifying a subject at risk of breast cancer by detecting the presence of polymorphic variations in the DLG1, KIAA0783, DPF3 or CENPC1 regions which are associated with breast cancer in a nucleic acid sample from a subject.
XX
PS Example 6; Page 91; 227pp; English.
XX
CC The present invention relates to a method for identifying a subject at risk of breast cancer. The method comprising detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The nucleic acid sample comprises the DLG1 region (ADO79402), KIAA0783 region (ADO79403), DPF3 region (ADO79404) or CENPC1 region (ADO79405). The gene DLG1 (discs, large homolog 1 (Drosophila)) is also known as synapse-associated protein 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783 has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a novel gene with unknown function, however, being a zinc finger protein, it likely to be a transcription factor. The gene DPF3 (D4, zinc and double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079 and 2810403B03Rik. DPF3 is a Rho family guanine-nucleotide exchange factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The gene CENPC1 (centromere protein C1) is also known as Centromere autoantigen C1. CENPC1 has been mapped to chromosomal position 4ql2-q13.3. CENPC1 is a centromere autoantigen and a component of the inner kinetochore plate. The CENPC1 protein is required for maintaining proper kinetochore size and a timely transition to anaphase. The method is useful for identifying a subject at risk of breast cancer, for early diagnosis, prevention and treatment of breast cancer, to analyze and predict a response to a breast cancer treatment, and in clinical drug trials. The present sequence was used in an example from the invention.
XX
SQ Sequence 18 BP; 6 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 398 TTCCTTACAATTCAGGG 415
Db 18 TTCCTTACAATTCATGG 1

RESULT 534
ADP82980/c
ID ADP82980 standard; DNA; 18 BP.
XX
AC ADP82980;
XX
DT 23-SEP-2004 (first entry)
XX
DE Nitrite hydratase related PCR primer, SEQ ID 32.
XX
KW Nitrite hydratase; enzyme; biocatalyst; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO2004056990-A1.
XX
PD 08-JUL-2004.
XX

PF 15-DEC-2003; 2003WO-JP016014.
XX
PR 19-DEC-2002; 2002JP-00368360.
PR 10-NOV-2003; 2003JP-00379280.
XX
PA (MITA) MITSUI CHEM INC.
PI Yamaki T, Banba S, Matoishi K, Ito K, Kobayashi H, Tanaka E;
PI Oikawa T;
XX
DR WPI; 2004-517682/49.
XX
PT Novel nitrile hydratase, useful for producing nitrile and amide
PT compounds, comprises alpha and beta subunit.
XX
PS Disclosure; SEQ ID NO 32; 345pp; Japanese.
XX
CC The present invention relates to novel pseudonocardia thermophila nitrile
CC hydratase (I) sequences. (I) efficiently converts a nitrile compound into
CC its corresponding amide compound and is useful for producing biocatalyst
CC substances. The present sequence is a PCR primer used to illustrate the
CC invention.
XX
SQ Sequence 18 BP; 3 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 CTGCCCCGGCCGTGGCAG 34
Db 18 CTGCTCGTCCGGGGCAG 1

RESULT 535
ADP83010/c
ID ADP83010 standard; DNA; 18 BP.
XX
AC ADP83010;
XX
DT 23-SEP-2004 (first entry)
XX
DE Nitrile hydratase related PCR primer, SEQ ID 62.
XX
KW Nitrile hydratase; enzyme; biocatalyst; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO2004056990-A1.
XX
PD 08-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-JP016014.
XX
PR 19-DEC-2002; 2002JP-00368360.
PR 10-NOV-2003; 2003JP-00379280.
XX
PA (MITA) MITSUI CHEM INC.
XX
PI Yamaki T, Banba S, Matoishi K, Ito K, Kobayashi H, Tanaka E;
PI Oikawa T;
XX
DR WPI; 2004-517682/49.
XX
PT Novel nitrile hydratase, useful for producing nitrile and amide
PT compounds, comprises alpha and beta subunit.
XX
PS Example 22; SEQ ID NO 62; 345pp; Japanese.
XX
CC The present invention relates to novel Pseudonocardia thermophila nitrile
CC hydratase (I) sequences. (I) efficiently converts a nitrile compound into
CC its corresponding amide compound and is useful for producing biocatalyst
CC substances. The present sequence is a PCR primer used to illustrate the

CC invention.
XX
SQ Sequence 18 BP; 1 A; 8 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 GGCTGCCCCGGCCGTGGC 32
Db 18 GCCGGCCCCGGCCGTGCG 1

RESULT 536
ADQ80462
ID ADQ80462 standard; DNA; 18 BP.
XX
AC ADQ80462;
XX
DT 23-SEP-2004 (first entry)
XX
DE MGB-probe to determine EV1 viral RNA levels.
XX
KW echovirus; &agr2; &bgr1; Cytostatic; Immunostimulant; immune response;
KW cancer; ss; probe.
XX
OS Unidentified.
XX
PN WO2004054613-A1.
XX
PD 01-JUL-2004.
XX
PF 18-DEC-2003; 2003WO-AU001688.
XX
PR 18-DEC-2002; 2002AU-00953436.
XX
PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
XX
PI Shafren D;
XX
DR WPI; 2004-488010/46.
XX
PT Treating abnormal cells in a mammal comprises treating the mammal with an
PT echovirus or its modified forms or combinations, which recognize
PT alpha2betat for killing at least some of the cells.
XX
PS Example 1; Page 23; 67pp; English.
XX
CC The present invention relates to treating abnormal cells in a mammal
CC comprises treating the mammal with an echovirus or its modified forms or
CC combinations, which recognize &agr; 2 &bgr; 1 for infectivity of the
CC cells, where at least some of the cells are killed by the virus. The
CC inoculant for generating echovirus is useful in the manufacture of
CC medicament for inducing an immune response against cancer cells in a
CC mammal. The present sequence represents a MGB probe to determine EV1
CC viral RNA levels.
XX
SQ Sequence 18 BP; 7 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 900 CCAAGAGCCTCAACATTT 917
Db 1 CCAATAGCTTCAACAATT 18

RESULT 537
ACC67229/c
ID ACC67229 standard; DNA; 17 BP.
XX
AC ACC67229;

XX 01-JUL-2003 (first entry)
DT Murine oligonucleotide associated with tumour supression, SEQ ID 4476.
XX
DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
XX WO2003025176-A2.
PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX
PS Disclosure; Page 554; 738pp; French.
XX
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 3.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CATGTGCACATG 533
| | | | | | | | | |
Db 16 CATGTGCACATG 5

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